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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 42.9294 Seconds
(without alignments)
4009.823 Million cell updates/sec

Title: US-09-019-441-1
Perfect score: 390
Sequence: 1 ATGCGTGGACTCTGCTCTT.....CCCGTTGACGTCCTAGGT 390

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	390	100.0	390	3	US-08-803-085-1
2	321.2	82.4	891	3	US-09-049-672A-23
3	319.6	81.9	902	2	US-08-378-939-11
4	285.2	75.7	548	4	US-09-404-879A-267
5	295.2	75.7	548	4	US-09-338-933-267
6	295.2	75.7	548	4	US-09-215-681-267
7	285.4	73.2	735	4	US-10-039-785-59
8	285.4	73.2	735	4	US-10-039-785-63
9	285.4	73.2	735	4	US-10-039-785-64
10	275.8	70.7	735	4	US-10-039-785-54
11	275.4	70.6	333	2	US-08-958-201-13
12	273.8	70.2	333	2	US-08-958-201-11
13	269.4	69.1	735	4	US-10-039-785-57
14	267.8	68.7	735	4	US-10-039-785-60
15	261.4	67.0	735	4	US-10-039-785-58
16	261.4	67.0	735	4	US-10-039-785-61
17	258.2	66.2	735	4	US-10-039-785-55
18	252.2	64.7	543	4	US-09-702-705-970
19	252.2	64.7	543	4	US-09-736-457-970
20	239.6	61.4	324	3	US-09-240-274-137
21	236.4	60.6	585	4	US-09-620-312D-551
22	234.6	60.2	935	3	US-09-049-672A-20
23	233	59.7	393	1	US-08-305-683A-3
24	225.8	57.9	771	3	US-08-991-789A-241
25	225.8	57.9	771	4	US-09-062-451-241
26	225.8	57.9	771	4	US-09-598-326-241
27	225.8	57.9	771	4	US-09-289-198-241

Sequence 138, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 25, Appli
Sequence 8, Appli
Sequence 27, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 133, Appl
Sequence 132, Appl
Sequence 1, Appli
Sequence 43, Appli
Sequence 62, Appli
Sequence 134, Appl
Sequence 5, Appli
Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-08-803-085-1
Sequence, Application US/08803085
Patent No. 6011138
GENERAL INFORMATION
APPLICANT: BEFF, Mitchell E.
APPLICANT: KLOETZER, William S.
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
TITLE OF INVENTION: ANTIBODIES AND USE THEREOF AS THERAPEUTICS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patencin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/803,085
FILING DATE: 20-FEB-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..390
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 58..390
US-08-803-085-1

Query Match 100.0%; Score 390; DB 3; Length 390;


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ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 902 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 32..739
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 89..739
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 32..86
US-08-378-939-11
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Query Match 81.9%; Score 319.6; DB 2; Length 902;
Best Local Similarity 88.7%; Pred. No. 3.5e-85;
Matches 346; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

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QY 1 ATGGCTGGACTCTGCTCCCTCGTCCCTCACTCAGGGCAGAGGATCTGGGCTCAG 60
DB 32 ATGGCTGGGCTCTGCTCCCTCACTCAGGGCAGAGGATCTGGGCTCAG 91
QY 61 TCTGCTGGACTCAGCTCCTCTGCTGGGCTCTCTGGACAGTCCGTCACCATCTCC 120
DB 92 TCTGCTGGACTCAGCTCCTCTGCTGGGCTCTCTGGACAGTCCGTCACCATCTCC 151
QY 121 TGCACTGGAAACGAGGATGAGTTGGTGTATTAATGATGCTCTGGTACCAACACAC 180
DB 152 TGCACTGGAAACGAGGATGAGTTGGGAGTTATAACCTTGTCTCTGGTACCAACAC 211
QY 181 CCAGGAAAGCCCCCAAACTCATGATTATGATGCTCTAGCGGGCTCAGGGTCTCT 240
DB 212 CCAGGAAAGCCCCCAAACTCATGATTATGATGCTCTAGCGGGCTCAGGGTCTCT 271
QY 241 GATCGCTTCTGCTCCAGTCTGGAACACAGGCTCCCTGACCATCTCTGGGCTCCAG 300
DB 272 AATCGCTTCTGCTCCAGTCTGGAACACAGGCTCCCTGACCAATCTCTGGGCTCCAG 331
QY 301 GCTGAGGACGAGGCTGATTATTACTTGTGTTTATATACACAGTACGACTTTGTTATTC 360
DB 332 GCTGAGGACGAGGCTGATTATTACTTGTGTTTATATACAGTACGACTTTGTTATTC 391
QY 361 GGAAGAGGAGGAGGCTGAGGCTCTAGGT 390
DB 392 GGCGGAGGAGGAGGAGGCTGAGGCTCTAGGT 421
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RESULT 4
US-09-404-879A-267
Sequence 267, Application US/09404879A
Patent No. 6468546
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C2
CURRENT APPLICATION NUMBER: US/09/404.879A
CURRENT FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 393
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 267
LENGTH: 548
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(548)
OTHER INFORMATION: n = A,T,C or G
US-09-404-879A-267

Query Match 75.7%; Score 295.2; DB 4; Length 548;
Best Local Similarity 87.7%; Pred. No. 4.9e-78;
Matches 343; Conservative 0; Mismatches 46; Indels 2; Gaps 2;

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QY 1 ATGGCTGGACTCTGCTCCCTCGTCCCTCACTCAGGGCAGAGGATCTGGGCTCAG 60
DB 47 ATGGCTGGGCTCTGCTCCCTCACTCAGGGCAGAGGATCTGGGCTCAG 106
QY 61 TCTGCTGGACTCAGCTCCCTCTGCTGGGCTCTCTGGACAGTCCGTCACCATCTCC 120
DB 107 TCTGCTGGACTCAGCTCCCTCTGCTGGGCTCTCTGGACAGTCCGTCACCATCTCC 166
QY 121 TGCACTGGAAACGAGGATGAGTTGGTGTATTAATGATGCTCTGGTACCAACACAC 180
DB 167 TGCACTGGAAACGAGGATGAGTTGGTGTATTAATGATGCTCTGGTACCAACACAC 226
QY 181 CCAGGAAAGCCCCCAAACTCATGATTATGATGCTCTAGCGGGCTCAGGGTCTCT 240
DB 227 CCAGGAAAGCCCCCAAACTCATGATTCTGAGGTCACTAAGCGGCTCAGGGTCTCT 286
QY 241 GATCGCTTCTGCTCCAGTCTGGAACACAGGCTCCCTGACCATCTCTGGGCTCCAG 300
DB 287 GATCGCTTCTGCTCCAGTCTGGAACACAGGCTCCCTGACCATCTCTGGGCTCCAN 346
QY 301 GCTGAGGACGAGGCTGATTATTACT-GTTGTTTATATACACAGTACGACTTTGTTATT 359
DB 347 GCTGAGGATGAGTCTGATTATTACTGGAAGCTCATATGAGGCAACACAAATTTGGTGT 406
QY 360 CGGAAG-AGGAGCCCCGTTGACCGTCTAGG 389
DB 407 CGGCGAAGGAGGAGGAGGCTGACCGTCTAAG 437
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RESULT 5
US-09-338-933-267
Sequence 267, Application US/09338933
Patent No. 6488931
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
OVARIAN CANCER
FILE REFERENCE: 210121.462C1
CURRENT APPLICATION NUMBER: US/09/338,933
CURRENT FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 312
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 267
LENGTH: 548
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(548)
OTHER INFORMATION: n = A,T,C or G
US-09-338-933-267

Query Match 75.7%; Score 295.2; DB 4; Length 548;
Best Local Similarity 87.7%; Pred. No. 4.9e-78;
Matches 343; Conservative 0; Mismatches 46; Indels 2; Gaps 2;

Qy 280 CTGACCATCTCTGGGCTCCAGGCTGAGGAGGAGGCTGATTATTACTGTTGTTTCATATACA 339
Db 625 CTGACCATCTCTGGGCTCCAGGCTGAGGAGGAGGCTGATTATTACTGAGCTCATATACA 684
Qy 340 ACCAGTAGCATTGTTATTTCGGAAGAGGAGGAGGCTGACCGTCTCTAGGT 390
Db 685 ACCAGCAACACTTGGGTGTTTCGGCGGAGGAGGAGGCTGACCGTCTCTAGGT 735

RESULT 8
US-10-039-785-63
; Sequence 63, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US/10/039,785
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/293,473
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 63
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding T1015A07 scFv
US-10-039-785-63

Query Match 73.2%; Score 285.4; DB 4; Length 735;
Best Local Similarity 88.3%; Pred. No. 4.2e-75;
Matches 310; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
Qy 40 GGACAGGATCTCTGGGCTCAGTCTGCCCGACTCAGGCTCCCTCTGTGTTGGGTCTCCT 99
Db 385 GGCGGTGGGGAAGTGCACAGTCTGCCCTGACTCAGCTGCCTCCATGTTGGGTCTCCT 444
Qy 100 GGACAGTGGTCAACATCTCTGACCTGGAACAGGAGGATGACGTTGGTGTATTAACAT 159
Db 445 GGACAGTGGTCAACATCTCTGACCTGGAACAGGAGGATGACGTTGGTGTATTAACAT 504
Qy 160 GTCTCTGGTACCAACACACCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 219
Db 505 GTCTCTGGTACCAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 564
Qy 220 AAGCGGGCTCAGGGGCTCTGTGCTGCTTCTCTGGCTCCAAGTCTGGCAACACGGGCTCC 279
Db 565 AATCGGCTCAGGGGTTCTTAATCGCTTCTCTGCTCCCAAGTCTGGCAACACGGGCTCC 624
Qy 280 CTGACCATCTCTGGGCTCCAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 339
Db 625 CTGACCATCTCTGGGCTCCAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 684
Qy 340 ACCAGTAGCATTGTTATTTCGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 390

Db 685 AGCAGCAACACTTGGGTGTTTCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 735
RESULT 9
US-10-039-785-64
; Sequence 64, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US/10/039,785
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/293,473
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 64
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding T1015E01 scFv
US-10-039-785-64

Query Match 73.2%; Score 285.4; DB 4; Length 735;
Best Local Similarity 88.3%; Pred. No. 4.2e-75;
Matches 310; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
Qy 40 GGACAGGATCTCTGGGCTCAGTCTGCCCGACTCAGGCTCCCTCTGTGTTGGGTCTCCT 99
Db 385 GGCGGTGGGGAAGTGCACAGTCTGCCCTGACTCAGCTGCCTCCATGTTGGGTCTCCT 444
Qy 100 GGACAGTGGTCAACATCTCTGACCTGGAACAGGAGGATGACGTTGGTGTATTAACAT 159
Db 445 GGACAGTGGTCAACATCTCTGACCTGGAACAGGAGGATGACGTTGGTGTATTAACAT 504
Qy 160 GTCTCTGGTACCAACACACCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 219
Db 505 GTCTCTGGTACCAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 564
Qy 220 AAGCGGGCTCAGGGGCTCTGTGCTGCTTCTCTGGCTCCAAGTCTGGCAACACGGGCTCC 279
Db 565 AATCGGCTCAGGGGTTCTTAATCGCTTCTCTGCTCCCAAGTCTGGCAACACGGGCTCC 624
Qy 280 CTGACCATCTCTGGGCTCCAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 339
Db 625 CTGACCATCTCTGGGCTCCAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 684
Qy 340 ACCAGTAGCATTGTTATTTCGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 390
Db 685 AGCAGCAACACTTGGGTGTTTCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 735
RESULT 10

US-10-039-785-54
; Sequence 54, Application US/10039785
; Patent No. 6538318
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 54
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding T1014A04 scFv
US-10-039-785-54

Query Match 70.7%; Score 275.8; DB 4; Length 735;
Best Local Similarity 86.6%; Pred. No. 2.9e-72;
Matches 304; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy 40 GGACAGATCTGGGCTCAGTCTGCCCGGACTCAGCCCTCCCTCTGTGTCTGGGTCCT 99
Db 385 GCGGCTGGGGAAGTGCACATCTGTGTCTGACTCAGCCACCTCGCGTCGGGTCTCT 444
Qy 100 GGACAGTCGGTCACCATCTCTGCACTGGAAACCAAGGATGACGTTGGTGTATACTAT 159
Db 445 GGACAGTCAGTCACCATCTCTGCACTGGAAACCAAGGATGACGTTGGTGTATACTAT 504
Qy 160 GTCTCTGGTACCAACACACCCAGGCAAGCCGCCCAACTCATGATTATGATGCTCT 219
Db 505 GTCTCTGGTACCAACACACCCAGGCAAGCCGCCCAACTCATGATTATGATGCTCAAT 564
Qy 220 AAGCGGGCTCAGGGGCTCTGTATCGTCTCTGTCTCAAGTCTGGCAACACGCGCTCC 279
Db 565 CAGCGGCTCTCAGGGGCTCTGTATCGTCTCTGTCTCAAGTCTGGCAACACGCGCTCC 624
Qy 280 CTGACCATCTCTGGGCTCAGGCTGAGGACGAGGCTGATTACTGTGTATATACA 339
Db 625 CTGACCGCTCTCTGGGCTCAGGCTGAGGATGAGGCTGATTACTGTGAGTTATATGCA 684
Qy 340 ACCAGTACCATTTGTTATTTCGGAAGAGGACCGGTTGACCGTCTTAGGT 390
Db 685 GGCAGCAAAATGGGTGTTTCGGGGAGGACCAAGCTGACCGTCTTAGGT 735

RESULT 11
US-08-958-201-13
; Sequence 13, Application US/08958201
; Patent No. 5977319
; GENERAL INFORMATION:
; APPLICANT: Pope, Anthony R

; APPLICANT: Pritchard, Kevin
; APPLICANT: Williams, Andrew J
; APPLICANT: Johnson, Kevin S
; TITLE OF INVENTION: Specific binding members for estradiol;
; TITLE OF INVENTION: materials and methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/958,201
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,897
; FILING DATE: 21-OCT-1996
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 333 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: 1C/2D
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..333
; US-08-958-201-13

Query Match 70.6%; Score 275.4; DB 2; Length 333;
Best Local Similarity 89.2%; Pred. No. 3e-72;
Matches 297; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 58 CAGTGTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTGGACAGTCGGTCACCATC 117
Db 1 CAGTGTGCTGTGACTCAGCCTCCCTCTGTGTCTGGGTCTCTGGACAGTCGGTCACCATC 60
Qy 118 TCCTGCACTGGACCAAGGATGACGTCGTTGGTGTATAAATATGTCCTCTGTTACCAAC 177
Db 61 TCCTGCACTGGACCAAGGATGACGTCGTTGGTGTATAAATATGTCCTCTGTTACCAAC 120
Qy 178 CACCCAGGCAAGCCCAAACTCATGATTATGATGTCGTAAGCGGGCTCAGGGGTC 237
Db 121 CACCCAGGCAAGCCCAAACTCATGATTATGATGTCGTAAGTCAGTAATCGGCCCTCAGGGGTT 180
Qy 238 TCCTGATCGCTTCTGTGGCTCCAAAGTCTGGCAACACGCGCTCCCTGACCATCTCTGGGCTC 297
Db 181 CCTAATCGCTTCTCAGGCTCCAAAGTCTGGCAACACGCGCTCCCTGACCATCTCTGGGCTC 240
Qy 298 CAGCTGAGGACAGGCTGATTATTACTGTGTTCATATACACAGTACAGTCTTTGTTA 357
Db 241 CAGCTGAGGACAGGCTGATTATTACTGTGAGCTCACTTACACGAGTACAGTCTGTGATC 300
Qy 358 TTCGGAAGAGGACCGGGTTGACGCTCTAGGT 390
Db 301 TTCGGAAGAGGACCGGGTTGACGCTCTAGGT 333

RESULT 12
US-08-958-201-11
; Sequence 11, Application US/08958201
; Patent No. 5977319
; GENERAL INFORMATION:
; APPLICANT: Pope, Anthony R
; APPLICANT: Pritchard, Kevin

APPLICANT: Williams, Andrew J
APPLICANT: Johnson, Kevin S
TITLE OF INVENTION: Specific binding members for estradiol;
TITLE OF INVENTION: materials and methods
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall O'Toole Gerstein Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/958,201
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,897
FILING DATE: 21-OCT-1996
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: D12 (light chain)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..333
US-08-958-201-11

Query Match 70.2%; Score 273.8; DB 2; Length 333;
Best Local Similarity 88.9%; Pred. No. 8.8e-72;
Matches 296; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
QY 58 CAGTCTGCGGACTCAGCCCTCTCTGTGTCGGTCTCTGACAGTGGTCCCATC 117
DB 1 CAGTCTGCTGACTCAGCCCTCTCTGTGTCGGTCTCTGACAGTGGTCCCATC 60
QY 118 TCCTGCACTGGAACAGGAGTGGTGGTTTAACTATGCTCTGTTACCAAC 177
DB 61 TCCTGCACTGGAACAGGAGTGGTGGTTTAACTATGCTCTGTTACCAAC 120
QY 178 CACCCAGGCAAGCCCAACTCATGTTATGATGTCGTAAGCGGCTCAGGGGTC 237
DB 121 CACCCAGGCAAGCCCAACTCATGTTTTCAGGTGAGTATCGGCCCTCAGGGGTT 180
QY 238 TCTGATCGCTTCTGCTGCTCAAGTCTGGCAACAGGCTCCCTGACCATCTCTGGGCTC 297
DB 181 CCTAATCGCTTCTCAGGCTCAGGCTGGCAACAGGCTCCCTGACCATCTCTGGGCTC 240
QY 298 CAGGCTGAGGAGGCTGATTATGTTGTTTATATACCAACAGGAGTCTTTGTTA 357
DB 241 CAGGTTGAGGAGGCTGATTATGTTGTTTATATACCAACAGGAGTCTTTGTTA 300
QY 358 TTCGGAAGGAGGAGGCTGACCGTCTCAGGT 390
DB 301 TTCGGAAGGAGGAGGCTGACCGTCTCAGGT 333

RESULT 13
US-10-039-785-57
Sequence 57 Application US/10039785
Patent No. 6538938
GENERAL INFORMATION:
APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
FILE REFERENCE: PF550
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/369,860
PRIOR FILING DATE: 2002-04-05

FILE REFERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/039,785
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/369,860
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/331,044
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 60/327,364
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/323,807
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/309,176
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/294,981
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/293,473
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ IDS: 66
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 57
LENGTH: 735
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: DNA encoding T1014A12 scFv
US-10-039-785-57

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Best Local Similarity 85.5%; Pred. No. 2.2e-70;
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QY 100 GGCAGTCTGGTCACTCTCTGCACTGGACCCAGGAGTGGTGGTGGTGGTGGTGGTGGTGGT 159
DB 445 GGCAGTCTGGTCACTCTCTGCACTGGACCCAGGAGTGGTGGTGGTGGTGGTGGTGGTGGT 504
QY 160 GTCTCTCTGGTACCAACACCAACCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCA 219
DB 505 GTCTCTCTGGTACCAACACCAACCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCA 564
QY 220 AAGCGGCGCTCAGGGGCTCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGGCTCC 279
DB 565 AGCGGCGCTCAGAGGTTCTAGTCTCTCTGGCTCCAAAGTCTGGCAACACGGGCTCC 624
QY 280 CTGACCATCTCTGGGCTCCAGGCTGAGGAGGCTGATTTACTGTTGTTTATATATA 339
DB 625 CTGACCATCTCTGGGCTCCAGGCTGAGGAGGCTGATTTACTGTTGTTTATATATA 684
QY 340 ACCAGTAGCACTTTGTTTATTTCCGAGAGGAGCCCGTTGACCGTCTCAGGT 390
DB 685 AGCAACCACTTTGGGTGTTGGCGGAGGAGCCAAAGTCAACCGTCTCAGGT 735

RESULT 14
US-10-039-785-60
Sequence 60 Application US/10039785
Patent No. 6538938
GENERAL INFORMATION:
APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
FILE REFERENCE: PF550
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/369,860
PRIOR FILING DATE: 2002-04-05

;; PRIOR APPLICATION NUMBER: 60/341,237
;; PRIOR FILING DATE: 2001-12-20
;; PRIOR APPLICATION NUMBER: 60/331,310
;; PRIOR FILING DATE: 2001-11-14
;; PRIOR APPLICATION NUMBER: 60/331,044
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;; PRIOR APPLICATION NUMBER: 60/327,364
;; PRIOR FILING DATE: 2001-10-09
;; PRIOR APPLICATION NUMBER: 60/323,807
;; PRIOR FILING DATE: 2001-09-21
;; PRIOR APPLICATION NUMBER: 60/309,176
;; PRIOR FILING DATE: 2001-08-02
;; PRIOR APPLICATION NUMBER: 60/294,981
;; PRIOR FILING DATE: 2001-06-04
;; PRIOR APPLICATION NUMBER: 60/293,473
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 66
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 60
;; LENGTH: 735
;; TYPE: DNA
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: DNA encoding T1014F08 scFv
US-10-039-785-60

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Best Local Similarity 85.2%; Pred. No. 6.6e-70;
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Db 445 GGACAGTCAGTCACCATCTCTGCACTGGAACACAGGATGAGTGGTGGTTATAAGTAT 504
Qy 160 GTCTCTGGTACCAACACACACCCAGGCAAGCCCAAACTCATGATTTATGATGTCGCT 219
Db 505 GTCTCTGGTACCAACACACACCCAGGCAAGCCCAAACTCATGATTTATGATGTCAGT 564
Qy 220 AAGCGGCTCAGGGTCTGTGATCGCTTCTGCTCCAGTCCAGTCTGGCAACACGCTCC 279
Db 565 ATGCGGCTCAGGGGTCGGGATCGCTTCTGCTCCAGTCCAGTCTGGCAACACGCTCC 624
Qy 280 CTGACCATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATTTACTGTTGTTCATATACA 339
Db 625 CTGACCGTCTCTGGGCTCCAGGCTGAGGATGAGGCTGATTTACTGCGCTCATATGCA 684
Qy 340 ACCAGTAGCACTTTGTTATTCGGAAGAGGACCCGGTTGACCGTCTTAGGT 390
Db 685 GGCAGCAAAATTTGGGTGTTCGGCGGAGGACCAAGCTGACCGTCTTAGGT 735

RESULT 15
US-10-039-785-58
; Sequence 58, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PFS50
; CURRENT APPLICATION NUMBER: US/10/039,785
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044

;; PRIOR FILING DATE: 2001-11-07
;; PRIOR APPLICATION NUMBER: 60/327,364
;; PRIOR FILING DATE: 2001-10-09
;; PRIOR APPLICATION NUMBER: 60/323,807
;; PRIOR FILING DATE: 2001-09-21
;; PRIOR APPLICATION NUMBER: 60/309,176
;; PRIOR FILING DATE: 2001-08-02
;; PRIOR APPLICATION NUMBER: 60/294,981
;; PRIOR FILING DATE: 2001-06-04
;; PRIOR APPLICATION NUMBER: 60/293,473
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 66
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 58
;; LENGTH: 735
;; TYPE: DNA
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: DNA encoding T1014B01 scFv
US-10-039-785-58

Query Match 67.0%; Score 261.4; DB 4; Length 735;
Best Local Similarity 84.0%; Pred. No. 5.2e-68;
Matches 295; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
Qy 40 GGCACAGATCTGGGCTCAGTCTGCCCGGACTCAGCTCCCTCTGTGTCCTGGGTCCTCT 99
Db 385 GCGGTGGCGAAGTGCACTGCCCTGTGCTGACGCGGCGCCCTCAGTGTCTGGGTCCTCT 444
Qy 100 GGACAGTCGGTCACCATCTCTGCACTGGAACACAGGATGAGTGGTGGTTATAACTAT 159
Db 445 GGACAGTCAGTCACCATCTCTGCACTGGAACACAGGATGAGTGGTGGTTATAATTAT 504
Qy 160 GTCTCTGGTACCAACACACACCCAGGCAAGCCCAAACTCATGATTTATGATGTCGCT 219
Db 505 GTCTCTGGTACCAACACACACCCAGGCAAGCCCAAACTCATGATTTATGATGTCAGT 564
Qy 220 AAGCGGCTCAGGGTCTGTGATCGCTTCTGCTCCAGTCCAGTCTGGCAACACGCTCC 279
Db 565 AAGCGGCTCAGGGGTCCTGATCGCTTCTGCTCCAGTCCAGTCTGGCAACACGCTCC 624
Qy 280 CTGACCATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATTTACTGTTGTTCATATACA 339
Db 625 CTGACCGTCTCTGGGCTCCAGGCTGAGGATGAGGCTGATTTACTGCGGCTCATATGCA 684
Qy 340 ACCAGTAGCACTTTGTTATTCGGAAGAGGACCCGGTTGACCGTCTTAGGT 390
Db 685 GGCAGCAAAATTTGGGTGTTCGGCGGAGGACCAAGCTGACCGTCTTAGGT 735

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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 1615.57 Seconds
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Title: US-09-019-441-1

Perfect score: 390

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Scoring table: IDENTITY_NUC

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Listing first 45 summaries

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17: em_hum.*

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19: em_mu.*

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21: em_or.*

22: em_ov.*

23: em_pat.*

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25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_man.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	340.4	87.3	473	9	HUMIGLDS	M75282 Human Ig la
3	340.4	87.3	473	9	HUMIGLDS	M75139 Human Ig re
4	338.8	86.9	435	9	HS285033	285033 H.sapiens I
5	335.6	86.1	435	9	HS285358	285358 H.sapiens I
6	334	85.6	435	9	HS285035	285035 H.sapiens I
7	334	85.6	435	9	HS285297	285297 H.sapiens I
8	334	85.6	435	9	HS285355	285355 H.sapiens I
9	334	85.6	605	6	AXJ79222	AXJ79222 Sequence
10	330.8	84.8	435	9	HS285038	285038 H.sapiens I
11	330.8	84.8	435	9	HS285362	285362 H.sapiens I
12	329.2	84.4	435	9	HS285034	285034 H.sapiens I
13	329.2	84.4	435	9	HS285360	285360 H.sapiens I
14	329.2	84.4	435	9	HS285364	285364 H.sapiens I
15	329.2	84.4	895	9	BC033102	BC033102 Homo sapi
16	327.6	84.0	435	9	HS285032	285032 H.sapiens I
17	327.6	84.0	453	9	HSU43772	U43772 Human immun
18	326	83.6	435	9	HS285029	285029 H.sapiens I
19	325.8	83.5	894	9	BC018749	BC018749 Homo sapi
20	324	83.1	375	9	HS285091	285091 H.sapiens I
21	322.8	82.8	435	9	HS285295	285295 H.sapiens I
22	322.8	82.8	435	9	HS285303	285303 H.sapiens I
23	322.8	82.8	450	9	HSWLRG	X62125 H.sapiens r
24	321.2	82.4	435	9	HS284919	284919 H.sapiens I
25	321.2	82.4	435	9	HS285036	285036 H.sapiens I
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34	318	81.5	400	9	HS285197	285197 H.sapiens I
35	318	81.5	435	9	HS285296	285296 H.sapiens I
36	317.8	81.5	916	9	BC030983	BC030983 Homo sapi
37	316.4	81.1	435	9	HS284924	284924 H.sapiens I
38	316.4	81.1	435	9	HS284925	284925 H.sapiens I
39	316.4	81.1	435	9	HS285030	285030 H.sapiens I
40	316.4	81.1	435	9	HS285040	285040 H.sapiens I
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45	314.6	80.7	435	9	HS285359	285359 H.sapiens I

ALIGNMENTS

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(24-17TIIIIH34) rearranged; Ig-Light-Lambda; VLambda.
ACCESSION 285043
VERSION 285043.1 GI:1834754
KEYWORDS antigen receptor; immunoglobulin; immunoglobulin light chain;
immunoglobulin superfamily; rearranged; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.

Db	270	AAATCGCTTCTCTGGCTCCAAAGTCTGGCAACAGCGCTCCTGTACCAATCTCTGGGCTCCAG	329
Qy	301	GCTGAGGACGAGGCTGATTATTACTGTGTTTCATATACCAACAGTAGTACACTTTGTTATTC	360
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Qy	361	GGAAAGAGGACCGGTTGACCGTCTTAGGT	390
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DEFINITION	H.sapiens Ig lambda light chain variable region gene (24-07ITIB176) rearranged; Ig-Light-Lambda; VLambda.		
ACCESSION	Z85033		
VERSION	Z85033.1	GI:1834744	
KEYWORDS	antigen receptor; immunoglobulin; immunoglobulin light chain; immunoglobulin superfamily; rearranged; variable region.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1		
TITLE	Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G. XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda Repertoire		
JOURNAL	J. Mol. Biol.		
REFERENCE	2 (bases 1 to 435)		
AUTHORS	Ignatovich,O.		
TITLE	Direct Submission		
JOURNAL	Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein Engineering, Hills Road, Cambridge CB2 2QH, UK		
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Qy	61	TCGTGCCCGACACTCAGCGCTCCCTGTGTCTGGGTCTCTGGACAGTCGGTCACCATCTCC	120
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Qy	121	TGCACCTGGAAACAGCGATGACGTTGGTGGTTATACTATGTCTCTGGTACCAACACCAC	180
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Qy	181	CCAGGCAAGGCCCCAAACTCATGATTTATGATGTGCGCTAAGCGGGCTCAGGGGTCTCT	240
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Qy 241 GATCGCTTCTGGCTCAAGCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTCCAG 300
Db 241 AATCGCTTCTTGGCTCAAGCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTCCAG 300
Qy 301 GCTGAGGACGAGGCTGATTATTACTGTTTTCATATACAACAGTAGCAGTCTTGTATTTC 360
Db 301 GCTGAGGACGAGGCTGATTATTACTGTTTTCATATACAACAGTAGCAGTCTTGTATTTC 360
Qy 361 GGAGAGGAGGACCGGTTGACCGTCTTAGGT 390
Db 361 GCGGAGGAGGACCAAGCTGACCGTCTTAGGT 390

RESULT 5
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LOCUS              H.sapiens Ig lambda light chain variable region gene (25-28SWIID60)
DEFINITION
ACCESSION          285358
VERSION            285358.1 GI:1835069
KEYWORDS            immunoglobulin superfamily; rearranged; variable region;
SOURCE              Homo sapiens
ORGANISM            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE           1
AUTHORS             Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.
TITLE               XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
                    Repertoire
JOURNAL             J. Mol. Biol.
REFERENCE           2 (bases 1 to 435)
AUTHORS             Ignatovich,O.
TITLE               Direct Submission
JOURNAL             Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
                    Engineering, Hills Road, Cambridge CB2 2QH, UK
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BASE COUNT          86 a 148 c 99 g 102 t
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Best Local Similarity 91.3%; Pred. No. 3.2e-84;
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Qy 1 ATGGCTGGACTCTGCTCCTCGTCACCTCTCTCACTCAGGGCAGAGGATCTGGGCTCAG 60
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Qy 301 GCTGAGGACGAGGCTGATTATTACTGTTTTCATATACAACAGTAGCAGTCTTGTATTTC 360
Db 301 GCTGAGGACGAGGCTGATTATTACTGTTTTCATATACAACAGTAGCAGTCTTGTATTTC 360
Qy 361 GGAAGAGGAGCCCGGTTGACCGTCTTAGGT 390
Db 361 GGAAGTGGGACCAAGGTAACCGTCTTAGGT 390

RESULT 6
HS285035          435 bp  DNA  linear  PRI 06-FEB-1997
LOCUS              H.sapiens Ig lambda light chain variable region gene
DEFINITION          (24-09ITIIIC195) rearranged; Ig-light-Lambda; VLambda.
ACCESSION          285035
VERSION            285035.1 GI:1834746
KEYWORDS            immunoglobulin superfamily; rearranged; variable region;
SOURCE              Homo sapiens
ORGANISM            Homo sapiens
                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE           1
AUTHORS             Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.
TITLE               XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
                    Repertoire
JOURNAL             J. Mol. Biol.
REFERENCE           2 (bases 1 to 435)
AUTHORS             Ignatovich,O.
TITLE               Direct Submission
JOURNAL             Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
                    Engineering, Hills Road, Cambridge CB2 2QH, UK
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Db 301 GCTGAGGACGAGCTGATTATTAATGCTGCTATATACACCAAGTACGACTTGTATTTC 360
QY 361 GGAAGAGGACCCCGTTGACCGTCTTAGGT 390
Db 361 GGAAGAGGACCCCGTTGACCGTCTTAGGT 390

RESULT 7
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LOCUS HSZ85297 435 bp DNA linear PRI 06-FEB-1997
DEFINITION H.sapiens Ig lambda light chain variable region gene (25-070IVE158)
rearranged; Ig-Lambda; VLambda.
ACCESSION Z85297.1 GI:1835008
VERSION 1
KEYWORDS antigen receptor; immunoglobulin; immunoglobulin light chain;
immunoglobulin superfamily; rearranged; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.
TITLE XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
Reertoire.
JOURNAL J. Mol. Biol.
REFERENCE 2 (bases 1 to 435)
AUTHORS Ignatovich,O.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
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/mol_type="genomic DNA"
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Matches 353; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
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QY 181 CCAGGCAAGCCCAAACTCATGATTATGATGCTAAGCGGCTCAGGGTCTCT 240
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Db 241 AATCGCTTCTTGCTCCAAAGTCTGGCAACACGGCTCCCTGACCAATCTCTGGGCTCCAG 300
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Db 301 GCTGAGGACGAGCTGATTATTAATGCTGCTATATACACCAAGTACGACTTGTATTTC 360
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RESULT 8
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DEFINITION H.sapiens Ig lambda light chain variable region gene (25-23SWIB16)
rearranged; Ig-Lambda; VLambda.
ACCESSION Z85355.1 GI:1835066
VERSION 1
KEYWORDS antigen receptor; immunoglobulin; immunoglobulin light chain;
immunoglobulin superfamily; rearranged; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.
TITLE XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
Reertoire.
JOURNAL J. Mol. Biol.
REFERENCE 2 (bases 1 to 435)
AUTHORS Ignatovich,O.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
FEATURES
Location/Qualifiers
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/clone_lib="cDNA library"
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Best Local Similarity 91.0%; Pred. No. 9.1e-84;
Matches 353; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
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QY 61 TCTGCCCCGACTAGCCCTCTGTGTCTGGGTCTCCTGGACAGTGGTCAACATCTCC 120
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QY 301 GCTGAGGACGAGCTGATTACTGTGTTCATATACACCAAGTACACTTTGTTATTC 360
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QY 361 GGAAGAGGACCGGTGACCGTCTTAGGT 390
Db 361 GCGGAGGAGCAAGGTGACCGTCTTAGGT 390

RESULT 11
HSZ85362 HSZ85362 435 bp DNA linear PRI 06-FEB-1997
LOCUS H.sapiens Ig lambda light chain variable region gene
DEFINITION (25-33SWIIE224) rearranged; Ig-Light-Lambda; VLambda.
ACCESSION Z85362.1 GI:1835073
VERSION 285362.1
KEYWORDS antigen receptor; immunoglobulin; immunoglobulin light chain;
immunoglobulin superfamily; rearranged; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.
TITLE XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
JOURNAL Repertoire
AUTHORS J. Mol. Biol.
REFERENCE 2 (bases 1 to 435)
AUTHORS Ignatovich,O.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
FEATURES
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/organism="Homo sapiens"
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Matches 353; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1 ATGSCCTGGACTCTGCTCTGTCACCTCTCTACTCAGGCGACAGGATCTGGGCTCAG 60
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Db 241 GATCGCTTCTCTGGCTCCAAAGTCTGGCAACAACCGGCTCTCCCTGACCATCTCTCGGGCTCTG 300
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Db 301 GCTGAGGATGAGGCTGATTACTGTGTTCATATACACCAAGTACACTTTGTTATTC 360
QY 361 GGAAGAGGACCGGTGACCGTCTTAGGT 390
Db 361 GCGGAGGAGCAAGGTGACCGTCTTAGGT 390

RESULT 12
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LOCUS H.sapiens Ig lambda light chain variable region gene
DEFINITION (24-08ITIIC194) rearranged; Ig-Light-Lambda; VLambda.
ACCESSION Z85034.1 GI:1834745
VERSION 285034.1
KEYWORDS antigen receptor; immunoglobulin; immunoglobulin light chain;
immunoglobulin superfamily; rearranged; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.
TITLE XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
JOURNAL Repertoire
AUTHORS J. Mol. Biol.
REFERENCE 2 (bases 1 to 435)
AUTHORS Ignatovich,O.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
FEATURES
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/organism="Homo sapiens"
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gene 1. .435
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Best Local Similarity 90.3%; Pred. No. 2.1e-82;
Matches 352; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 1 ATGSCCTGGACTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60
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Db      301  |||||
QY      361  GGAAGAGGAGCCCGGTTGACCGTCTAGGT 390
Db      361  |||||

RESULT 13
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LOCUS      H.sapiens Ig lambda light chain variable region gene
DEFINITION (25-31SWIID182) rearranged; Ig-Light-Lambda; VLambda.
ACCESSION  Z85360.1 GI:1835071
VERSION     antigen receptor; immunoglobulin; immunoglobulin light chain;
KEYWORDS    immunoglobulin superfamily; rearranged; variable region.
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.
TITLE       XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
JOURNAL     Repertoire.
REFERENCE   2 (bases 1 to 435)
AUTHORS     Ignatovich,O.
TITLE       Direct Submission
JOURNAL     Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
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Matches 352; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY      1  ATGGCTCGGACTCTGCTCCTGTCACCTCTCTCACTCAGGGCACAGGATCCTGGGCTCAG 60
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Db      301  |||||
QY      361  GGAAGAGGAGCCCGGTTGACCGTCTAGGT 390
Db      361  |||||

RESULT 14
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LOCUS      H.sapiens Ig lambda light chain variable region gene
DEFINITION (25-36SWIIF166) rearranged; Ig-Light-Lambda; VLambda.
ACCESSION  Z85364.1 GI:1835075
VERSION     antigen receptor; immunoglobulin; immunoglobulin light chain;
KEYWORDS    immunoglobulin superfamily; rearranged; variable region.
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.
TITLE       XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
JOURNAL     Repertoire.
REFERENCE   2 (bases 1 to 435)
AUTHORS     Ignatovich,O.
TITLE       Direct Submission
JOURNAL     Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
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QY      1  ATGGCTCGGACTCTGCTCCTGTCACCTCTCTCACTCAGGGCACAGGATCCTGGGCTCAG 60
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QY      61  TCTGCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTTGACAGTGGTCAACATCTCC 120
Db      61  |||||
QY      121  TGCACCTGAACACGAGTACGTTGGTGGTTATTAATCTATGTCCTCTGTAACCAACACCAC 180
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361 GGAAGAGGACGCGGTTGACCGCTCTAGGT 390
361 GCGGAGGACCAAGCTGACCGTCTCTAGGT 390
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RESULT 15
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LOCUS
DEFINITION
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MGC:45681 IMAGE:4851128, mRNA, complete cds.
ACCESSION
BC033102
VERSION
BC033102.1 GI:21619847
KEYWORDS
MGC.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 895)
Strausberg, R.
Direct Submission
Submitted (25-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NTH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabs-x@mail.nih.gov
Tissue Procurement: Louis Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smalls, Michael Smith, Lorraine Spence, Jeff Scott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 43 Row: 9 Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: Genomescan gene prediction, Similarity but not identity to protein.

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Best Local Similarity 90.3%; Pred. No. 2e-82;
Matches 352; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 1 ATGGCCCTGGACTCTGCTCTGCTCGTCAACCTCCCTCCTCAGGGCACAGATCCTGGGCTCAG 60
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Db 151 TGCACCTGGAAACAGCAGATGACGTTGGTGTGTTATTAATATGTCTCTCTGGTACCAACACAC 210
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QY 361 GGAAGAGGACCGCGGTTGACCGTCTCTAGGT 390
Db 391 GGAAGAGGACCGCGGTTGACCGTCTCTAGGT 420
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 1687.58 Seconds
(without alignments)
5616.780 Million cell updates/sec

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Perfect score: 390
Sequence: 1 ATGGCTGGACTGCTGCTCT.....CCCGGTGACCGTCTTAGGT 390

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: em_esthum.*
3: em_estin.*
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24: em_gss_pro.*
25: em_gss_rod.*
26: em_gss_phg.*
27: em_gss_vrl.*
28: gb_gss1.*
29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	334	85.6	843	10 BG756493	BG756493 602715633
4	334	85.6	1078	12 BM914350	BM914350 AGENCOURT

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6	330.8	84.8	787	12	BI820758	BI820758 603034354
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9	329.2	84.4	716	9	AV693754	AV693754 AV693754
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12	329.2	84.4	889	10	BG756342	BG756342 602713662
13	329.2	84.4	908	10	BG756874	BG756874 602710363
14	329.2	84.4	953	10	BG756229	BG756229 602245104
15	329.2	84.4	980	10	BG397302	BG397302 602439086
16	327.6	84.0	487	9	AW404692	AW404692 UI-HF-BL0
17	327.6	84.0	710	9	AV694861	AV694861 AV694861
18	327.6	84.0	751	9	AV699040	AV699040 AV699040
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21	327.6	84.0	868	10	BG483745	BG483745 602503383
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23	326	83.6	479	10	BG059377	BG059377 nah50e11.
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25	326	83.6	658	10	BG397577	BG397577 602438617
26	326	83.6	804	10	BG564971	BG564971 602583943
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30	322.8	82.8	523	12	BM831030	BM831030 K-EST0104
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35	321	82.3	553	12	BM830982	BM830982 K-EST0104
36	321	82.3	554	12	BM830988	BM830988 K-EST0104
37	321	82.3	604	12	BM773502	BM773502 K-EST0057
38	321	82.3	710	12	BM769463	BM769463 K-EST0052
39	319.6	81.9	831	10	BG541853	BG541853 602569746
40	319.2	81.8	840	10	BG397282	BG397282 602439065
41	318.2	81.6	824	10	BG536723	BG536723 602564852
42	318	81.5	426	12	BM825633	BM825633 K-EST0097
43	318	81.5	479	12	BM830794	BM830794 K-EST0104
44	318	81.5	754	12	B1823608	B1823608 603040988
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ALIGNMENTS

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DEFINITION 880 bp mRNA linear EST 22-JAN-2001
BF975970
MRNA sequence.
BF975970
EST.
BF975970.1 GI:12343185
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 880)
AUTHORS NTH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Prepared by: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L12CM1211 row: c column: 19
High quality sequence stop: 759.

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 Site_2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."
 BASE COUNT 151 a 230 c 177 g 128 t

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 Best Local Similarity 90.3%; Pred. No. 4.3e-77;
 Matches 352; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
 QY 1 ATGGCTGGACTCTGCTCTGTCACCTCTCACTCAGGCGACAGGATCTGGGCTCAG 60
 Db 32 ATGGCTGGGCTCTGCTCTGTCACCTCTCACTCAGGCGACAGGATCTGGGCTCAG 91
 QY 61 TCTGCCCGACTCAGCCTCCTGTCGTCGGGTCCTCTGACAGTGGTCAACATCTCC 120
 Db 92 TCTGCCCTGACTCAGCCTCCTGTCGTCGGGTCCTCTGACAGTGGTCAACATCTCC 151
 QY 121 TGCATCGAACACGAGTACGTTGGTGGTTTAACTATGTTCTCTGTTACCAACAC 180
 Db 152 TGCATCGAACACGAGTACGTTGGTGGTTTAACTATGTTCTCTGTTACCAACAC 211
 QY 181 CCAGCAAGCCCGCAACTCATGTTTATGTCGTCGTAAGCGGCTCAGGGTCTCT 240
 Db 212 CCAGCAAGCCCGCAACTCATGTTTATGTCGTCGTAAGCGGCTCAGGGTCTCT 271
 QY 241 GATGCTTCTCTGGCTCCAACTCTGGCAACAGGCTCCCTGACCATCTCTGGGCTCCAG 300
 Db 272 GATGCTTCTCTGGCTCCAACTCTGGCAACAGGCTCCCTGACCATCTCTGGGCTCCAG 331
 QY 301 GCTGAGGACGAGGCTGATTATTACTGTTTATATACAAACAGTACGATCTTTGTTATTC 360
 Db 332 GCTGAGGATGAGGCTGATTATTACTGACGTCATATGACGAGCAGCAACAATTATGTTCTC 391
 QY 361 GGAAGAGGACCGGTTGACCGTCTCCTAGGT 390
 Db 392 GGAAGTGGGACCAAGGTCACCGTCTCCTAGGT 421

RESULT 9
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 ACCESSION AV693754
 VERSION AV693754.1 GI:10295617
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 716)
 Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,
 Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,
 Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X.,
 Hu, G., Gu, J., Chen, Z. and Han, Z.
 Insight into hepatocellular carcinogenesis at transcriptome level
 by comparing gene expression profiles of hepatocellular carcinoma
 with those of corresponding noncancerous liver
 Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
 21625106
 11752456
 JOURNAL MEDLINE
 PUBMED
 COMMENT Contact: Zeguang Han
 Chinese National Human Genome Center at Shanghai

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919 (ex. 45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn
 This clone is available at CHGC in Shanghai.

FEATURES

source
 1. 716
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 /db_xref="taxon:9606"
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 BASE COUNT 148 a 240 c 183 g 144 t 1 others
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 Best Local Similarity 90.3%; Pred. No. 4.3e-77;
 Matches 352; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
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 QY 361 GGAAGAGGACCGGTTGACCGTCTCCTAGGT 390
 Db 389 GGCAGGAGCAACAGTACCGTCTCTAGGT 418

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 DEFINITION AV697043
 ACCESSION AV697043
 VERSION AV697043.1 GI:10298906
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 767)
 Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,
 Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,
 Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X.,
 Hu, G., Gu, J., Chen, Z. and Han, Z.
 Insight into hepatocellular carcinogenesis at transcriptome level
 by comparing gene expression profiles of hepatocellular carcinoma
 with those of corresponding noncancerous liver
 Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
 21625106
 11752456
 JOURNAL MEDLINE
 PUBMED
 COMMENT Contact: Zeguang Han
 Chinese National Human Genome Center at Shanghai

10


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301 GCTGAGGACGAGCTGATTATTACTGTTGTTTCATATACAAACAGTAGCAGCTTTGTTATTC 360
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VERSION BF976229
KEYWORDS GI:12343444
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 953)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
    Email: cgabbs-remail.nih.gov
    Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
    cDNA Library Preparation: Ling Hong/Rubin Laboratory
    cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
    DNA Sequencing by: Incyte Genomics, Inc.
    Clone distribution: MGC clone distribution information can be
    found through the I.M.A.G.E. Consortium/LLNL at:
    http://image.llnl.gov
    Plate: LLCM1208 row: h column: 02
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            Directionally cloned into EcoRI/XhoI sites using the
            following 5' adaptor: GGCACGAG(G). Size-selected >500bp
            for average insert size 1.8kb. Library constructed by Ling
            Hong in the laboratory of Gerald M. Rubin (University of
            California, Berkeley) using ZAP-cDNA synthesis kit
            (Stratagene) and Superscript II RT (Life Technologies).
            Note: this is a NIH_MGC Library."
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QY 121 TGCACTGGAACCAAGCAGATGAGTTGGTGGTTATTAATGTTCTCTGGTACCAACACCAC 180
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QY 241 GATCGCTTCTCTGGCTCCAAAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTCCAG 300
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ACCESSION BG397302
VERSION BG397302
KEYWORDS GI:13290750
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 980)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
    Email: cgabbs-remail.nih.gov
    Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
    cDNA Library Preparation: Ling Hong/Rubin Laboratory
    cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
    DNA Sequencing by: Incyte Genomics, Inc.
    Clone distribution: MGC clone distribution information can be
    found through the I.M.A.G.E. Consortium/LLNL at:
    http://image.llnl.gov
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            /lab_host="DH10B (phage-resistant)"
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            /note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
            Site 2: EcoRI; cDNA made by oligo-dT priming.
            Directionally cloned into EcoRI/XhoI sites using the
            following 5' adaptor: GGCACGAG(G). Size-selected >500bp
            for average insert size 1.8kb. Library constructed by Ling
            Hong in the laboratory of Gerald M. Rubin (University of
            California, Berkeley) using ZAP-cDNA synthesis kit
            (Stratagene) and Superscript II RT (Life Technologies).
            Note: this is a NIH_MGC Library."
BASE COUNT 233 a 293 c 263 g 190 t
ORIGIN
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    Best Local Similarity 90.3%; Pred. No. 5e-77;
    Matches 352; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 1 ATGGCCTGGACTGCTCTCGTCACCCCTCTACTCAGGCGACAGGATCTGGGCTCAG 60
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Db 33 ATGGCCTGGGCTCTGCTCTCTCTCCTCCTCCTCCTCAGGCGACAGGCTCTGGGCCAC 92
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Qy 181 CCAGGCAAGCCCCCAACTCATGATTTATGATGTGCTAAGCGGGCTCAGGGTCTCT 240
Db 213 CCAGGCAAGCCCCCAACTCATGATTTATGAGGTCAATAGCGGCCCTCAGGGTCCCT 272
Qy 241 GATGCTTCTCTGGTCCAGTCTGGCAACACGGCCCTCCCTGACCATCTCTGGGCTCCAG 300
Db 273 GATGCTTCTCTGGTCCAGTCTGGCAACACGGCCCTCCCTGACCATCTCTGGGCTCCAG 332
Qy 301 GCTGAGGACGAGGCTGATTATTACTTGTGTTTCATATACAACAGTAGCATTGTTATTTC 360
Db 333 GCTGCGATGAGGCTGATTATTACTGAGCTCATATGCGGCGACAGTTTCTGCTGTC 392
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 19:01:43 ; Search time 563.449 Seconds
(without alignments)
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Title: US-09-019-441-1
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2244575 seqs, 1713117285 residues

Total number of hits satisfying chosen parameters: 4489150

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	324.4	83.2	408	11	US-09-918-995-36573
6	324.4	83.2	421	11	US-09-918-995-16692
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12	300.6	77.1	2667	15	US-10-158-646-76
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19	285.4	73.2	735	13	US-10-139-785-59	Sequence 59, Appl
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25	284.4	72.9	735	15	US-10-151-882-4	Sequence 4, Appl
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27	275.8	70.7	735	13	US-10-139-785-54	Sequence 54, Appl
28	275.8	70.7	735	14	US-10-039-785-54	Sequence 54, Appl
29	275	70.5	552	13	US-10-029-386-1351	Sequence 1351, Ap
30	275	70.5	707	13	US-10-027-632-18093	Sequence 18093, A
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32	272	69.7	379	13	US-10-029-386-15053	Sequence 15053, A
33	269.4	69.1	735	13	US-10-139-785-57	Sequence 57, Appl
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36	267.8	68.7	735	13	US-10-139-785-60	Sequence 60, Appl
37	267.8	68.7	735	14	US-10-039-785-60	Sequence 436, App
38	265.2	68.0	518	13	US-10-029-386-436	Sequence 63, Appl
39	264.6	67.8	741	13	US-10-322-673-63	Sequence 59, Appl
40	262	67.2	765	13	US-10-360-828-59	Sequence 18, Appl
41	261.8	67.1	358	13	US-10-010-729-18	Sequence 58, Appl
42	261.4	67.0	735	13	US-10-139-785-58	Sequence 61, Appl
43	261.4	67.0	735	13	US-10-139-785-61	Sequence 58, Appl
44	261.4	67.0	735	14	US-10-039-785-58	Sequence 61, Appl
45	261.4	67.0	735	14	US-10-039-785-61	

ALIGNMENTS

RESULT 1

US-09-019-441-1
; Sequence 1, Application US/09019441
; Publication No. US2003008621A1
; GENERAL INFORMATION:
; APPLICANT: REFF, Mitchell E.
; KLOETZER, William S.
; NAKAMURA, Takehiko
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
; ANTIBODIES AND USE THEREOF AS THERAPEUTICS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/019,441
; FILING DATE: 05-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/803,085
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012172-502
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:

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SEQUENCE CHARACTERISTICS:
LENGTH: 390 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..390
NAME/KEY: mat_peptide
LOCATION: 58..390
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-019-441-1

Query Match      100.0%; Score 390; DB 11; Length 390;
Best Local Similarity 100.0%; Pred. No. 6.1e-118;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCCTGGACTCTGCTCCTCGTCAACCTCCTCACTCAGGGCAGAGGATCTGGGCTCAG 60
Db 1 ATGGCCTGGACTCTGCTCCTCGTCAACCTCCTCACTCAGGGCAGAGGATCTGGGCTCAG 60

Qy 61 TCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTTGACAGTCTGGTCAACATCTCC 120
Db 61 TCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTTGACAGTCTGGTCAACATCTCC 120

Qy 121 TGCACCTGAAACAGGATGAGCTGGTGGTGTATTAACATATGCTCTCTGTTACCAACACAC 180
Db 121 TGCACCTGAAACAGGATGAGCTGGTGGTGTATTAACATATGCTCTCTGTTACCAACACAC 180

Qy 181 CCAGGCAAGCCCCCAACTCATGATTTATGATGCTGCTAAGCGGCTCAGGGTCTCT 240
Db 181 CCAGGCAAGCCCCCAACTCATGATTTATGATGCTGCTAAGCGGCTCAGGGTCTCT 240

Qy 241 GATCGCTTCTTGCTCCAACTGCGCAACAGGCTCCCTGACCATCTCTGGGCTCCAG 300
Db 241 GATCGCTTCTTGCTCCAACTGCGCAACAGGCTCCCTGACCATCTCTGGGCTCCAG 300

Qy 301 GCTGAGGACGAGGCTGATTATTAACATGTTGTTTATATACAAACAGTAGCATTGTTATTC 360
Db 301 GCTGAGGACGAGGCTGATTATTAACATGTTGTTTATATACAAACAGTAGCATTGTTATTC 360

Qy 361 GGAAGAGGAGCCCGGTTGACCGTCTTAGGT 390
Db 361 GGAAGAGGAGCCCGGTTGACCGTCTTAGGT 390
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RESULT 2
US-10-103-686-1
; Sequence 1, Application US/10103686
; Publication No. US20030059424A1
; GENERAL INFORMATION:
; APPLICANT: REFF, Mitchell E.
; NAKAMURA, Takehiko
; KLOETZER, William S.
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
; ANTIBODIES AND USE THEREOF AS THERAPEUTICS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/103,686
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; FILING DATE: 25-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/803,085
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 390 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..390
; NAME/KEY: mat_peptide
; LOCATION: 58..390
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-103-686-1

Query Match      100.0%; Score 390; DB 15; Length 390;
Best Local Similarity 100.0%; Pred. No. 6.1e-118;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCCTGGACTCTGCTCCTCGTCAACCTCCTCACTCAGGGCAGAGGATCTGGGCTCAG 60
Db 1 ATGGCCTGGACTCTGCTCCTCGTCAACCTCCTCACTCAGGGCAGAGGATCTGGGCTCAG 60

Qy 61 TCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTTGACAGTCTGGTCAACATCTCC 120
Db 61 TCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTTGACAGTCTGGTCAACATCTCC 120

Qy 121 TGCACCTGAAACAGGATGAGCTGGTGGTGTATTAACATATGCTCTCTGTTACCAACACAC 180
Db 121 TGCACCTGAAACAGGATGAGCTGGTGGTGTATTAACATATGCTCTCTGTTACCAACACAC 180

Qy 181 CCAGGCAAGCCCCCAACTCATGATTTATGATGCTGCTAAGCGGCTCAGGGTCTCT 240
Db 181 CCAGGCAAGCCCCCAACTCATGATTTATGATGCTGCTAAGCGGCTCAGGGTCTCT 240

Qy 241 GATCGCTTCTTGCTCCAACTGCGCAACAGGCTCCCTGACCATCTCTGGGCTCCAG 300
Db 241 GATCGCTTCTTGCTCCAACTGCGCAACAGGCTCCCTGACCATCTCTGGGCTCCAG 300

Qy 301 GCTGAGGACGAGGCTGATTATTAACATGTTGTTTATATACAAACAGTAGCATTGTTATTC 360
Db 301 GCTGAGGACGAGGCTGATTATTAACATGTTGTTTATATACAAACAGTAGCATTGTTATTC 360

Qy 361 GGAAGAGGAGCCCGGTTGACCGTCTTAGGT 390
Db 361 GGAAGAGGAGCCCGGTTGACCGTCTTAGGT 390
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RESULT 3
US-10-198-846-13206/c
; Sequence 13206, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
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Matches	350;	Conservative	0;	Mismatches	39;	Indels	0;	Gaps	0;
QY	2	TGGCCTTGGACTCTGCTCTCGTCA	CCCTCCTCACTCAGGGCACAGATCCTGGGCTCAGT	61					
Db	1529	TGGCCTTGGGCTCTGCTGCTCCTG	ACCTCCTCACTCAGGGCACAGGGTCTGGGGCCAGT	1470					
QY	62	CTGCCCCGACTCAGCTCCCTCTG	TGCTGGGTCTCCTGGACAGTCGGTCAACCATCTCCT	121					
Db	1469	CTGCCCCGACTCAGCTCCCTCTG	TGCTGGGTCTCCTGGACAGTCGATCACCATCTCCT	1410					
QY	122	GCACGTGAACACAGCGATGACG	TGTTGGTGTATAAATATGTCTCCTGGTACCAACACCACC	181					
Db	1409	GCAATTGGAACCTTCAATGAC	ATTGGTAGTTATAAATATGTCTCCTGGTACCAACACCACC	1350					
QY	182	CAGGCAAAAGCCCCAAATCAT	GATTTATGATTCGCTAAGCGGGCTCTAGGGGTCTCTG	241					
Db	1349	CAGGCAAAAGCCCCAAATCCT	GATTATGATGTCAGTAATCGGCCCTCAGGGGTTTCTA	1290					
QY	242	ATCGCTTCTCTGGTCCCAAGT	CTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGG	301					
Db	1289	ATCGCTTCTCTGGTCCCAAGT	CTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGG	1230					
QY	302	CTGAGGACGAGGCTGATTATT	ACTGTGTTCATATACAACCACTAGACACTTTGTTATTCTG	361					
Db	1229	CTGAGGACGAGGCTGATTATT	ACTGACGCTCATATACACGACGACACTCTGGTATTCTG	1170					
QY	362	GAAGAGGGACCCGGTTGAC	CGTCTTAGT 390						
Db	1169	GCGGAGGGACCAAGCTG	ACCGTCTCTGGT 1141						

RESULT 5

US-09-918-995-36573

Sequence 36573, Application US/09918995

Publication No. US20030073623A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES

FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 36573

LENGTH: 408

TYPE: DNA

ORGANISM: Homo sapiens

US-09-918-995-36573

Query Match

Best Local Similarity

Matches

349;

Conservative

0;

Mismatches

41;

Indels

0;

Gaps

0;

QY	1	ATGGCCTGGACTCTGCTCCTCGT	CACCCCTCCTCACTCAGGGCACAGGATCCTGGGCTCAG	60					
Db	19	ATGGCCTGGGCTCTGCTGCTCCT	CACCCCTCCTCACTCAGGGCACAGGATCCTGGGCTCAG	78					
QY	61	TTTGCCCCGACTCAGCCTCCCTC	TGTGTCTGGGTCTCTGGACAGTCGGTCAACATCTCC	120					
Db	79	TCTGCCCTGACTCAGCCTCGCT	CGTGTCTGGGTCTCCTGGGACAGTCGATCACCATCTCC	138					
QY	121	TGCACCTGGAACGACGATGACG	TGGTGGTTATAACTGTCTCCTGGTACCAACACCAC	180					
Db	139	TGCACCTGGAACGACGATGAC	ATTGGTTCGTTACAACTATGTCTCTGGTACCAACACAC	198					
QY	181	CCAGGCAAAAGCCCCAAACTCA	TGATTTATGATTCGCTAAGCGGGGCTCAGGGGTCTCT	240					
Db	199	CCAGGCAAAAGCCCCAAACTCA	TAAATTTATGAGTCAGTAACTCGGCCCTCAGGGGTTTCT	258					
QY	241	GATCGCTTCTCTGGCTCCAGT	CTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG	300					

Db 265 AATCGTTCTCTGCTCAAGTCTGGCAACACGGCTCCCTGACCGTCTCTGGGCTCCAG 324
Qy 301 GCTGAGACGAGGCTGATTATTACTGTGTTTCATATACACCACTAGACATCTTGTATTTC 360
Db 325 GCTGAGACGAGGCTGCTTATTATGCGCTTCATATACCAACCGGCATCACTTATGTCTTC 384
Qy 361 GGAAGAGGACCGGTTGACCGTCTCTAGGT 390
Db 385 GGAGGTGGACCTGGGTACCGTCTCTATGT 414

RESULT 11
US-10-158-646-73
; Sequence 73, Application US/10158646
; Publication No. US20030073105A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy K.W.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0030-1 US
; CURRENT APPLICATION NUMBER: US/10/158,646
; PRIOR FILING DATE: 2002-05-29
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PERL Program
; SEQ ID NO 73
; LENGTH: 883
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030073105A1 1329913.2
US-10-158-646-73

Query Match 77.4%; Score 301.8; DB 15; Length 883;
Best Local Similarity 87.3%; Pred. No. 8.2e-89;
Matches 343; Conservative 0; Mismatches 47; Indels 3; Gaps 1;

Qy 1 ATGCGCTGGACTCTGCTCTCGTCAACCTCTCTCACTCAGGGCAGAGGATCTGGGCTCAG 60
Db 39 ATGCGCTGGGCTCTGCTCTCTCACTCTCTCACTCAGGACACAGGGTCTGGGCCCCAG 98
Qy 61 TCTGCCCCGACTCAGCTCCCTCTGTCTGGGTCTCTGACAGTGGTCAACCATCTCC 120
Db 99 TCTGCCCCGACTCAGCTCCCTCTGTCTGGGTCTCTGACAGTGGTCAACCATCTCC 158
Qy 121 TGCACCTGGAACACGAGTGGTGGTTTATTAATCTCTCTCTGATCAACACAC 180
Db 159 TGCACCTGGAAGTGGGCTGAGCTGGTCTTATTAATCTCTCTCTGATCAACACAC 218
Qy 181 CCAGCAAGCCCCCAAACTCATGATTTATGATGTCGTAAGCGGCTCAGGGTCTCT 240
Db 219 CCAGCAAGCCCCCAAACTCATGATTTATGATGTCATTAATCGGCCCTCAGGGTCTCT 278
Qy 241 GATCGCTTCTGCTGCTCAAGTCTGGCAACAGGCTCCCTGACCATCTCTGGGCTCCAG 300
Db 279 AATCGGTTCTCTGGCTTCAAGTCTGGCAACAGGCTCCCTGACAACTCTCTGGGCTCCAG 338
Qy 301 GCTGAGGACGAGGCTGATTATTACTGTGTTTCATATACCAACAGTAGACATTT--TGTTA 357
Db 339 GCTGAGGATGAGGCTTATTATTACTGCTCTCTCAATTTGACGTAGTACATCTCTGTGTTA 398
Qy 358 TTCGGAAGAGGACCGGTTGACCGTCTCTAGGT 390
Db 399 TTCGCGGAGGACCAAGGTGACCGTCTCTAGGT 431

RESULT 12
US-10-158-646-76/c
; Sequence 76, Application US/10158646
; Publication No. US20030073105A1
; GENERAL INFORMATION:

; APPLICANT: Lasek, Amy K.W.
; APPLICANT: Sornasse, Thierry
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0030-1 US
; CURRENT APPLICATION NUMBER: US/10/158,646
; PRIOR FILING DATE: 2002-05-29
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PERL Program
; SEQ ID NO 76
; LENGTH: 2667
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030073105A1 1329881.6
US-10-158-646-76

Query Match 77.1%; Score 300.6; DB 15; Length 2667;
Best Local Similarity 87.2%; Pred. No. 3e-88;
Matches 341; Conservative 0; Mismatches 49; Indels 1; Gaps 1;

Qy 1 ATGCGCTGGACTCTGCTCTCTGTCACCTCTCACTCAGGGCAGAGGATCTGGGCTCAG 60
Db 2635 ATGCGCTGGGCTCTGCTCTCTCACTCAGGGCAGAGGCTCTGGGCCCCAG 2576
Qy 61 TCTGCCCCGACTCAGCTCCCTCTGTCTGGGTCTCTGACAGTGGTCAACCATCTCC 120
Db 2575 TCTGCCCCGACTCAGCTCCCTCGTCTCGGTCTCTGACAGTGGTCAACCATCTCC 2516
Qy 121 TGCACCTGGAACACGAGTGGTGGTTTATAAATCTCTCTCTGATCAACACAC 180
Db 2515 TGCACCTGGAACAGGCTGAGTGGTGGTTTATAAATCTCTCTCTGATCAACACAC 2456
Qy 181 CCAGGCAAGCCCCCAAACTCATGATTTATGATGTCGTAAGCGGCTCAGGGTCTCT 240
Db 2455 CCAGGCAAGCCCCCAAACTCATGATTTATGATGTCGTAAGCGGCTCAGGGTCTCT 2396
Qy 241 GATCGCTTCTCTGGCTCCAAAGTCTGGCAACAGGCTCCCTGACCATCTCT--GGGCTCCA 299
Db 2395 AATCGCTTCTCTGGCTCCAAAGTCTGGCAACAGGCTCCCTGACCATCTCTGGGCTCCA 2336
Qy 300 GGCTGAGGACGAGCTGATTATTACTGTTTCATATACCAACAGTAGACATTTGTTATT 359
Db 2335 GTCTGACGATGAGGCTGATTATTATTGATGATTTGGCCAAAGTAATGATTATGCTATT 2276
Qy 360 CGGAAGAGGACCGGTTGACCGTCTCTAGGT 390
Db 2275 TGGCGGAGGACCAAGTTGACCGTCTCTAGGT 2245

RESULT 13
US-09-884-441-267
; Sequence 267, Application US/09884441
; Patent No. US20020119158A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C7
; CURRENT APPLICATION NUMBER: US/09/884,441
; CURRENT FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 267
; LENGTH: 548
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(548)

Qy	241	GATCGTTCTCTGGCTCCAGCTGGCAACACGGCTCCCTGACCAATCTCTGGGCTCCAG	300
Db	287	GATCGTTCTCTGGCTCCAGCTGGCAACACGGCTCCCTGACCAATCTCTGGGCTCCAN	346
Qy	301	GCTGAGGACGAGGCTGATTATTACT-GTTGTTCTATATACCAACAGTAGCACTTTGTTATT	359
Db	347	GCTGAGGATGANGCTGATTATTACTGGAAGCTCATATGCGGCAACAACAAATTGGGTGTT	406
Qy	360	CGGAAG-AGGGACCCGGTTGACCGTCTCTAGG	389
Db	407	CGGCGAAGGACCAAGCTGACCGTCTTAAG	437

Search completed: December 30, 2003, 03:42:07
Job time : 565.449 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 170.16 Seconds
(without alignments)
6187.013 Million cell updates/sec

Title: US-09-019-441-1

Perfect score: 390

Sequence: 1 ATGCGCTGGACTCTGCTCCT.....CCCGGTGACCGTCTTAGGT 390

Scoring table: IDENTITY_NUC.

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseq 19Jun03:*

- 1: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
- 2: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
- 3: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
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- 22: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
- 23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
- 24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
- 25: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	390	100.0	390	19 AAV33307	Anti-human CD23 6G
2	334	85.6	605	24 ABK29738	Colon adenocarcino
3	322.4	82.7	1460	25 ABK32194	Human ovarian spec
4	321.2	82.4	891	22 AAC65528	Human immune syste
5	319.6	81.9	902	14 AAQ35100	Antibody D lambda
6	316.4	81.1	889	23 AAS77073	DNA encoding novel
7	313.6	80.4	763	23 AAS83480	DNA encoding novel
8	313.2	80.3	726	25 ABX12863	DNA encoding monoc

9	310	79.5	448	23 AAS77070	DNA encoding novel
10	307.2	78.8	7528	22 ABF30316	Bicistronic idioty
11	307	78.7	387	24 ABX00199	Mouse DNA encoding
12	307	78.7	387	24 ABK71405	DNA encoding throm
13	306.8	78.7	756	23 AAS83477	DNA encoding novel
14	306.8	78.7	866	23 AAS87037	DNA encoding novel
15	305.4	78.3	1636	23 ABV22585	Human prostate exp
16	305.4	78.3	1636	23 ABV28405	Human prostate exp
17	305.2	78.3	453	23 AAS77071	DNA encoding novel
18	303.6	77.8	637	23 AAS77074	DNA encoding novel
19	298.8	76.6	783	23 AAS83483	DNA encoding novel
20	298.6	76.6	414	23 AAS77069	DNA encoding novel
21	297	76.2	863	23 AAS83485	DNA encoding novel
22	295.6	75.8	876	23 AAS83478	Human ovarian carc
23	295.2	75.7	548	21 AAAG9957	Ovarian carcinoma
24	295.2	75.7	548	24 ABN72851	Human prostate exp
c	295.2	75.7	1636	23 ABV22585	Human prostate exp
c	295.2	75.7	1636	23 ABV28405	Human autoantibody
25	292.4	75.0	351	22 AAI68755	Nucleotide sequenc
28	284.8	73.0	5464	25 ABV77130	Nucleotide sequenc
29	284.8	73.0	6877	25 ABV77133	Nucleotide sequenc
30	284.6	73.0	628	14 AQO36134	MH4H7 Mab light ch
31	284.6	73.0	1044	12 AAQ12840	Variable region of
32	284.4	72.9	351	22 AAI68765	Human autoantibody
33	284.4	72.9	726	25 ABZ25504	APRIL binding scfv
34	281.2	72.1	747	21 AAC67868	Recombinant human
35	281.2	72.1	816	24 ABK43226	DNA encoding anti
36	280.8	72.0	333	22 AAH42401	Nucleotide sequenc
37	280.8	72.0	333	22 AAH42407	Nucleotide sequenc
38	278.4	71.4	9071	13 AAQ22491	Human U266 lambda
39	278.4	71.4	9071	13 AAQ23370	U266-Lambda gene a
40	276.8	71.0	792	24 ABX00205	DNA encoding singl
41	276.8	71.0	792	24 ABK71411	DNA encoding singl
42	276.8	71.0	822	24 ABX00208	DNA encoding singl
43	276.8	71.0	822	24 ABK71414	DNA encoding throm
44	275.8	70.7	330	24 ABX00191	Mouse DNA encoding
45	275.8	70.7	330	24 ABK71397	Thrombopoietin (TP

ALIGNMENTS

RESULT 1
AAV33307
ID AAV33307 standard; DNA; 390 BP.

XX AAV33307;

XX AC

XX 25-MAR-2003 (updated)

XX 18-NOV-1998 (first entry)

XX DE Anti-human CD23 6G5 monoclonal antibody light chain variable region DNA.

XX DE Anti-human CD23 6G5 monoclonal antibody; light chain variable region;

XX DE human CD23; IGE; FcεR1i/CD23; gamma-1 constant region;

XX DE gamma-3 constant region; allergy; inflammation; autoimmune disease;

XX DE allergic rhinitis; conjunctivitis; autoimmune haemolytic anaemia; ss.

XX OS Macaca fascicularis

XX OS

XX PH Key Location/Qualifiers

XX FT CDS 1..390

XX FT /tag= a

XX FT /product= "anti-human CD23 6G5 light chain variable

XX FT region"

XX FT /note= "CDS does not contain a stop codon"

XX FT sig_peptide 1..57

XX FT /tag= b

XX FT mat_peptide 58..390

XX FT /tag= c

XX FT misc_feature 124..165

XX FT /tag= d

XX FT /note= "encodes CDR 1 region"

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FT misc_feature 211..231
FT /*tag= e
FT /note= "encodes CDR 2 region"
FT 328..357
FT /*tag= f
FT /note= "encodes CDR 3 region"
XX
XX WO9837099-A1.
XX
XX PD 27-AUG-1998.
XX
XX PF 17-FEB-1998; 98WO-US02253.
XX
XX PR 20-FEB-1997; 97US-0803085.
XX
XX PR 05-FEB-1998; 98US-0019441.
XX
XX PA (IDEC-) IDEC PHARM CORP.
XX
XX PA (SEKG) SEIKAGAKU CORP.
XX
XX PI Klotzer WS, Nakamura T, Reff ME;
XX
XX WPI; 1998-467495/40.
XX
XX DR P-PSDB; AAW70377.
XX
XX PR New anti-human CD23 monoclonal antibody - used for inhibiting IgE
XX
XX PT expression to treat or prevent allergic, inflammatory and
XX
XX PT auto-immune conditions
XX
XX PS Example 1; Pages 102-104; 146pp; English.
XX
XX CC The present sequence represents a DNA sequence encoding the light
XX
XX CC chain variable region of primate monoclonal antibody anti-human CD23 6G5.
XX
XX CC The invention provides primate monoclonal antibodies which specifically
XX
XX CC bind human CD23, the low affinity receptor for IgE (FcεRI/CD23),
XX
XX CC and comprise either of a human gamma-1 or human gamma-3 constant region
XX
XX CC that binds to human Fc gamma receptors and inhibits IgE expression.
XX
XX CC The monoclonal antibodies of the invention are claimed to be useful
XX
XX CC for inhibiting induced IgE production for treating or preventing
XX
XX CC allergic, inflammatory and autoimmune conditions e.g. allergic rhinitis
XX
XX CC conjunctivitis, autoimmune haemolytic anaemia, etc.
XX
XX CC (Updated on 25-MAR-2003 to correct PR field.)
XX
XX SQ Sequence 390 BP; 74 A; 123 C; 96 G; 97 T; 0 other;

Query Match 100.0%; Score 390; DB 19; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.7e-109;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCCTGGACTGCTCCTCGTACCCCTCCTCACTCAGGCGACAGGATCCTGGGCTCAG 60
Db 1 ATGGCCTGGACTGCTCCTCGTACCCCTCCTCACTCAGGCGACAGGATCCTGGGCTCAG 60
Qy 61 TCTGCCCGGACTCAGCCTCCCTCTGTGCTGGGTCTCCTGGACAGTCGGTCACCATCTCC 120
Db 61 TCTGCCCGGACTCAGCCTCCCTCTGTGCTGGGTCTCCTGGACAGTCGGTCACCATCTCC 120
Qy 121 TGCACCTGAACACAGGATGAGCTGGTGGTTATTAACCTATGCTCTCTGTATCAACACAC 180
Db 121 TGCACCTGAACACAGGATGAGCTGGTGGTTATTAACCTATGCTCTCTGTATCAACACAC 180
Qy 181 CCAGCAAGGCCCCCAACTCATGATTTATCATGTCGCTAAGCGGGCTCAGGGGTCTCT 240
Db 181 CCAGCAAGGCCCCCAACTCATGATTTATGATGTCGCTAAGCGGGCTCAGGGGTCTCT 240
Qy 241 GATCGCTTCTCTGGTCCCAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTCCAG 300
Db 241 GATCGCTTCTCTGGTCCCAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTCCAG 300
Qy 301 GCTGAGGACGAGGCTGATTTATCTGTTGTTTCATATACAACAGTAGACATTTGTTATTC 360
Db 301 GCTGAGGACGAGGCTGATTTATCTGTTGTTTCATATACAACAGTAGACATTTGTTATTC 360
Qy 361 GGAAGAGGGACCCGGTTGACCGTCTAGGT 390

```

```

Db 361 GGAAGAGGGACCCGGTTGACCGTCTAGGT 390
|||||
RESULT 2
ABK29738
ID ABK29738 standard; cDNA; 605 BP.
XX
XX AC ABK29738;
XX
XX DT 23-APR-2002 (first entry)
XX
XX DE Colon adenocarcinoma-specific cDNA #264.
XX
XX KW Human; colon adenocarcinoma; colon cancer; tumour; gene; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200196389-A2.
XX
XX PD 20-DEC-2001.
XX
XX PF 07-JUN-2001; 2001WO-US18574.
XX
XX PR 09-JUN-2000; 2000US-210667P.
XX
XX PR 22-NOV-2000; 2000US-252614P.
XX
XX PA (CORI-) CORIXA CORP.
XX
XX PI Meagher MJ, King GE, Xu J, Secrist H;
XX
XX WPI; 2002-098052/13.
XX
XX PT New isolated polynucleotide encoding a polypeptide comprising a portion
XX
XX PT of colon tumour protein, for detection, diagnosis and therapy of human
XX
XX PT colon cancer
XX
XX PS Claim 1; Page 181-182; 21pp; English.
XX
XX CC The invention relates to an isolated polynucleotide (I) encoding a
XX
XX CC polypeptide (II) comprising a portion of a colon tumour protein. A new
XX
XX CC oligonucleotide (III) that hybridises to (I) is useful for
XX
XX CC determining the presence of a cancer in a patient. (II) or antigen
XX
XX CC presenting cells expressing (I) are useful for stimulating and/or
XX
XX CC expanding T cells specific for a tumour protein, by contacting T cells
XX
XX CC with (I), (II) or antigen-presenting cells that express (I). (I), (II),
XX
XX CC or antigen presenting cells that express (II) are useful for treating
XX
XX CC colon cancer in a patient by incubating CD4+ and/or CD8+ T cells isolated
XX
XX CC from a patient with (I), (II), or antigen presenting cells that express
XX
XX CC (II), so that T cells proliferate, and administering to the patient an
XX
XX CC effective amount of the proliferated T cells, thus inhibiting the
XX
XX CC development of a cancer in the patient. A new composition is useful for
XX
XX CC stimulating an immune response in a patient. (I) or (II) is useful in
XX
XX CC vaccines and pharmaceutical compositions for prevention and treatment of
XX
XX CC colon cancer and for the diagnosis and monitoring of the cancers. (I),
XX
XX CC (II) or an antibody against (II) is useful for detection, diagnosis and/
XX
XX CC or therapy of human colon cancer. (I) is useful as a probe or primer for
XX
XX CC nucleic acid hybridisation, and in the design and preparation of ribozyme
XX
XX CC molecules for inhibiting expression of (II) in tumour cells. ABK29475-
XX
XX CC ABK29851 represent human colon adenocarcinoma-specific cDNA sequences of
XX
XX CC the invention.
XX
XX SQ Sequence 605 BP; 123 A; 198 C; 154 G; 128 T; 2 other;

Query Match 85.6%; Score 334; DB 24; Length 605;
Best Local Similarity 91.0%; Pred. No. 2.9e-92;
Matches 355; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Qy 1 ATGGCCTGGACTGCTCCTCGTACCCCTCCTCACTCAGGCGACAGGATCCTGGGCTCAG 60
Db 33 ATGGCCTGGGCTCTGCTATTCTCCTACCTCCTCACTCAGGCGACAGGATCCTGGGCTCAG 92
Qy 61 TCTGCCCGGACTCAGCCTCCCTCTGTGCTGGGTCTCCTGGACAGTCGGTCACCATCTCC 120

```


Qy	241	GATCGCTTCTCGGCTCCAAAGTGTGGCGAACGGCGCTCCCTGACCAATCTCTGGGCTCCAG	300
Db	256	GATCGCTTCTCGGCTCCAAAGTGTGGCGAACGGCGCTCCCTGACCAATCTCTGGGCTCCAG	315
Qy	301	GCTGAGGACGAGCTGATTATTACTGTGTTGTTTCATATACACCAAGTAGCAC-----TTTGT	354
Db	316	GCTGAGGATGAGCTGATTATTACTGTGCTCATATGAGGCGATACACCCGGCGGTG	375
Qy	355	TTATTTCGNAAGGAGACCGGTGACCGTCTCAGGT	390
Db	376	GTTTTTCGGCGGAGGACCAAGTGAACGCTCTCAGGT	411

RESULT 9

RD001 2
AAS77070

ID AAS77070 standard; cDNA: 448 BP.

AC AAS77070:

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #12874.

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

30-MAR-2001; 2001WO-US08631.

31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI: 2001-639362/73.

DR P-PSDB; ABG12883.

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -

PS Claim 1; SEQ ID No 12874; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published pct sequences.

XX

Seq	Sequence	448 BP;	89 A;	142 C;	113 G;	104 T;	0 other;
Query Match	79.5%;	Score	310;	DB	23;	Length	448;
Best Local Similarity	87.2%;	Pred. NO.	5.9e-85;				
Matches	340;	Conservative	0;	Mismatches	50;	Indels	0;
Gaps							
Qy	1	ATGGCTGTGACTGTGCTCTCTGTCACCCCTCTCACTCAGGCGACAGATCCTCGGCTCAG	60				
Db	48	ATGGCTTGGGCTCTGCTGCTCTCACTCTCTCTCACTGAGCACAGGTCCTGGGCCAG	107				
Qy	61	TCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTTGGACAGTCGGTTCACCATCTCC	120				
Db	108	TCTGCCCCTGACTCAGCCTGCCTCCGCTCTGGGTCTCTTGGACAGTCGATCACCATCTCC	167				
Qy	121	TGCACCTGGAAACACAGCATGACGTTGGTGGTTATACTATGTCTCTGGTACCAACACCAC	180				
Db	168	TGCACCTGGAAACACAGCAGTGATGTTGGAAATATTAACCTTGTCTCTGGTACCAACAGCAC	227				
Qy	181	CCAGGCCAAAGCCCCCAAACTCATGATTTATGATGTGCTTAAGCGGGCCTCAGGGGTCTCT	240				
Db	228	CCAGGCCAAAGCCCCCAAACTCATATTTATGAGGGCAGTAAGCGCCCTCAGGATTTCT	287				
Qy	241	GATCGCTTCTCTGGCTCCAAAGTCTGGGAACAACGGCCCTCCCTGACCAATCTCTGGGCTCCAG	300				
Db	288	AGTCGCTTCTCTGGCTCCAAAGTCTGGGAACAACGGCCCTCCCTGACCAATGTCTGGGCTCCAG	347				
Qy	301	GCTGAGGACGAGGCTCATATTACTGTGTTTACATACAAACAGTAGTAGCATTTGTTATTTC	360				
Db	348	GCTGAGGACGAGGCTGATTTACTGCTGCTCTCATATGACAGTAGTAGCATTTATGCTTTC	407				
Qy	361	GGAAAGGACCCGGTTGACCGGTCCTTAGGT	390				
Db	408	GGACCTTGGGACCAAGGTCACCGTCTTAGGT	437				

RESULT 10

AAAF30316

ID AAF30316 standard; cDNA; 7528 BP.

AC AAF30316;

14-MAY-2001 (first entry)

XX
DE
Bicistronic idiotypic plasmid VR1642.

AA Flt-3 ligand; Fms-like tyrosine kinase; mouse; human; vaccine;
 KW immunotherapy; therapy; tumour; lymphoma; gene therapy; VR1642;
 KW plasmid VAXIP; antibody; idiotype; vector; ss.

OS Chimeric - Cytomegalovirus.

OS Chimeric - *Cycomegavovirus*
OS Chimeric - *Mus musculus*.

OS Chimeric - Homo sapiens.

OS Chimeric - Bos taurus.

PN WO200109303-A2.

08-FEB-2001

XX
PF
31-III-2000-2000WO-IIS20679

XX
PR 30-JUL-1999: 99US-0146170-

XX (VTCAL-) VTCAL- TNC.

XX
PT
Hermann CG:XX
WPB: 2001-123319/13

Immunogenic compositions comprising Flt-3 ligand encoding polynucleotide and one or more antigen, or cytokine encoding polynucleotides, useful for suppressing tumour growth and for treating autoimmune diseases (e.g. rheumatoid arthritis) -

Search completed: December 29, 2003, 16:25:33
Job time : 172.16 secs

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XX 20-FEB-2001; 2001WO-US05171.
XX 17-FEB-2000; 2000US-183319P.
XX 16-MAR-2000; 2000US-189862P.
XX 25-MAY-2000; 2000US-207454P.
XX 09-JUN-2000; 2000US-211314P.
XX 18-JUL-2000; 2000US-219007P.
XX 13-DEC-2000; 2000US-255281P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
XX Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer -
XX
XX Claim 1; Page 3949; 11750pp; English.
XX The invention relates to an isolated nucleic acid molecule (I) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX specification or its complement. (I) is useful for:
XX (a) assessing whether a patient is afflicted with prostate cancer;
XX (b) monitoring the progression of prostate cancer in a patient;
XX (c) assessing the efficacy of a test compound to inhibit prostate
XX cancer in a patient;
XX (d) assessing the efficacy of a therapy for inhibiting prostate cancer
XX in a patient;
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX (f) assessing the prostate cell carcinogenic potential of a compound;
XX (g) determining whether prostate cancer has metastasized in a patient;
XX (h) assessing the aggressiveness or indolence of prostate cancer in a
XX patient;
XX (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
XX Sequence 1636 BP; 345 A; 470 C; 479 G; 342 T; 0 other;
XX
Query Match      78.3%; Score 305.4; DB 23; Length 1636;
Best Local Similarity 89.2%; Pred. No. 2.5e-83;
Matches 354; Conservative 0; Mismatches 36; Indels 7; Gaps 2;
Qy      1  ATGGCCCTGGACTCTGCTCCCTCGTCACCTCTCACTCAGGGCAGGATCTGGGCTCAG 60
Db      |||||
Qy      60  ATGGCCCTGGGCTCTGCTGCTCCTCACCCTCTCACTCAGGGCAGGATCTGGGCTCAG 119
Db      |||||
Qy      61  TCTGCCCCGACTCAGCCTCCCTCTGTCTCTGGGTCTCTGGACAGTCGGTCACCATCTCC 120
Db      |||||
Qy      120  TCTGCCCTGACTCAGCCTGCTCGTCTCTGGGTCTCTGGACAGTCGATCACCATCTCC 179
Db      |||||
Qy      121  TGCATCGGAACCGAGTAGAGTTGGTGGTTATAA-CTATGTCTCTGGTACCAACCA 179
Db      |||||
Qy      180  TGCATCGGAACCGAGTAGAGTTGGGCGTTATAACCTATGTCTCTCTGGTATCAACA 239
Db      |||||
Qy      180  CCCAGGCAAGCCCAACCTCATGATTATGATGCTGCTAAGCGGGCTCAGGGTCTC 239
Db      |||||
Qy      240  CCCAGGCAAGCCCAACCTCATGATTATGATGCTGAGTATCGGGCTCAGGGGTTT 299
Db      |||||
Qy      240  TGATCGCTTCTCTGGCTCCAAAGTCTGGCAACACAGGCTCCCTGACCATCTCTGGGCTCCA 299
Db      |||||
Qy      300  TATCGCTTCTCTGGCTCCAAAGTCTGGCAACACAGGCTCCCTGACCATCTCTGGGCTCCA 359
Db      |||||
Qy      300  GGCTGAGGACGAGGCTGATTATTACTGTGTTTCATATACCAACAGTAGCACT-----TT 353
Db      |||||
Qy      360  GGCTGAGGACGAGGCTGATTATTACTGCAGCTCATATACAAGCAGCAGCACTCTCTCTATT 419
Db      |||||
Qy      354  GTTATTCGGAAGAGGGACCGGTTGACCGTCTTAGGT 390
Db      |||||
Qy      420  TGTCTTCGGAACCTGGGACCAAGGTACCCGCTCTAGGT 456
Db      |||||
```

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 1752.27 Seconds
(without alignments)
9875.644 Million cell updates/sec

Title: US-09-019-441-2

Perfect score: 423

Sequence: 1 ATGAACACCTGTGCTTCTT.....TCCTGGTCACCGTCTCTCTCA 423

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

15: em.ba.*

16: em.fun.*

17: em.hum.*

18: em.in.*

19: em.mu.*

20: em.om.*

21: em.or.*

22: em.ov.*

23: em.pat.*

24: em.ph.*

25: em.pl.*

26: em.ro.*

27: em.sts.*

28: em.un.*

29: em.vi.*

30: em.htg.hum.*

31: em.htg.inv.*

32: em.htg.other.*

33: em.htg.mus.*

34: em.htg.pln.*

35: em.htg.rod.*

36: em.htg.mam.*

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38: em.sy.*

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40: em.htgo.mus.*

41: em.htgo.other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	328.6	77.7	435	9	AF416358 Papio cyn
2	327	77.3	441	9	AF416359 Papio cyn
3	323.8	76.5	420	9	MMU57560 Macaca mula
4	319	75.4	420	9	MMU57565 Macaca mula
5	318.2	75.2	411	9	MMU57563 Macaca mula
6	315.6	74.6	423	9	HSIGHXX28
7	314.6	74.4	414	9	MMU57568 Macaca mula
8	313.2	74.0	1431	6	AR108867 Sequence
9	313.2	74.0	1431	6	AR265201 Sequence
10	313.2	74.0	1431	6	BD063039 Identific
11	312.4	73.9	426	9	AF062120 Homo sapi
12	311	73.5	420	9	HSIGHXX25
13	310	73.3	420	9	HUMIGHRH
14	309.8	73.2	468	9	HUMIGHZF
15	305.6	72.2	414	9	HST2X26
16	305	72.1	414	9	HSIGHXX23
17	303.4	71.7	435	9	MMU57566 Macaca mula
18	302.8	71.6	423	9	AF174036
19	301.8	71.3	432	9	HSIGHXX26
20	301.2	71.2	423	9	HSIGHXX20
21	299.8	70.9	1404	6	AR135375 Sequence
22	299.8	70.9	1404	6	AR135376 Sequence
23	299.8	70.9	1404	6	AR135377 Sequence
24	299.6	70.8	423	9	AF062258 Homo sapi
25	298.6	70.8	486	9	AF417843 Homo sapi
26	298.6	70.6	423	9	HST14X12
27	298.2	70.5	423	6	AR008995 Sequence
28	298.2	70.5	423	6	I61194 Sequence 19
29	298.2	70.5	423	6	I78743 Sequence 19
30	298.2	70.5	453	9	HSE5444
31	298.2	70.5	2149	9	BC011857 Homo sapi
32	297.6	70.4	447	9	AF416357 Papio cyn
33	297	70.2	423	9	HST14X24
34	296.6	70.1	429	9	AF062232 Homo sapi
35	296.6	70.1	481	6	BD182342 Ant1 CD40
36	296.4	70.1	619	6	AX427527 Sequence
37	295.2	69.8	420	6	AR006813 Sequence
38	295.2	69.8	420	6	AR135372 Sequence
39	295.2	69.8	420	6	I71325 Sequence 10
40	295	69.7	420	9	AF062220 Homo sapi
41	294.8	69.7	423	9	HSIGHXX29
42	294.8	69.7	426	9	AF062278 Homo sapi
43	294.6	69.6	416	9	HSIGHXX27
44	292.4	69.1	1431	6	AR108863 Sequence
45	292.4	69.1	1431	6	AR265197 Sequence

ALIGNMENTS

RESULT 1
AF416358
LOCUS
DEFINITION
ACCSSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

AF416358
Papio cynocephalus anubis clone VH4-4 immunoglobulin heavy chain
variable region mRNA, partial cds.
AF416358
AF416358.1 GI:19744277
Papio anubis (olive baboon)
Papio anubis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
Cercopitheciinae; Papio.
1 (bases 1 to 435)
Scincariello,F., Jayashankar,L. and Attanasio,R.

435 bp
mRNA
linear
PRI 27-MAR-2002

Pred. No. is the number of results predicted by chance to have a


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Db      178  CCAGGAGGGCGTGGAGTGGGAGTATCTATGTAGTGTGGGAGCACCGAATAC 237
Qy      241  AACCGTCCCTCAAGAGTCGAGTCATATTTTCAACAAGACAGTCACGAACACGATTTCTCC 300
Db      238  AACCCCTCCCTCAAAAGTCGAGCCACCATTTTCAAGAGACACAGTCACGAACACGATTTCTCC 297
Qy      301  CTGACCTGAACCTGTGACCGCGCGACACGCGGCGTGTATTCTGTGCGCAGAGATTGG 360
Db      298  CTGAAGGTGAGCTCTGTACCGCGCGGACACGCGCGTGTATTCTGTGCGGAGGAGAC 357
Qy      361  GCCCAATAGCTGGAACACGCTAGGCTTCTGGGCGCAGGAGTCCTGGTCAACCGTCTCC 420
Db      358  TACAGTACCACTGTGTACTTTCGAGTTCCTGGGCGCAGGCGCGCTGTGTACCGTCTCC 417
Qy      421  TCA 423
Db      418  TCA 420

RESULT 5
MMU57563
LOCUS      411 bp mRNA linear PRI 11-FEB-1998
DEFINITION Macaca mulatta Ig rearranged heavy chain variable region, anti-RBC
ACCESSION U57563
VERSION   U57563.1 GI:1575073
KEYWORDS  antibody, mRNA, partial cds.
SOURCE    Macaca mulatta (rhesus monkey)
ORGANISM  Macaca mulatta
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopitheciinae; Macaca.
REFERENCE 1 (bases 1 to 411)
AUTHORS   Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Roubinet,F.,
          Blacher,A. and Capra,J.D.
TITLE     Variable region gene segment utilization in rhesus monkey
          hybridomas producing human red blood cell-specific antibodies:
          predominance of the VH4 family but not VH4-21 (V4-34)
JOURNAL   Mol. Immunol. 34 (3), 237-253 (1997)
MEDLINE   97368199
PUBMED    9224966
REFERENCE 2 (bases 1 to 411)
AUTHORS   Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Blacher,A.
          and Capra,J.D.
TITLE     Direct Submission
JOURNAL   Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center,
          University of Texas Southwestern Medical Center, 6000 Harry Hines
          Blvd., Dallas, TX 75235-9140, USA
FEATURES  Location/Qualifiers
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            1..411
             /organism="Macaca mulatta"
             /mol_type="mRNA"
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             /note="hybridoma 1B4"
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            1..>411
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             /db_xref="GI:1575074"
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BASE COUNT 81 a 124 c 115 g 91 t
ORIGIN
Query Match 75.2%; Score 318.2; DB 9; Length 411;
Best Local Similarity 88.2%; Pred. No. 1.2e-75;
Matches 373; Conservative 0; Mismatches 38; Indels 12; Gaps 2;
Qy      1  ATGAACACCTGTGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCCAG 60
Db      1  ATGAACACCTGTGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCCAG 60

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Qy      61  CTGCAGTCGAGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCTCCCTCACC 120
Db      61  GTGCAGTCGAGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCTCCCTCACC 120
Qy      121  TGCCTGTCTCTCTGTGGTCTGTGCAGCAGTAGTAACCTGTGGACCTTGGATCCGCGACGCC 180
Db      121  TGCCTGTCTCTCTGTGGTCT---CATCAGCAGTAACCTACTTGGAGCTGGATCCGCGACGCC 177
Qy      181  CCAGGAGGAGGAGTCGGAGTGGATGGACGTATCTCTGGTAGTGGTGGGGCCACCACTAC 240
Db      178  CCAGGAGGAGGAGTCGGAGTGGATTTGGAGCTTTCTATGGTACTAGTGGAGGACCTACTAT 237
Qy      241  AACCCGTCCTCAAGAGTCGAGTCATCATTTTCAACAACACGTCCTCAAGAACCACTTCTCC 300
Db      238  AACCCCTCCCTCAGAGTCGAGTCACCATTTTCAACAGACAGTCCCAAGAACCACTTCTCC 297
Qy      301  CTGAACCTGAACCTCTGTGACCGCGCGGACACCGCGCTGTATTACTCTGTGCAGAGATTGG 360
Db      298  CTGAAGCTGAGCTCTGTGACCGCGCGGACACCGCGCTGTATTACTCTGTGCAGGATAT--- 354
Qy      361  GCCCAATAGCTGGAACACGCTAGGCTTCTGGGCGCAGGAGTCCTGGTCAACCGTCTCC 420
Db      355  -----ACAGTAAGTAAGGCTTTTGACTCTGGGCGCAGGAGTCTTGGTCAACCGTCTCC 408
Qy      421  TCA 423
Db      409  TCA 411

RESULT 6
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LOCUS      423 bp mRNA linear PRI 26-JUL-1997
DEFINITION H.sapiens mRNA for XLA IG heavy chain VDJ region (LE 4-8).
ACCESSION X65910 S58678
VERSION   X65910.1 GI:395108
KEYWORDS  diversity region; Ig heavy chain; immunoglobulin; joining region;
          variable region.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 423)
AUTHORS   Schiff,C.
TITLE     Direct Submission
JOURNAL   Submitted (08-APR-1992) C. Schiff, Centre D'Immunologie de
          Marseille, Case 906, 13288 Marseille, Cedex 9, FRANCE
REFERENCE 2 (bases 1 to 423)
AUTHORS   Milili,M., Le Deist,F., de Saint-Basile,G., Fischer,A.,
          Fougereau,M. and Schiff,C.
TITLE     Bone marrow cells in X-linked agammaglobulinemia express
          pre-B-specific genes (lambda-like and V pre-B) and present
          immunoglobulin V-D-J gene usage strongly biased to a fetal-like
          repertoire
JOURNAL   J. Clin. Invest. 91 (4), 1616-1629 (1993)
MEDLINE   93232287
PUBMED    8473505
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           misc_feature 378..423
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 Db 241 AACCGTCCCTCAGAGTCGAGTCATCATTTTCAAGACAGCTCCAGAACCACTTCTCC 300
 Qy 301 CTGAACCTGAACCTCTGTGACCGCGGACACGCGCGTGTATTACTGTGCGAGAGATTGG 360
 Db 301 CTGAAGCTGAACCTCTATACCGCGCGGACACGCGCGTGTATTACTGTGTGAGAGATCGT 360
 Qy 361 GCCCAATAGCTGGACAA-----CGTAGGCTTCTGGGGCCAGGAGTC 405
 Db 361 CTTTTCAGTGTGGAAATGGTTTACAACTGGTTTCGATGTCGTGGGGCCCGGAGTC 420
 Qy 406 CTGCTACCGTCTCTCTCA 423
 Db 421 CTGGTCACCGTCTCTCTCA 438

RESULT 11
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 LOCUS AF062120 426 bp mRNA linear PRI 08-MAY-2001
 DEFINITION Homo sapiens clone 21u-39 immunoglobulin heavy chain variable region (IGH) mRNA, partial cds.
 ACCESSION AF062120
 VERSION AF062120.1 GI:3170702
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 426)
 AUTHORS Wang, X. and Stollar, B.D.
 TITLE Immunoglobulin VH gene expression in human aging
 JOURNAL Clin. Immunol. 93 (2), 132-142 (1999)
 MEDLINE 99459182
 PUBMED 10527689
 REFERENCE 2 (bases 1 to 426)
 AUTHORS Wang, X. and Stollar, B.D.
 TITLE Direct Submission
 JOURNAL Submitted (22-APR-1998) Biochemistry Department, Tufts University School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA
 FEATURES
 Location/Qualifiers
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 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
 /chromosome="14"
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 /clone="21u-39"
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 1. >426
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Matches 369; Conservative 0; Mismatches 51; Indels 6; Gaps 2;
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 Db 61 GTGCAGCTGCAGGAGTGGGCCCCAGGAGTGGTGAAGCTTTCGGAGACCTGTGCTCCAC 120
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 Db 121 TGGCTGTCTCTGGTGGTCCATCAGCAGTAGTAACCTGGTGGAGTGGGTCCGCCAGCCC 180
 Qy 181 CCAGGGAAGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAACTAC 240
 Db 181 CCAGGGAAGGCTGGAGTGGATTGGGAATCTATCATTA---GTGGAGACCAACTAC 237
 Qy 241 AACCCGTCCCTCAAGAGTCGAGTCATCATTTTCAAGACACGTCCTCAAGAACCACTTCTCC 300
 Db 238 AACCCGTCCCTCAAGAGTCGAGTCATCATTTTCAAGAACCACTTCTCTCC 297
 Qy 301 CTGAACCTGAACCTCTGTGACCGCGGACACGCGCGTGTATTACTGTGCGAGAGATTGG 360
 Db 298 CTGAAGCTGAGCTCTGTGACCGCGGACACGCGCGTGTATTACTGTGCGAGAGAGCCCC 357
 Qy 361 GCCCAATAGCTGGAAACACG---CTAGGCTTCTGGGGCCAGGAGTCTCTGGTCCACGTC 417
 Db 358 CCGACTACCGTGGTACAGTACTTTGACTACTGGGGCCAGGAAACCTTGGTCCACGTC 417
 Qy 418 TCCTCA 423
 Db 418 TCCTCA 423
 RESULT 12
 HSIHGX25
 LOCUS HSIHGX25 420 bp mRNA linear PRI 26-JUL-1997
 DEFINITION H. sapiens mRNA for XLA IG heavy chain VDJ region (LE 4-5).
 ACCESSION X65907.58702
 VERSION X65907.1 GI:395105
 KEYWORDS diversity region; Ig heavy chain; immunoglobulin; joining region; variable region.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 420)
 AUTHORS Schiff, C.
 TITLE Direct Submission
 JOURNAL Submitted (08-APR-1992) C. Schiff, Centre D'Immunologie de Marseille, Case 906, 13288 Marseille, Cedex 9, FRANCE
 REFERENCE 2 (bases 1 to 420)
 AUTHORS Millili, M., Le Deist, F., de Saint-Basile, G., Fischer, A., Fougereau, M. and Schiff, C.
 TITLE Bone marrow cells in X-linked agammaglobulinemia express pre-B-specific genes (lambda-like and v pre-B) and present immunoglobulin V-D-J gene usage strongly biased to a fetal-like repertoire
 J. Clin. Invest. 91 (4), 1616-1629 (1993)
 JOURNAL 93232287
 MEDLINE
 PUBMED 8473505
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 /db_xref="taxon:9606"
 /chromosome="14"
 /clone="LE 4-5"
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 /tissue_type="bone marrow"
 /clone_lib="LE library"
 1. 57
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 1830.37 Seconds
(without alignments)
5616.780 Million cell updates/sec

Title: US-09-019-441-2
Perfect score: 423
Sequence: 1 ATGAACACCTGTGTTCTT.....TCTGTGTCACCGTCTCCTCA 423

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

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5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_est3:*

12: gb_est4:*

13: gb_est5:*

14: gb_est6:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	301.6	71.3	453	9 AW402337	AW402337 UI-HF-BK0
2	301.4	71.3	502	13 BX283435	BX283435 BX283435
3	301.4	71.3	862	10 BG397580	BG397580 602438620
4	299	70.7	867	10 BG685428	BG685428 602637281

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

5	297.4	70.3	890	13	BX324929	BX324929
6	297.4	70.3	1036	13	BQ072430	BQ072430 AGENCOURT
7	294.8	69.7	925	13	BQ710876	BQ710876 AGENCOURT
8	294	69.5	921	13	BQ710000	BQ710000 AGENCOURT
9	293.8	69.5	532	2	HSM070357	BX480350 Homo sapi
10	292.6	69.2	1201	13	BX377045	BX377045 BX377045
11	291.8	69.0	467	14	CB138507	CB138507 K-EST0191
12	291.8	69.0	527	14	CB147325	CB147325 K-EST0203
13	291.8	69.0	537	14	CB135937	CB135937 K-EST0188
14	291.8	69.0	552	14	CB135635	CB135635 K-EST0187
15	291.8	69.0	574	14	CB148794	CB148794 K-EST0205
16	291.8	69.0	588	14	CB146592	CB146592 K-EST0202
17	291.8	69.0	600	14	CB135761	CB135761 K-EST0188
18	291.8	69.0	603	14	CB121483	CB121483 K-EST0169
19	291.8	69.0	607	14	CB135254	CB135254 K-EST0187
20	291.6	68.9	939	13	BQ708070	BQ708070 AGENCOURT
21	290.8	68.7	1058	13	BX337642	BX337642 BX337642
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23	290.8	68.7	1201	13	BX396323	BX396323 BX396323
24	290.8	68.7	1201	13	BX399725	BX399725 BX399725
25	290.8	68.7	1201	13	BX439041	BX439041 BX439041
26	290.2	68.6	798	12	BI771905	BI771905 603058919
27	290	68.6	1050	9	AL552672	AL552672 AL552672
28	288.6	68.2	501	14	CB133184	CB133184 K-EST0183
29	288.4	68.2	850	10	BG686474	BG686474 602637417
30	288.4	68.2	1019	13	BQ072420	BQ072420 AGENCOURT
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32	286.8	67.8	680	14	CB551642	CB551642 WMS00006
33	286.8	67.8	904	13	BQ710488	BQ710488 AGENCOURT
34	286.8	67.8	1201	13	BX399940	BX399940 BX399940
35	286.6	67.8	955	13	BQ711653	BQ711653 AGENCOURT
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37	285.4	67.5	820	12	BI770055	BI770055 603053578
38	285.2	67.4	915	13	BQ711871	BQ711871 AGENCOURT
39	285.2	67.4	923	13	BQ707945	BQ707945 AGENCOURT
40	285.2	67.4	928	13	BQ707875	BQ707875 AGENCOURT
41	285.2	67.4	959	13	BQ709473	BQ709473 AGENCOURT
42	285	67.4	680	10	BG684306	BG684306 602636046
43	285	67.4	977	13	BX396901	BX396901 BX396901
44	285	67.4	1201	13	BX336959	BX336959 BX336959
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ALIGNMENTS

RESULT 1:
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LOCUS UI-HF-BK0-aal-c-02-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
DEFINITION IMAGE:3053955 5', mRNA sequence.
ACCSSION AW402337
VERSION AW402337.1 GI:6921023
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 453)
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.


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QY 301 CTGAACCTGAACTCTGTGACCGCCCGGACACAGCGCGGTGTATTACTGTGCGAGAGATTGG 360
DB 321 CTGAAGCTGAGTCTGTGACCGCCCGGACACAGCGCGGTGTATTACTGTGCGAGAGTTGGG 380
QY 361 GCCAAATAGCTGGAACACGCTAGCTTCTGGGCGCAGGGAGTCTCTGTCACGCTCTCC 420
DB 381 AGACATCTACTACTA--CGGTATGACGCTGTGGGCGCAAGGACACCGGTCAACGCTCTCC 438
QY 421 TCA 423
DB 439 TCA 441

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LOCUS BX324929 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS01086YJ13 5-PRIME, mRNA sequence.
ACCESSION BX324929
VERSION BX324929.1 GI:30338413
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 890)
AUTHORS Li.W.B., Gruber.C., Jessee.J. and Polayes.D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7198.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0A1086CE07QPl&cluster=7198.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0A1086CE07QPl.
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/notes="1st strand cDNA was primed with a NotI-oligo(dT)
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sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 186 a 291 c 236 g 177 t
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Best Local Similarity 87.2%; Pred. No. 3.6e-65;
Matches 374; Conservative 0; Mismatches 46; Indels 9; Gaps 4;
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DB 418 TGTAGTGGTATAGCTCTACCTCGCCTTTGACTACTTGGGCGCCAGGGAACCTGTGCCACC 477
QY 415 GTCTCCTCA 423
DB 478 GTCTCCTCA 486

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5', mRNA sequence.
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VERSION BX072430.1 GI:19901476
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1036)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: csapsb-@email.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI2810 row: h column: 21
High quality sequence stop: 626.
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/lab_host="DH10B"
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/notes="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
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anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."

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products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells *E. coli* Top10F' with electroporation method."

BASE COUNT 106 a 180 c 148 g 118 t
ORIGIN

Query Match 69.0%; Score 291.8; DB 14; Length 552;
Best Local Similarity 83.9%; Pred. No. Be-64; 62; Indels 6; Gaps 2;
Matches 355; Conservative 0; Mismatches 62; Indels 6; Gaps 2;

QY 1 ATGAACACCTGTGGTTCTTCTCTCTGTCGAGCTCCAGATGGTCTCTGCCAG 60
Db ATGAACACCTGTGGTTCTTCTCTCTGTCGAGCTCCAGATGGTCTCTGCCAG 98

QY 61 CTGCAGCTGCAGAGTCGGGCCAGAGTGTGAAGCCTTGGAGACCTGTCCCTCACC 120
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QY 121 TCGCGTGTCTGTGGGTCTGTACAGTACTGAGTGTGACCTGTGGAGCCTGTCCCTCACC 180
Db TCGCGTGTCTGTGGGTCTGTACAGTACTGAGTGTGACCTGTGGAGCCTGTCCCTCACC 218

QY 181 CCAGGGAAGGAGTGGAGTGGATGGAGCTATCTCTGTGTAGTGGTGGGCCCAACCACTAC 240
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Db AACCGTCTCTCAAGAGTCGAGTATCATTTTCAAGAGTCAAGAACCACTCTCTCT 335

QY 301 CTGAACCTGAACTCTGTACCGCCGACACGCGGTGTTATCTGTGCGCAGAGATTGG 360
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QY 361 GCCCAATAGTGGAAACACGCTAGGCTTCTGGGGCCAGGGAGTCTCTGTCCACCGTCTCC 420
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QY 421 TCA 423
Db 453 TCA 455

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5', mRNA sequence.
ACCESSION CB148794
VERSION CB148794.1 GI:28131443
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 574)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
21C Frontier Korean EST Project 2001
JOURNAL Unpublished
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel.: +82-42-860-4470
Fax: +82-42-860-4409

Email: yongseung@mail.kribb.re.kr
Plate: 21 row: A column: 09
High quality sequence stop: 574.
Location/Qualifiers
1. 574
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L7N800102s1-21-A09"
/sex="M"
/lab_host="Top10F'"
/clone_lib="L7N800102s1"
/note="Organ: Liver; Vector: pcNS-D2; Site.1: EcoRI;
Site.2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with *E. coli* DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells *E. coli* Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 - 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promoter as 5' primer and N(dt)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells *E. coli* Top10F' with electroporation method."

FEATURES

source

BASE COUNT 111 a 188 c 154 g 121 t
ORIGIN

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Best Local Similarity 83.9%; Pred. No. 8.1e-64;
Matches 355; Conservative 0; Mismatches 62; Indels 6; Gaps 2;

QY 1 ATGAACACCTGTGGTTCTTCTCTCTGTCGAGCTCCAGATGGTCTCTGCCAG 60
Db ATGAACACCTGTGGTTCTTCTCTCTGTCGAGCTCCAGATGGTCTCTGCCAG 98

QY 61 CTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCCGAGACCTGTCCCTCACC 120
Db GTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCCGAGACCTGTCCCTCACC 158

QY 121 TCGCCTGTCTGTGGTCTGTGACGAGTACTGTTGGACCTGTGGACCTGGACGCC 180
Db TCGCCTGTCTGTGGTCTGTGACGAGTACTGTTGGACCTGTGGACCTGGACGCC 218

QY 181 CCAGGGAAGGAGTGGAGTGGATGGAGCTATCTCTGTGTAGTGGTGGGCCCAACCACTAC 240
Db CCAGGGAAGGAGTGGAGTGGATGGAGCTATCTCTGTGTAGTGGTGGGCCCAACCACTAC 275

QY 241 AACCGTCTCTCAAGAGTCGAGTATCATTTTCAAGACAGCTCAAGAACCACTCTCC 300
Db AACCGTCTCTCAAGAGTCGAGTATCATTTTCAAGAGTCAAGAACCACTCTCTCT 335

QY 301 CTGAACCTGAACTCTGTGACCGCCGACACGCGGTGTTATCTGTGCGCAGAGATTGG 360
Db CTGAACCTGAACTCTGTGACCGCCGACACGCGGTGTTATCTGTGCGCAGAGATTGG 395

QY 361 GCCCAATAGTGGAAACACGCTAGGCTTCTGGGGCCAGGGAGTCTCTGTCCACCGTCTCC 420

Db 396 TCGCCTCGGACTG---GTGCTTTGACCTCTGCGGCCAGGAGACCTGTGTACCGTCTCC 452
Qy 421 TCA 423
Db 453 TCA 455

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Job time : 1834.37 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 184.558 Seconds
(without alignments)
6187.013 Million cell updates/sec

Title: US-09-019-441-2
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
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1	423	100.0	423 19	AAV33308	Anti-human CD23 6G	
2	313.2	74.0	1431 18	AAT62513	Primate anti-hu	
3	313.2	74.0	1431 19	AAV35489	Macaque primatized	
4	313.2	74.0	1431 24	AAV37247	DNA sequence of a	
5	301.2	71.2	423 21	AAZ39331	Nucleotide sequenc	
6	299.8	70.9	1404 18	AAT62868	Human gamma-4 heav	
7	299.8	70.9	1404 18	AAT62869	Human gamma-4E hea	
8	299.8	70.9	1404 18	AAT62870	Human gamma-4PE he	

9	298.2	70.5	420	21	AAZ39335	Nucleotide sequenc
10	298.2	70.5	423	14	AAQ35903	Anti-CD4 VH coding
11	298.2	70.5	423	18	AAT91564	Anti-CD4 cynomolg
12	298.2	70.5	423	19	AAV31428	Anti-CD4 antibody
13	298.2	70.5	423	19	AAV05695	Monkey anti-CD4 he
14	298.2	70.5	423	25	ABX76616	DNA encoding cynom
15	296.6	70.1	481	22	ABT31871	Anti-CD40 monoclon
16	296.4	70.1	619	22	AAV30348	Human diagnostic a
17	295.2	69.8	420	18	AAT95167	Monkey anti-human
18	295.2	69.8	420	18	AAT62865	Monkey anti-CD4 he
19	295.2	69.8	420	19	AAV23760	Anti-CD4 antibody
20	293.8	69.5	496	20	AAZ24416	Human bladder tumo
21	293.4	69.4	417	21	AAZ52907	Human LH1238 mono
22	292.4	69.1	1431	18	AAT62510	Primate anti-hu
23	292.4	69.1	1431	19	AAV35485	Macaque primatized
24	292.4	69.1	1431	24	AAV17243	DNA sequence of a
25	290	68.6	1634	21	AAZ50012	Human immune syste
26	289.6	68.5	1567	22	AAZ66522	Human immune syste
27	287.6	68.0	614	20	AAV86218	Human PTHrp monoc
28	286	67.6	417	21	AAV13938	Human bladder tumo
29	281.4	66.5	397	20	AAZ24417	Anti-CD40 monoclon
30	278.8	65.9	462	25	ABT31873	Anti-TRAIL-R antib
31	278.4	65.8	467	25	ABZ59692	Human ovarian anti
32	277	65.5	629	24	ABQ56276	Human IGFAM-2 immu
33	276.2	65.3	1746	21	AAZ27382	Vh 71-4. Homo sap
34	275.6	65.2	348	14	AAQ42697	VH411. Homo sapie
35	275.6	65.2	348	14	AAQ42699	VH415. Homo sapie
36	275.6	65.2	348	14	AAQ42700	Anti-TRAIL-R antib
37	275.2	65.1	467	25	ABZ59694	VH416. Homo sapie
38	274	64.8	348	14	AAQ42701	Human bladder tumo
39	273.6	64.7	457	20	AAZ24423	Human immunoglobul
40	273.4	64.6	1507	21	AAV09695	Anti-hTNFSP13b hum
41	272.8	64.5	426	25	ABZ80001	Human antibody 4A5
42	272.8	64.5	462	25	ABZ80006	Monoclonal antibod
43	272.8	64.5	1431	17	AAT18059	Anti-TRAIL-R antib
44	271.2	64.1	490	25	ABZ59696	Mouse DNA encoding
45	270.4	63.9	426	24	ABX00190	

ALIGNMENTS

RESULT 1
AAV33308
ID AAV33308 standard; DNA; 423 BP.
XX AAV33308;
AC AAV33308;
XX
XX 25-MAR-2003 (updated)
DT 18-NOV-1998 (first entry)
XX
DE Anti-human CD23 6G5 monoclonal antibody heavy chain variable region DNA.
XX
XX Anti-human CD23 6G5 monoclonal antibody; heavy chain variable region;
XX human CD23; IGE; FcRii/CD23; gamma-1 constant region;
XX gamma-3 constant region; allergy; inflammation; autoimmune disease;
XX allergic rhinitis; conjunctivitis; autoimmune haemolytic anaemia; ss.
XX
XX Macaca fascicularis
XX
XX Key Location/Qualifiers
FH CDS 1..423
FT /tag= a
FT /product= "anti-human CD23 6G5 heavy chain variable
FT region"
FT /note= "CDS does not contain a stop codon"

FT sig_peptide 1..57
FT /tag= b
FT mat_peptide 58..423
FT /tag= c
FT misc_feature 148..165
FT /tag= d
FT /note= "encodes CDR 1 region"

[illegible]

QY 361 GCCCAATAGCTGGAACAACAGCTAGGCTTCTGGGGCCAGGAGCTCTGGTCAACGGTCTCC 420
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QY 421 TCA 423
 Db 418 TCA 420

RESULT 9
 AAZ39335
 ID AAZ39335 standard; DNA; 420 BP.
 AC AAZ39335;
 DT 15-FEB-2000 (first entry)
 XX Nucleotide sequence of Cynomolgus VH cDNA clone 2-10.
 XX Complementarity determining region; antibody; primate; immunogenicity;
 XX Old World ape; Old World monkey; antigen-binding affinity; ss.
 XX Macaca cynomolgus.
 OS WO955369-A1.
 PN 04-NOV-1999.
 PD 28-APR-1999; 99WO-US09131.
 PF 28-APR-1998; 98US-0083367.
 PR (SMIK) SMITHKLINE BEECHAM CORP.
 PA Taylor AH;
 PI WPI; 2000-023265/02.
 DR P-PSDB; AAY56667, AAY56732.
 XX Antibodies containing donor complementarity determining regions and
 PT non-human primate acceptor frameworks, having reduced immunogenicity in
 PT humans -
 XX Example 3; Page 84-85; 123pp; English.

XX The invention provides an antibody (Ab) comprising donor CDRs
 CC (complementarity determining regions) derived from a non-human antigen-
 CC specific donor antibody, and an acceptor framework from a non-human
 CC primate. The Abs are prepared by grafting CDRs from a non-human antigen-
 CC specific donor antibody onto homologous Old World ape or monkey acceptor
 CC frameworks. The Abs have reduced immunogenicity and are better tolerated
 CC in humans (because of the close similarity between the human and primate
 CC proteins), but retain the full antigen-binding affinity of the donor
 CC antibody.

XX Sequence 420 BP; 80 A; 125 C; 113 G; 102 T; 0 other;
 SQ Query Match 70.5%; Score 298.2; DB 21; Length 420;
 Best Local Similarity 83.2%; Pred. No. 1.5e-67;
 Matches 352; Conservative 0; Mismatches 68; Indels 3; Gaps 1;

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 Db 1 ATGAAGCACCTGTGGTTCTTCTCTCTGCTGCGAGCTCCAGATGGGTCTGTCCAG 60

QY 61 CTGACGTGCGAGGAGTGGGGCCAGGAGTGGTGAAGCTTCGGAGACCTGTCCCTCACC 120
 Db 61 GTTCACTACAGAGTGGGGCCAGGAGTGGTGAAGCTTCGGAGACCTGTCCCTCACC 120

QY 121 TGCCTGTCTGTGGTGGCTGTGTGACGAGTGTAACTGGTGACCTGGATCCGCCAGCCC 180
 Db 121 TGCCTGTCTGTGGTGGCTGTGTGACGAGTGTAACTGGTGACCTGGATCCGCCAGTCC 180

QY 181 CCAGGAAGGAGCTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAACTAC 240
 Db 181 CCGGGAAGGGGCTGGAAATGGATTGGAAGTTCTTATATCTACTTGAATACTCTCTCC 240

QY 241 AACCCGTCCCTCAAGAGTGCAGTCAATTTTCAAGACACGTCCAGAACCAAGTCTCC 300
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QY 301 CTGAACCTGAACCTGTGACCGCGGACACGGCGGTGTATTACTGTGCGAGATTGG 360
 Db 301 CTGAGACTGACCTGTGACCGCGGACACGGCGGTGTATTACTGTGCGAGATTGG 357

QY 361 GCCCAATAGCTGGAACAACAGCTAGGCTTCTGGGGCCAGGAGTCTCTGGTCAACGGTCTCC 420
 Db 358 CTCTATAGCAGCGGCTATAAATTTTACTACTGGGGCCAGGAGTCTCTGGTCAACGGTCTCC 417

QY 421 TCA 423
 Db 418 TCA 420

RESULT 10
 AAQ35903
 ID AAQ35903 standard; DNA; 423 BP.
 XX AAQ35903;
 AC AAQ35903;
 DT 25-MAR-2003 (updated)
 DT 08-JUN-1993 (first entry)
 XX Anti-CD4 VH coding sequence.
 XX PCR; amplify; clone; heavy; light; chain; variable; region; lambda;
 KW immortalised B-cell; vector; TCAE 6; human; IgG1; constant; antigen;
 KW recombinant; antibody; chimpanzee; Ig; Ag; Old world monkey; eczema;
 KW immunoglobulin; therapeutic; rheumatoid arthritis; ss.
 XX Simian sp.
 OS WO9302108-A1.
 PN 04-FEB-1993.
 PD 24-JUL-1992; 92WO-US06194.
 PF 25-JUL-1991; 91US-0735064.
 PR 23-MAR-1992; 92US-0856281.
 XX (IDEC-) IDEC PHARM CORP.
 XX Hanna N, Newman RA, Raab RW;
 DR WPI; 1993-058729/07.
 DR P-PSDB; AAR31948.
 XX Recombinant antibodies including Old World monkey portion and
 PT human portion - used for treatment of auto-immune diseases,
 PT infectious diseases, AIDS, tumours, diabetes, proliferative
 PT diseases, intestinal inflammations and allergies, etc.
 XX Disclosure; Page 53-54; 92pp; English.

XX The sequences given in AAQ35903-04 encode the Simian anti CD4 VH and
 CC V-lambda sequences respectively. These sequences were derived using
 CC the primer sequences given in AAQ35901-02. The amplification products
 CC were sequentially cloned into the vector TCAE 6, which contains human
 CC IgG1 and human lambda constant regions. The amplified sequences could
 CC be used in the production of a recombinant antibody, comprising a
 CC human, chimpanzee or old world monkey immunoglobulin (Ig) constant
 CC region and an antigen (Ag) binding portion of an old world monkey Ig
 CC variable region, where the old world monkeys may be the same or
 CC different. The recombinant antibody may be used as a therapeutic
 CC agent for the treatment of rheumatoid arthritis, eczema and


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112 GTGCAGCTGCAGGAGTCTGGGCCCGCAGAGCTTGTGAAGCCTTCGAGAGACCCCTGTCCCTCACC 171
121 TGGCGTGTCTCTGGTGGCTCTGTTCAGCAGTATGTAACCTGGTGAACCTCGATCCGCCAGCCCC 180
172 TGCACCTGTCTCTGGTGGCTC--CATCAGTGGTTACTACTGGAGCTGGATCCGGCAGCCCC 228
181 CCAGGGAAGGGAAGTGGAGTGGATTTGGACGTATCTCTGTGTAGTGGTGGGGCCACCAACTAC 240
229 CCAGGGAAGGGAAGTGGAGTGGATTTGGGTATATCTATTACA---GTGGGAGACCAACTAC 285
241 AACCCGTCCCTCAAAGAGTCCGAGTCATCATTTCAAGAAGACACGTCCAAAGAACCCAGTTCTCC 300
286 AATCCCTCCCTCAAAGAGTCCGAGTCACCATATCAGTAGACACGTCCTCAAAGAACCCAGTTCTCC 345
301 CTGAACCTGAACCTCTGTGACCGCCGGGACACGGCCGCTGTATTTACTGTGTCGAGAGATTGG 360
346 CTGAAGCTGAATTTCTGTGACCGCTGCGGACACGGCCGCTGTATTTACTGTGTCGAGAGCCCC 405
361 GCCCAATAGCTGGAAACAGCGTAGGCTTCTGGGGCCAGGAGTCTCTGTGTCAACCGTCTCC 420
406 TTGCACGGTGACTACAAATGGTTCCACCCCTGTGGGCCAGGGAACCCCTGTGTCAACCGTCTCC 465
421 TCA 423
466 TCA 468

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QY	421	TCA 423
Db	421	TCA 423
RESULT 15		
ABT31871	ABT31871 standard; DNA; 481 BP.	
XX	AC	ABT31871;
XX	DT	01-MAY-2003 (first entry)
XX	XX	Anti-CD40 monoclonal antibody related DNA SEQ ID No 43.
XX	XX	Anti-Allergic; haemostatic; immunomodulator; cytostatic; antibody;
KW	KW	human CD40; IL-12; LPS; lipopolysaccharide; IFNgamma; interferon gamma;
KW	KW	dendritic cell; high G28-5; CD95 expression; high G28-5; B cell line;
KW	KW	immunoreactivator; anti-tumour agent; immunosuppressant; allergy;
KW	KW	autoimmune disease; coagulation factor VIII inhibitor; anti-CD40; gene;
XX	XX	db.
XX	XX	Unidentified.
OS	XX	WO200288186-A1.
PN	XX	07-NOV-2002.
PD	XX	26-APR-2002; 2002WO-JP04292.
PF	XX	27-APR-2001; 2001WO-US13672.
PR	XX	11-MAY-2001; 2001JP-0142482.
PR	XX	05-OCT-2001; 2001JP-0310535.
PR	XX	26-OCT-2001; 2001US-0040244.
XX	XX	(KIRI) KIRIN BEER KK.
PA	XX	Mikayama T, Yoshida H, Force WR, Chen X, Takahashi N;
PI	XX	WPI; 2003-120463/11.
DR	XX	P-PSDB; ABJ36929.
DR	XX	Anti-CD40 monoclonal antibody with antagonist/agonist activity to CD40,
PT	XX	or functional fragment, is useful in the treatment of e.g. autoimmune
PT	XX	diseases or cancer
PS	XX	Claim 26; Page 50; 94pp; Japanese.
PS	XX	The invention relates to an antibody to human CD40, or its functional
CC	XX	fragment, has at least one of the following properties: acting on
CC	XX	dendritic cells to produce IL-12 in the presence of LPS
CC	XX	(lipopolysaccharide) and IFNgamma (interferon gamma); acting on dendritic
CC	XX	cells to activate maturation of the dendritic cells with high G28-5
CC	XX	antibody; and activating CD95 expression with high G28-5 antibody against
CC	XX	B cell line. Such antibodies or functional fragments can be used as
CC	XX	immunoreactivators, anti-tumour agents, immunosuppressants, and as remedies
CC	XX	for autoimmune diseases, allergy or coagulation factor VIII inhibitors
CC	XX	syndrome. This polynucleotide sequence represents a coding DNA sequence
CC	XX	relating to the anti-CD40 monoclonal antibody of the invention.
XX	XX	Sequence 481 BP; 101 A; 146 C; 130 G; 104 T; 0 other;
XX	XX	Query Match 70.18; Score 296.6; DB 25; Length 481;
XX	XX	Best Local Similarity 84.6%; Pred. No. 4.1e-67;
XX	XX	Matches 359; Conservative 0; Mismatches 59; Indels 6; Gaps 2;
QY	1	ATGAACACCTGTGGTTCTTCTCTCTGTGGCAGCTCCAGATGGGTCTGTCCAG 60
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QY	61	CTGCAGCTGCAGAGTCGGCCACGAGTGGTGAAGCCTTCGGAGACCTGTCCCTCACC 120

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 19:01:43 ; Search time 611.125 Seconds
(without alignments)
2371.523 Million cell updates/sec

Title: US-09-019-441-2

Perfect score: 423

Sequence: 1 ATGAACACCTGGTGTCTT.....TCTGTGTCACGCTCCTCA 423

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2244575 seqs, 1713117285 residues

Total number of hits satisfying chosen parameters: 4489150

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	313.2	74.0	1431	13	US-10-124-807-11
5	313.2	74.0	1431	13	US-10-291-532-11
6	313.2	74.0	1431	14	US-10-124-905-11
7	313.2	74.0	1431	14	US-10-073-138-6
8	301.2	71.2	423	9	US-09-905-243-40
9	299.8	70.9	1404	15	US-10-211-357-7
10	299.8	70.9	1404	15	US-10-211-357-9
11	299.8	70.9	1404	15	US-10-211-357-11
12	298.2	70.5	420	9	US-09-905-243-44
13	298.2	70.5	423	10	US-09-850-165-15
14	295.2	69.8	420	15	US-10-211-357-1
15	293.4	69.4	417	13	US-10-300-675-1

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Sequence 114, App
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Sequence 16699, A
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Sequence 963, App
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18 292.4 69.1 1431 13 US-10-291-532-3
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27 266.6 63.0 393 9 US-09-925-299-198
28 266.6 63.0 393 11 US-09-925-299-198
29 264.2 62.5 417 9 US-09-905-243-7
30 262.6 62.1 472 14 US-10-040-739-963
31 261.6 61.8 429 9 US-09-905-243-1
32 261.2 61.7 1341 13 US-10-194-801C-7
33 261.2 61.7 2674 13 US-10-194-801C-1
34 257.4 60.9 450 13 US-10-390-986-13
35 256.2 60.6 2288 13 US-09-814-353-21201
36 255.6 60.4 531 14 US-10-040-739-1375
37 254.2 60.1 438 11 US-09-918-995-16650
38 252.8 59.8 829 14 US-10-040-739-210
39 251.8 59.5 414 15 US-10-153-437-4
40 251.6 59.5 407 9 US-09-905-243-43
41 251 59.3 655 10 US-09-920-345-4
42 248.6 58.8 747 13 US-10-182-132-1
43 248 58.6 2244 15 US-10-198-846-13582
44 243 57.4 3128 13 US-10-027-632-114467
45 243 57.4 3128 14 US-10-027-632-114467

ALIGNMENTS

RESULT 1

US-09-019-441-2
Sequence 2, Application US/09019441
Publication No. US20030086921A1

GENERAL INFORMATION:

APPLICANT: REFF, Mitchell E.
KLOETZER, William S.
NAKAMURA, Takehiko

TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL

ANTIBODIES AND USE THEREOF AS THERAPEUTICS

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/019,441

FILING DATE: 05-Feb-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/803,085

FILING DATE: 20-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-502

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 2:

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SEQUENCE CHARACTERISTICS:
LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..423
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 58..423
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-019-441-2

Query Match      100.0%; Score 423; DB 11; Length 423;
Best Local Similarity 100.0%; Pred. No. 2.3e-116;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAACACCTGTGGTTCTCTCTCTGTGGCAGTCCAGATGGTCTCTCCAG 60
Db |||||
Qy 1 ATGAACACCTGTGGTTCTCTCTCTGTGGCAGTCCAGATGGTCTCTCCAG 60
Db |||||
Qy 61 CTGCAGCTGCAGGAGTGGGCCAGGAGTGTGAAGCCTTCGGAGACCTGTCTCACC 120
Db |||||
Qy 61 CTGCAGCTGCAGGAGTGGGCCAGGAGTGTGAAGCCTTCGGAGACCTGTCTCACC 120
Db |||||
Qy 121 TGGCTGTCTCTGTGGTCTGTGCAGCAGTAGTAACCTGTGGACCTGGATCCGCGGCC 180
Db |||||
Qy 121 TGGCTGTCTCTGTGGTCTGTGCAGCAGTAGTAACCTGTGGACCTGGATCCGCGGCC 180
Db |||||
Qy 181 CCAGGGAAGGAGTGGAGTGGATTCCTGTAGTGGTGGGCCACCACTAC 240
Db |||||
Qy 181 CCAGGGAAGGAGTGGAGTGGATTCCTGTAGTGGTGGGCCACCACTAC 240
Db |||||
Qy 241 AACCCGTCCCTCAAGAGTCCAGTTCATTCATTCACAGACAGCTCCAAAGACCACTTCC 300
Db |||||
Qy 241 AACCCGTCCCTCAAGAGTCCAGTTCATTCATTCACAGACAGCTCCAAAGACCACTTCC 300
Db |||||
Qy 301 CTGAACCTGAACCTGTGTGACCGCGGACACGCGCGGTATTACTGTGCGAGAGATTGG 360
Db |||||
Qy 301 CTGAACCTGAACCTGTGTGACCGCGGACACGCGCGGTATTACTGTGCGAGAGATTGG 360
Db |||||
Qy 361 GCCCAATAGCTGGAACACGCTAGGCTTCTGGGGCCAGGGAGTCTGTCACCGTCTCC 420
Db |||||
Qy 361 GCCCAATAGCTGGAACACGCTAGGCTTCTGGGGCCAGGGAGTCTGTCACCGTCTCC 420
Db |||||
Qy 421 TCA 423
Db |||
Qy 421 TCA 423
Db |||

RESULT 2
US-103-686-2
; Sequence 2, Application US/10103686
; Publication No. US20030059424A1
; GENERAL INFORMATION:
; APPLICANT: REFF, Mitchell E.
; KLOETZER, William S.
; NAKAMURA, Takehiko
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

SEQUENCE CHARACTERISTICS:
LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..423
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 58..423
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-103-686-2

Query Match      100.0%; Score 423; DB 15; Length 423;
Best Local Similarity 100.0%; Pred. No. 2.3e-116;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAACACCTGTGGTTCTCTCTCTGTGGCAGTCCAGATGGTCTCTCCAG 60
Db |||||
Qy 1 ATGAACACCTGTGGTTCTCTCTCTGTGGCAGTCCAGATGGTCTCTCCAG 60
Db |||||
Qy 61 CTGCAGCTGCAGGAGTGGGCCAGGAGTGTGAAGCCTTCGGAGACCTGTCTCACC 120
Db |||||
Qy 61 CTGCAGCTGCAGGAGTGGGCCAGGAGTGTGAAGCCTTCGGAGACCTGTCTCACC 120
Db |||||
Qy 121 TGGCTGTCTCTGTGGTCTGTGCAGCAGTAGTAACCTGTGGACCTGGATCCGCGGCC 180
Db |||||
Qy 121 TGGCTGTCTCTGTGGTCTGTGCAGCAGTAGTAACCTGTGGACCTGGATCCGCGGCC 180
Db |||||
Qy 181 CCAGGGAAGGAGTGGAGTGGATTCCTGTAGTGGTGGGCCACCACTAC 240
Db |||||
Qy 181 CCAGGGAAGGAGTGGAGTGGATTCCTGTAGTGGTGGGCCACCACTAC 240
Db |||||
Qy 241 AACCCGTCCCTCAAGAGTCCAGTTCATTCATTCACAGACAGCTCCAAAGACCACTTCC 300
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Qy 241 AACCCGTCCCTCAAGAGTCCAGTTCATTCATTCACAGACAGCTCCAAAGACCACTTCC 300
Db |||||
Qy 301 CTGAACCTGAACCTGTGTGACCGCGGACACGCGCGGTATTACTGTGCGAGAGATTGG 360
Db |||||
Qy 301 CTGAACCTGAACCTGTGTGACCGCGGACACGCGCGGTATTACTGTGCGAGAGATTGG 360
Db |||||
Qy 361 GCCCAATAGCTGGAACACGCTAGGCTTCTGGGGCCAGGGAGTCTGTCACCGTCTCC 420
Db |||||
Qy 361 GCCCAATAGCTGGAACACGCTAGGCTTCTGGGGCCAGGGAGTCTGTCACCGTCTCC 420
Db |||||
Qy 421 TCA 423
Db |||
Qy 421 TCA 423
Db |||

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10103686
FILING DATE: 25-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/803,085
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..423
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 58..423
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-103-686-2

Query Match      100.0%; Score 423; DB 15; Length 423;
Best Local Similarity 100.0%; Pred. No. 2.3e-116;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAACACCTGTGGTTCTCTCTCTGTGGCAGTCCAGATGGTCTCTCCAG 60
Db |||||
Qy 1 ATGAACACCTGTGGTTCTCTCTCTGTGGCAGTCCAGATGGTCTCTCCAG 60
Db |||||
Qy 61 CTGCAGCTGCAGGAGTGGGCCAGGAGTGTGAAGCCTTCGGAGACCTGTCTCACC 120
Db |||||
Qy 61 CTGCAGCTGCAGGAGTGGGCCAGGAGTGTGAAGCCTTCGGAGACCTGTCTCACC 120
Db |||||
Qy 121 TGGCTGTCTCTGTGGTCTGTGCAGCAGTAGTAACCTGTGGACCTGGATCCGCGGCC 180
Db |||||
Qy 121 TGGCTGTCTCTGTGGTCTGTGCAGCAGTAGTAACCTGTGGACCTGGATCCGCGGCC 180
Db |||||
Qy 181 CCAGGGAAGGAGTGGAGTGGATTCCTGTAGTGGTGGGCCACCACTAC 240
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Qy 181 CCAGGGAAGGAGTGGAGTGGATTCCTGTAGTGGTGGGCCACCACTAC 240
Db |||||
Qy 241 AACCCGTCCCTCAAGAGTCCAGTTCATTCATTCACAGACAGCTCCAAAGACCACTTCC 300
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Qy 301 CTGAACCTGAACCTGTGTGACCGCGGACACGCGCGGTATTACTGTGCGAGAGATTGG 360
Db |||||
Qy 301 CTGAACCTGAACCTGTGTGACCGCGGACACGCGCGGTATTACTGTGCGAGAGATTGG 360
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Qy 361 GCCCAATAGCTGGAACACGCTAGGCTTCTGGGGCCAGGGAGTCTGTCACCGTCTCC 420
Db |||||
Qy 361 GCCCAATAGCTGGAACACGCTAGGCTTCTGGGGCCAGGGAGTCTGTCACCGTCTCC 420
Db |||||
Qy 421 TCA 423
Db |||
Qy 421 TCA 423
Db |||

RESULT 3
US-09-948-429B-11
; Sequence 11, Application US/09948429B
; Patent No. US20020177689A1
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TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1431
NAME/KEY: mat peptide
LOCATION: 1..1431
US-10-124-905-11

Query Match 74.0%; Score 313.2; DB 14; Length 1431;
Best Local Similarity 84.5%; Pred. No. 1.6e-83;
Matches 370; Conservative 0; Mismatches 53; Indels 15; Gaps 1;
Qy 1 ATGAACACCTGTGGTCTCTCTCTGTGGCAGCTCCAGATGGTCTCTCCAG 60
Db 1 ATGAACACCTGTGGTCTCTCTCTGTGGCAGCTCCAGATGGTCTCTCCAG 60
Qy 61 CTGCAGCTGCAGAGTCCGGCCAGGAGTGGTGAAGCTTCGGAGACCTGTCTCCACC 120
Db 61 CTGCAGCTGCAGAGTCCGGCCAGGAGTGGTGAAGCTTCGGAGACCTGTCTCCACC 120
Qy 121 TGCCTGTCTCTGGTGGCTCTGTCTCAGCAGTAGTAACCTGGTGACCTGGATCCGCCAGCCC 180
Db 121 TGCCTGTCTCTGGTGGCTCTGTCTCAGCAGTAGTAACCTGGTGACCTGGATCCGCCAGCCC 180
Qy 181 CCAGGGAAGGACTGGAGTGGATGGACGATATCTCTGTAGTGGTGGGCCACCACTAC 240
Db 181 CCAGGGAAGGACTGGAGTGGATGGACGATATCTCTGTAGTGGTGGGCCACCACTAC 240
Qy 241 AACCCGTCCTCAAGAGTCCAGTCAATTTCAACAGACAGCTCCAGAACCACTCTCC 300
Db 241 AACCCGTCCTCAAGAGTCCAGTCAATTTCAACAGACAGCTCCAGAACCACTCTCC 300
Qy 301 CTGAAGCTGAACCTGTGACCGCCGACACGCGCGTATTAATCTGTGCGAGAGATTGG 360
Db 301 CTGAAGCTGAACCTGTGACCGCCGACACGCGCGTATTAATCTGTGCGAGAGATTGG 360
Qy 361 GCCCAATAGCTGAACAA-----CGTAGGCTTCTGGGCCAGGAGTGC 405
Db 361 CTTTTCAGTGTGGTGAATGGTTTAAACAACAGTGGTTCGATGTCTGGGCCCGGAGTC 420
Qy 406 CTGCTACCGTCTCTCTCA 423
Db 421 CTGCTACCGTCTCTCTCA 438

RESULT 7

US-10-073-138-6
Sequence 6, Application US/10073138
Publication No. US20020187146A1
GENERAL INFORMATION:
APPLICANT: ANDERSON, Darrell R.
HANNA, Nabil
BRAMS, Peter

TITLE OF INVENTION: IDENTIFICATION OF UNIQUE BINDING
INTERACTIONS BETWEEN CERTAIN ANTIBODIES AND THE HUMAN B7.1
AND B7.2 CO-STIMULATORY ANTIGENS

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/073.138
FILING DATE: 13-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/746.361
FILING DATE: 08-NOV-1996
APPLICATION NUMBER: US 08/487.550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-256
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1431 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1431
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-073-138-6

Query Match 74.0%; Score 313.2; DB 14; Length 1431;
Best Local Similarity 84.5%; Pred. No. 1.6e-83;
Matches 370; Conservative 0; Mismatches 53; Indels 15; Gaps 1;

Qy 1 ATGAACACCTGTGGTCTCTCTCTGTGGCAGCTCCAGATGGTCTCTCCAG 60
Db 1 ATGAACACCTGTGGTCTCTCTCTGTGGCAGCTCCAGATGGTCTCTCCAG 60
Qy 61 CTGCAGCTGCAGAGTCCGGCCAGGAGTGGTGAAGCTTCGGAGACCTGTCTCCACC 120
Db 61 CTGCAGCTGCAGAGTCCGGCCAGGAGTGGTGAAGCTTCGGAGACCTGTCTCCACC 120
Qy 121 TGCCTGTCTCTGGTGGCTCTGTCTCAGCAGTAGTAACCTGGTGACCTGGATCCGCCAGCCC 180
Db 121 TGCCTGTCTCTGGTGGCTCTGTCTCAGCAGTAGTAACCTGGTGACCTGGATCCGCCAGCCC 180
Qy 181 CCAGGGAAGGACTGGAGTGGATGGACGATATCTCTGTAGTGGTGGGCCACCACTAC 240
Db 181 CCAGGGAAGGACTGGAGTGGATGGACGATATCTCTGTAGTGGTGGGCCACCACTAC 240
Qy 241 AACCCGTCCTCAAGAGTCCAGTCAATTTCAACAGACAGCTCCAGAACCACTCTCC 300
Db 241 AACCCGTCCTCAAGAGTCCAGTCAATTTCAACAGACAGCTCCAGAACCACTCTCC 300
Qy 301 CTGAAGCTGAACCTGTGACCGCCGACACGCGCGTATTAATCTGTGCGAGAGATTGG 360
Db 301 CTGAAGCTGAACCTGTGACCGCCGACACGCGCGTATTAATCTGTGCGAGAGATTGG 360
Qy 361 GCCCAATAGCTGAACAA-----CGTAGGCTTCTGGGCCAGGAGTGC 405
Db 361 CTTTTCAGTGTGGTGAATGGTTTAAACAACAGTGGTTCGATGTCTGGGCCCGGAGTC 420
Qy 406 CTGCTACCGTCTCTCTCA 423
Db 421 CTGCTACCGTCTCTCTCA 438

RESULT 8

US-09-905-243-40
Sequence 40, Application US/09905243
Patent No. US20020062009A1
GENERAL INFORMATION:
APPLICANT: Taylor, Alexander H
TITLE OF INVENTION: Monoclonal Antibodies with Reduced

us-09-019-441-2.open.rnpb

Search completed: December 30, 2003, 03:42:09
Job time : 613.125 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 46.5619 Seconds
(without alignments)
4009.823 Million cell updates/sec

Title: US-09-019-441-2

Perfect score: 423

Sequence: 1 ATGMAACACGTGGTGTCTT.....TCTGTGTCACCGTCTCTCTCA 423

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*

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4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*

5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq.*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	423	100.0	423	3	US-08-803-085-2
2	313.2	74.0	1431	3	US-08-487-550-11
3	313.2	74.0	1431	4	US-09-526-098-11
4	299.8	70.9	1404	3	US-08-523-894-7
5	299.8	70.9	1404	3	US-08-523-894-9
6	299.8	70.9	1404	3	US-08-523-894-11
7	298.2	70.5	423	1	US-08-379-072A-19
8	298.2	70.5	423	1	US-08-481-869-19
9	298.2	70.5	423	1	US-08-476-237-15
10	295.2	69.8	420	1	US-08-478-039-107
11	295.2	69.8	420	1	US-08-476-349A-107
12	295.2	69.8	420	3	US-08-523-894-1
13	292.4	69.1	1431	3	US-08-487-550-3
14	292.4	69.1	1431	4	US-09-526-098-3
15	289.6	68.5	1567	3	US-09-049-672A-17
16	268	63.4	426	2	US-08-480-774A-1
17	266.2	62.9	403	3	US-09-042-353-357
18	266.2	62.9	403	4	US-08-758-417A-205
19	263.8	62.4	404	3	US-09-042-353-355
20	263.8	62.4	404	4	US-08-758-417A-203
21	261.2	61.7	1341	4	US-09-372-425A-7
22	261.2	61.7	1341	4	US-09-372-425A-1
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24	257.8	60.9	524	4	US-08-758-417A-219
25	257.8	60.9	4926	3	US-09-042-353-418
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28	257.6	60.9	413	4	US-08-758-417A-199
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43	236.6	55.9	622	3	US-08-545-809A-59
44	227.2	53.7	1418	4	US-08-793-450-7
45	223.6	52.9	631	3	US-08-545-809A-31

ALIGNMENTS

RESULT 1

US-08-803-085-2

; Sequence 2, Application US/08803085

; Patent No. 6011138

; GENERAL INFORMATION:

; APPLICANT: REFF, Mitchell E.

; APPLICANT: KLOETZER, William S.

; APPLICANT: NAKAMURA, Takehiko

; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL

; TITLE OF INVENTION: ANTIBODIES AND USE THEREOF AS THERAPEUTICS

; NUMBER OF SEQUENCES: 35

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/803,085

; FILING DATE: 20-FEB-1997

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Teskin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/DOCKET NUMBER: 012712-353

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 423 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..423

; FEATURE:

; NAME/KEY: mat_peptide

; LOCATION: 58..423

US-08-803-085-2

Query Match 100.0%; Score 423; DB 3; Length 423;

RESULT 4
US-08-523-894-7
; Sequence 7, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil . . .

Query Match	70.9%;	Score 299.8;	DB 3;	Length 1404;
Best Local Similarity	83.5%;	Pred. No. 6.8e-78;		
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DB	1	ATGAACACCTGGGTCTCTTCCTCCTCGTGGGCGAGCCCCACAGATGGGTCTGTGCCAG	60	
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DB	181	CCAGGGAAGGGACTGGAGTGGATCGGCTACATCTATGGCAGTGGTGGGGCCACCAATTAC	240	
QY	241	AACCCCTCCCTCAAGAGTTCGAGTCATCATTTCAACAGACACGTCCTCAAGAACCCAGTTCTCC	300	
DB	241	AATCCCTCCCTCAACAATCGAGTCTCCATTTCAATAGACACGTCCTCAAGAACCTCTTCTCC	300	
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QY 421 TCA 423
Db 418 TCA 420

RESULT 5
US-08-523-894-9
; Sequence 9, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; TITLE OF INVENTION: Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/523,894
; FILING DATE: 06-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1404 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: heavy chain gamma 4 with the E mutation
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1404
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: 1..1404
US-08-523-894-9

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Best Local Similarity 83.5%; Pred. No. 6.8e-78;
Matches 353; Conservative 0; Mismatches 67; Indels 3; Gaps 1;

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Db 121 TGCAGTGTCTCTGCTGCTGCTCCATCAGCGGTGACTATTATTGGTCTCTGGATCCGCGAC 180
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QY 421 TCA 423
Db 418 TCA 420

RESULT 6
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; Sequence 11, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; TITLE OF INVENTION: Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/523,894
; FILING DATE: 06-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1404 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: heavy chain gamma 4 with the P and E
; CHROMOSOME/SEGMENT: mutation

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

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and is derived by analysis of the total score distribution.

SUMMARIES

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3	342.2	88.4	729	6	BD090625	BD090625 Drug cont
4	342.2	88.4	729	6	E40896	E40896 Humanized a
5	340.6	88.0	388	9	HSAS48508	AJS48508 Homo sapi
6	334.2	86.4	390	9	MMU57571	E12918 Macaca mula
7	334.2	86.4	396	6	E12918	E12918 Human mRNA
8	334.2	86.4	438	6	BD015544	BD015544 Human mon
9	334.2	86.4	438	6	BD094922	BD094922 Human mon
10	332.6	85.9	406	9	HUMIGKPFAN	M87478 Human reary
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12	331	85.5	962	9	BC034141	BC034141 Homo sapi
13	330.8	85.5	432	9	HUMIGKVC	L01279 Homo sapien
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28	321.4	83.0	390	9	HSFOGIL	X64163 H.sapiens m
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ALIGNMENTS

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LOCUS 19040 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for integrating genes at specific sites in mammalian cells
via homologous recombination and vectors for accomplishing the

same.
ACCESSION BD075127
VERSION BD075127.1 GI:22620730
KEYWORDS JP 2001516221-A/3.
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 19040)
AUTHORS Reff.M.E., Barnett,R.S. and Mclachlan,K.R.
TITLE Method for integrating genes at specific sites in mammalian cells

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 TITLE Potentially disease-modifying effects of apoptotic-cell specific
 immune responses
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 388)
 AUTHORS Pal, R.
 JOURNAL Direct Submission
 TITLE Submitted (25-FEB-2003) Pal R., Immunoenocrinology Lab, National
 Institute of Immunology, Aruna Asaf Ali Marg, JNU Complex, New
 Delhi, 110067, INDIA
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 DB 361 GGCCAGGACCAAGTGGAAATCAA 387

RESULT 6
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LOCUS MMU57571 390 bp mRNA linear PRI 02-OCT-1996
 DEFINITION Macaca mulatta Ig rearranged light chain variable region, anti-RBC
 antibody, mRNA, Partial cds.
 ACCESSION U57571
 VERSION U57571.1 GI:1575089
 KEYWORDS
 SOURCE Macaca mulatta (rhesus monkey)
 ORGANISM Macaca mulatta
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 Cercopitheinae; Macaca.
 REFERENCE 1 (bases 1 to 390)
 AUTHORS Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A.
 and Capra, J.D.
 TITLE Variable Region Gene Segment Utilization in Rhesus Monkey
 Hybridomas Producing Human Red Blood Cell-Specific Antibodies:
 Predominance of the VH4 Family but not VH4-21 (V4-34)
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 390)
 AUTHORS Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A.
 and Capra, J.D.
 TITLE Direct Submission
 JOURNAL Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center,
 University of Texas Southwestern Medical Center, 6000 Harry Hines
 Blvd., Dallas, TX 75235-9140, USA
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 97 a 108 c 94 g 91 t
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 Best Local Similarity 91.5%; Pred. No. 2.5e-98;
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 DB 361 GGCCAGGACCAAGTGGAAATCAA 387

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RESULT 7
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DEFINITION monoclonal antibody CLN''1-IgM,complete cds.
ACCESSION E12918
VERSION E12918.1 GI:3251749
KEYWORDS JP 1997100300-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 396)
Hagiwara,H., Aozuka,Y. and Miyahara,J.
AMINO ACID SEQUENCE OF ANTICANCER HUMAN MONOCLONAL ANTIBODY AND DNA
BASE SEQUENCE CODING FOR THE SAME
Patent: JP 1997100300-A 2 15-APR-1997;
HAGIWARA YOSHIHIDE
OS Homo sapiens (human)
PN JP 1997100300-A/2
PD 15-APR-1997
PF 03-OCT-1995 JP 1995278266
PI HAGIWARA HIDEAKI, AOZUKA YASUYUKI, MIYAHARA JUNICHI PC
C07K16/42,C07H21/04,C12N15/02,C12N15/09//A61K39/395,C12N5/10, PC
C12P21/08
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Query Match 86.4%; Score 334.2; DB 6; Length 396;
Best Local Similarity 91.5%; Pred. No. 2.5e-98;
Matches 354; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
QY 1 ATGGACATGAGGTCCTCCGCTCAGCTCTGGGGTCTCTGCTGCTGCTCCAGGTGCC 60
DB 1 ATGGACATGAGGTCCTCCGCTCAGCTCTGGGGTCTCTGCTGCTGCTCCAGGTGCC 60
QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGTCATCTGTAGGGGACAGA 120
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DEFINITION medicinal use thereof.
ACCESSION BD015544
VERSION BD015544.1 GI:22556681
KEYWORDS JP 2001206899-A/6.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 438)
Sakamoto,S. and Kamada,M.
Human monoclonal antibody against TGF-beta-II receptor and
medicinal use thereof
Patent: JP 2001206899-A 6 31-JUL-2001;
JAPAN TOBACCO INC
OS Homo sapiens (human)
PN JP 2001206899-A/6
PD 31-JUL-2001
PF 08-NOV-2000 JP 2000340216
PI SHINJI SAKAMOTO,MASAFUMI KAMADA
PC C07K16/28,A61K39/395,A61P1/16,A61P9/04,A61P9/10,A61P9/10, PC
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Best Local Similarity 91.5%; Pred. No. 2.5e-98;
Matches 354; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
QY 1 ATGACATGAGGTCCTCCGCTCAGCTCTGGGGTCTCTGCTGCTGCTCCAGGTGCC 60
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 QY 361 GGCAGGAGGACCAAGGTGGAATCAAA 387
 Db 361 GGCAGGAGGACCAAGGTGGAATCAAA 387

RESULT 9
 BD094922
 LOCUS Human monoclonal antibody for human TGF-beta type II receptor and 438 bp DNA linear PAT 27-AUG-2002
 DEFINITION pharmaceutical use thereof.

ACCESSION BD094922
 VERSION BD094922.1 GI:22640510
 KEYWORDS WO 0136642-A/6.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 438)
 Sakamoto, S. and Kamada, M.
 Human monoclonal antibody for human TGF-beta type II receptor and
 pharmaceutical use thereof

JOURNAL JAPAN TOBACCO INC, SHINJI SAKAMOTO, MASAFUMI KAMADA
 COMMENT OS WO 0136642-A/6
 PN WO 0136642-A/6
 PD 25-MAY-2001
 PF 17-NOV-2000 WO 2000JP008129
 PR 18-NOV-1999 JP 99P 328681, 08-NOV-2000 JP 00P 340216 PI
 SHINJI SAKAMOTO, MASAFUMI KAMADA
 PC C12N15/13, C07K16/28, C12N5/16, A61K39/395, A61P43/00, A61P13/12,
 A61P11/00,
 PC A61P1/16, A61P9/08, A61P9/10, A61P17/06, A61P17/04, A61P17/02, PC
 A61P19/02,
 PC A61P29/00
 CC Human monoclonal antibody for human TGF-beta type II receptor
 and
 pharmaceutical use thereof
 PH Key Location/Qualifiers
 FT CDS Location/Qualifiers

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FEATURES
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BASE COUNT 103 a 123 c 111 g 101 t
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 Best Local Similarity 91.5%; Pred. No. 2.5e-98;
 Matches 354; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 1 ATGGACATGAGGTCCTCGCTCAGCTCTGGGGCTCTTCTGCTCTGCTCCAGGTGCC 60
 Db 1 ATGGACATGAGGTCCTCGCTCAGCTCTGGGGCTCTTCTGCTCTGCTCCAGGTGCC 60
 QY 61 AGATGTGATCCAGATCAGCCAGTCTCCATCTTCCCTGCTGTCATCTGTAGGGGACAGA 120

Db 61 AGGTGTGATCCAGATGATCCAGTCTCCATCTCCCTGTCATCTGTAGGAGACAGA 120
 QY 121 GTACCATCACTTGCAGGCAAGTCAGGACATTAGGTATTATTTAAATTCGTATCAGCAG 180
 Db 121 GTACCATCACTTGCAGGCAAGTCAGGCAATTAGAAATGATTTAGGCTGTATCAGCAG 180
 QY 181 AAACAGGAAAGCTTCCTAAGCTCTGATCTATGTTGCATCCAGTTTGCAGTTTGCAGGCTC 240
 Db 181 AAACAGGAAAGCTTCCTAAGCTCTGATCTATGTTGCATCCAGTTTGCAGTTTGCAGGCTC 240
 QY 241 CCATCAAGTTTCAGCGGAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
 Db 241 CCATCAAGTTTCAGCGGAGTGGATCTGGGACAGAGTTCACTCTCACCAATCAGCAGCCTG 300
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 QY 361 GGCAGGAGGACCAAGGTGGAATCAAA 387
 Db 361 GGCAGGAGGACCAAGGTGGAATCAAA 387

RESULT 10
 HUMIGKFAN

LOCUS Human rearranged Igk mRNA 406 bp mRNA linear PRI 28-OCT-1994
 DEFINITION Human rearranged Igk mRNA VJC region.

ACCESSION M87478

VERSION M87478.1 GI:185950

KEYWORDS C-region; J-region; V-region; immunoglobulin kappa-chain; immunoglobulin light chain.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 406)
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Aucouturier, P., Bauwens, M., Khamlichi, A.A., Denoroy, L.,

Spinelli, S., Touchard, G., Preud'homme, J.L. and Cogné, M.
 Monoclonal Ig L chain and L chain V domain fragment crystallization

in myeloma-associated Fanconi's syndrome

J. Immunol. 150 (8 Pt 1), 3561-3568 (1993)

93224763

PUBMED 8468490

COMMENT Original source text: Homo sapiens (individual isolate patient

CHEB) bone marrow cDNA to mRNA.

FEATURES Location/Qualifiers

source

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v_region


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Best Local Similarity 91.4%; Pred. No. 2.4e-97;
Matches 351; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

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DB 1 GACATGAGGGTCCCGCTCAGCTCCCTGGGGCTCCTGCTCTGGGTCCCGAGGTGCC 60
QY 64 TGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGTCATCTGTAGGGGACAGATC 123
DB 61 TGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGTCATCTGTAGGGGACAGATC 120
QY 124 ACCATCACTTCAGGGCAAGTCAGGACATAGTATATTTAAATTTGGTATCAGCAGAA 183
DB 121 ACCATCACTTCAGGGCAAGTCAGGACATAGTATATTTAAATTTGGTATCAGCAGAA 180
QY 184 CCAGGAAAAGTCTCTAAGCTCCTGATCTATTTGTCATCCAGTTTGCAGAGTGGGGTCCCA 243
DB 181 CCAGGAAAAGTCTCTAAGCTCCTGATCTCTGATCCATGTCATCCAGTTTGCAGAGTGGGGTCCCA 240
QY 244 TCAAGGTTTCAGCGGACAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAG 303
DB 241 TCAAGGTTTCAGTGGCAGTGGATCTGGGACAGAGTTTCACTCTCACCATCAGCAGTCTGCAA 300
QY 304 CTGGAAGATTTTCGACATTTACTCTGTACAGTTTATAGTACCCCTCGGAGCTTCGGC 363
DB 301 CTGGAAGATTTTCGACATTTACTCTGTCAACAGAGTTACAGTACCCCTCGGAGCTTCGGC 360

RESULT 12
BC034141 962 bp mRNA linear PRI 08-JUL-2002
LOCUS Homo sapiens, similar to anti TNF-alpha antibody light-chain Fab
DEFINITION fragment, clone MGC:32713 IMAGE:4691280, mRNA, complete cds.
ACCESSION BC034141
VERSION BC034141.1 GI:21707883
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 962)
JOURNAL Strausberg,R.
Direct Submission
National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

/note="V1-J1 region"
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BASE COUNT 97 a 113 c 102 g 94 t
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Best Local Similarity 91.2%; Pred. No. 8.5e-98;
Matches 353; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 ATGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCGAGGTGCC 60
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QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGTCATCTGTAGGGGACAG 120
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QY 241 CCATCAAGGTTTCAGCGGACAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
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DB 302 CAACCTGAAGATTTTGGACATTTACTGTCTCAACAGAGTTACAGTATCCCGTGGACGTT 361
QY 361 GGCCAAAGGACCAAGTGGAAATCAA 387
DB 362 GGCCAAAGGACCAAGTGGAAATCAA 388

RESULT 11
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LOCUS Homo sapiens clone BUS immunoglobulin light chain variable region
DEFINITION gene, partial cds.
ACCESSION AF228327
VERSION AF228327.1 GI:9295292
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 400)
JOURNAL Maloum,K., Dighiero,G. and Magnac,C.C.
Unpublished
Direct Submission
Physiopathology, Institut Pasteur, 28 rue
Submitted (13-JAN-2000)
du DR Roux, Paris 75015, France
Location/Qualifiers
1..400
/organism="Homo sapiens"
/mol_type="genomic DNA"

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REMARK
COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: CLONTECH
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arranged by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
 Series: tRAI Plate: 41 Row: j Column: 19
 This clone was selected for full length sequencing because it
 passed the following selection criteria: GenomesScan gene
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FEATURES
source

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 DB 26 ATGGACATGAGGTCCTCCGCTCAGCTCTGGGGCTCTTCTGCTCTGCTCCAGGTGCC 85
 QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGTCATCTGTAGGGGACAGA 120
 DB 86 AGATGTGACATCCAGTCTGACCCAGTCTCCATCTTCCCTGCTGTCATCTGTAGGGGACAGA 145
 QY 121 GTCACATCACTTGCAGGGCAGTGCAGGACATAGGATTAATTAATTTGGTATCAGCAG 180
 DB 146 GTCACATCACTTGCAGGGCAGTGCAGGACATAGGATTAATTAATTTGGTATCAGCAG 205
 QY 181 AAACAGGAAGAGCTCCTAAGCTCTGATCTATGTCATCCAGTTTCGAAAGTGGGTC 240
 DB 206 AAACAGGAAGAGCTCCTAAGCTCTGATCTATGTCATCCAGTTTCGAAAGTGGGTC 265
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 QY 361 GGCCAAAGGACCAAGGTGGAAATCAA 387

Db 386 GGCGGAGGACCAAGTGGAGATCAAA 412

RESULT 13
 HUMIGKVCA 432 bp mRNA linear PRI 05-MAY-2000
 LOCUS Homo sapiens immunoglobulin kappa light chain VC region (IGK) mRNA,
 DEFINITION partial cds.
 ACCESSION L01279.1 GI:185984
 VERSION L01279.1
 KEYWORDS Homo sapiens (human)
 SOURCE ORGANISM
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 432)
 AUTHORS Friedman,D.P., Moore,J.S., Eriksen,J., Manz,J., Goldman,J.,
 Nowell,P.C. and Silberstein,L.E.
 TITLE Variable region gene analysis of an isotype-switched (IgA) variant
 of chronic lymphocytic leukemia
 JOURNAL Blood 80 (9), 2287-2297 (1992)
 MEDLINE 93043344
 PUBMED 1421400
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 Best Local Similarity 92.3%; Pred. No. 3.3e-97;
 Matches 360; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

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 Qy 358 TTGCGCCCAAGGACCAAGGTGGAATCAA 387
 Db 361 TTGCGCCCAAGGACCAAGGTGGAATCAA 390

RESULT 14
 MMU57579 390 bp mRNA linear PRI 02-OCT-1996
 LOCUS Macaca mulatta Ig rearranged light chain variable region, anti-RBC
 DEFINITION antibody, mRNA, partial cds.
 ACCESSION U57579
 VERSION U57579.1 GI:1575105
 KEYWORDS

SOURCE Macaca mulatta (rhesus monkey)

ORGANISM Macaca mulatta
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 Cercopithecinae; Macaca.

REFERENCE 1 (bases 1 to 390)
 Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A.
 and Capra, J.D.

TITLE Variable Region Gene Segment Utilization in Rhesus Monkey
 Hybridomas Producing Human Red Blood Cell-Specific Antibodies:
 Predominance of the VH4 Family but not VH4-21 (V4-34)

JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 390)
 Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A.
 and Capra, J.D.

TITLE Direct Submission
 JOURNAL Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center,
 University of Texas Southwestern Medical Center, 6000 Harry Hines
 Blvd., Dallas, TX 75235-9140, USA

FEATURES Location/Qualifiers

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BASE COUNT 94 a 110 c 98 g 88 t
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Query Match 85.1%; Score 329.4; DB 9; Length 390;
 Best Local Similarity 90.7%; Pred. No. 9.5e-97;
 Matches 351; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 1 ATGACATGAGGGTCCCGCTCAGCTCTGGGGTCTCTGCTGCTGGCTCCAGGTGCC 60

Db 1 ATGACATGAGGGTCCCGCTCAGCTCTGGGGTCTCTGCTGCTGGCTCCAGGTGCC 60

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RESULT 15

AX305000 974 bp DNA linear PAT 11-DEC-2001
 LOCUS Sequence 29 from Patent EP1158004.
 DEFINITION AX305000
 ACCESSION AX305000
 VERSION AX305000.1 GI:17644678

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 Takashi, T., Katsunari, T.P. and Nobuaki, H.

AUTHORS Human monoclonal antibody against a costimulatory signal
 transduction molecule a11m and pharmaceutical use thereof

JOURNAL Patent: EP 1158004-A 29 28-NOV-2001;
 Japan Tobacco Inc. (JP)

FEATURES Location/Qualifiers

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CDS 39..749

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BASE COUNT 246 a 282 c 232 g 214 t

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Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGATCTGTAGGGGACAGA 120

Db 99 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGATCTGTAGGGGACAGA 158

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Db 219 AAACCCAGGAAAGCCCTTAAACTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGTC 278
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Db 339 CAGCCTGAAGATTTTTCGCACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTTC 398
Qy 361 GGCCNAGGGACCAAGGTGGAATCAAA 387
Db 399 GGCCNAGGGACCAAGGTGGAATCAAA 425

Search completed: December 29, 2003, 19:01:27
Job time : 1605.14 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 1674.6 Seconds
(without alignments)
5616.780 Million cell updates/sec

Title: US-09-019-441-3

Perfect score: 387

Sequence: 1 ATGCACATGAGGTCCCGC.....GGACCAAGGTGGAATCAAA 387

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_est3:*

12: gb_est4:*

13: gb_est5:*

14: gb_est6:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	343.4	88.7	493	9	AW405753
2	342.2	88.4	819	14	CB985931
3	340.6	88.0	724	14	CB959008
4	340.6	88.0	923	13	BQ882857

5	339	87.6	799	14	CB984750
6	339	87.6	969	13	BU899279
7	337.4	87.2	769	14	CB986208
8	335.8	86.8	708	14	CB956923
9	335.8	86.8	745	14	CB958128
10	334.2	86.4	763	14	CB985168
11	332.6	85.9	750	14	CB985395
12	332.6	85.9	891	10	BG540787
13	331.6	85.7	891	13	BX336281
14	331	85.5	743	14	CB957909
15	331	85.5	764	14	CB956251
16	331	85.5	943	13	BQ707106
17	329.6	85.2	724	10	BG537031
18	329.4	85.1	464	2	HSM070437
19	329.4	85.1	748	14	CB956867
20	329.4	85.1	756	14	CB958365
21	329.4	85.1	809	14	CB986250
22	329.4	85.1	867	10	BG754732
23	329.4	85.1	886	10	BG756818
24	327.8	84.7	830	14	CB985233
25	327.8	84.7	864	10	BG548281
26	326.6	84.4	391	9	AW404992
27	326.2	84.3	453	9	AW383563
28	326.2	84.3	683	14	CB984699
29	326.2	84.3	741	14	CB955999
30	326.2	84.3	933	13	BQ899146
31	326.2	84.3	992	13	BQ708832
32	325.2	84.0	719	14	CB956636
33	325.2	84.0	964	13	BQ706786
34	325	84.0	834	14	CB987081
35	324.6	83.9	447	9	AW405752
36	324.6	83.9	633	12	BM769550
37	324.6	83.9	703	14	CB955760
38	324.6	83.9	730	14	CB984911
39	324.6	83.9	791	14	CB984519
40	324.6	83.9	797	14	CB987347
41	324.6	83.9	939	13	BQ705876
42	323	83.5	732	14	CB957611
43	323	83.5	742	14	CB984723
44	323	83.5	747	14	CB955983
45	323	83.5	748	14	CB957590

ALIGNMENTS

RESULT 1
AW405753
LOCUS
DEFINITION
UI-HF-BL0-abp-a-02-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3057250 5', mRNA sequence.
493 bp mRNA linear EST 16-FEB-2000
ACCESSION
AW405753
VERSION
AW405753.1 GI:6924810
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 493)
TITLE
NIH-MGC http://mgs.nci.nih.gov/
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabs@email.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES

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FEATURES
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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3057290"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_lib="NIH_MGC_37"
/notes="vector: p713-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
117 a 138 c 119 g 119 t
BASE COUNT
ORIGIN

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BASE COUNT	117 a	138 c	119 q	119 t

Query Match	88.7%	Score 343.4;	DB 9;	Length 493;
Best Local Similarity	93.2%	Pred. No. 6.6e-92;		
Matches 359: Conservative	0;	Mismatches 26;	Indels 0;	Gaps 0;

3	Qy	GGACATAGAGGTCCCCGCTCAGCTCCCTGGGGCTCCTTCTGCTCTGGGTCCAGTGCAG	62
8	Db	GGACATAGAGGTCCCCGCTCAGCTCCCTGGGGCTCCTGCTACTCTCTGGGTCCGAGTGCAG	67
63	Qy	ATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCATCTCTAGGGGACAGGT	122
68	Db	ATGTGACATCCAGATGACCCAGTCTCCATCTCCTCTGCTGCATCTCTAGGAGACAGGT	127
123	Qy	CACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAGAA	182
128	Db	CACCATCACTTGCAGGGCAAGTCAGGACATTAGCAGCTATTTAAATTGGTATCAGCAGAA	187
183	Qy	ACCAGGAAAAGCTCCTAAGCTCTCGATCTATGTTTGCATCCAGTTTGCAAAAGTGGGGTCCC	242
188	Db	ACCAGGAAAAGCCCTAAGCTCTCGATCTATGCTGCATCCAGTTTGCAAAAGTGGGGTCCC	247
243	Qy	ATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGAGTTTCACTCTCACCTCAGCAGCCGTGCA	302
248	Db	ATCAAGGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCTGTGCA	307
303	Qy	GCCTGAAGATTTTGCAGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGAGCTTCGG	362
308	Db	ACCTGAAGATTTTGCACACTTACTACTCTCAACAGAGTTACAGTACCCCTCGGAGCTTCGG	367
363	Qy	CCAAGGACCAAGGTGGAAATCAAA	387
368	Db	CCAAGGACCAAGGTGGAAATCAAA	392

RESULT 2
CB985931

LOCUS	CB985931	819 bp	mRNA	linear	EST	01-MAY-2000
DEFINITION	AGENCOURT_13604097 NIH_MCC184 Homo sapiens CDNA clone IMAGE:30328622 5', mRNA sequence.					

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE	1 (bases 1 to 819)
AUTHORS	NTH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs@emall.nih.gov Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arraved by: The I.M.A.G.E. Consortium (LNLN)

DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDCM139 row: 1 column: 15
 High quality sequence stop: 499.
 Location/Qualifiers

source

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1. .819
/organism="Homo sapiens"
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/lab_host="PH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_184"
/notes="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
SfiI (ggccattagcgc); Site_2: SfiI (ggccgctcggcc);
Library is oligo-dr primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyroid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGCGGCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGCGCGAGCGCGCATG-3'(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH MGC Library."

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BASE COUNT	211 a	233 c	193 g	182 t
ORIGIN				

Query Match 88.4%; Score 342.2; DB 14; Length 819;
Best Local Similarity 92.8%; Pred. No. 2e-91;
Matches 359; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy	1	ATGGACATGAGGCTCCCGCTCAGCTCTGGGGCTCTTCTGCTCTGGCTCCAGGTGCC	80
Db	31	ATGGACATGAGGCTCCCGCTCAGCTCTGGGGCTCTTCTGCTCTGGCTCCAGGTGCC	90
Qy	61	AGATGTGACATCAGATGACCCAGTCTCATTCTTCCTGTCTGCATCTGTAGGGACAGA	120
Db	91	AGATGTGACATCAGATGACCCAGTCTCATTCTTCCTGTCTGCATCTGTAGGGACAGA	150
Qy	121	GTCAACATCACTGTGAGGGCAAGTCAGGACATTAGGTATTATTAAATTCGGTATCAGCAG	180
Db	151	GTCAACATCACTGTGCGGGCAAGTCAGGACATTAGGACCTATTAAATTCGGTATCAGCAG	210
Qy	181	AAACCAAGGAAAAGCTCTTAAGCTCTGATCTATGTTTGCATCCAGTTTGCAAAGTGGGGTC	240
Db	211	AAACCAAGGAAAAGCTCTTAAGCTCTGATCTATGTTTGCATCCAGTTTGCAAAGTGGGGTC	270
Qy	241	CCATCAAGGTTTCAGCGCAGTGGATCTGGGACAGAGTTTCACTCTCAACGTCAGCAGCCTG	300
Db	271	CCATCAAGGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCAACATCAGCAGCTG	330
Qy	301	CAGCCTGAAGATTTTGGGACTTATTACTGTCTACAGGTTTATAGTACCCCTCCGACGTTTC	360
Db	331	CAACCTGAAGATTTTGGCACTTACTGTCTCAACAGAGTTTACAGTACCCCTCCGACGTTTC	390
Qy	361	GGCCAGGACCAAGGTGGAAATCAAA	387
Db	391	GGCCAAATGGACCAAGGTGGAAATCAAA	417

RESULT 3
CB959008

LOCUS	CB959008	AGENCOURT	13664954	NIH_MGC_184	Homo sapiens	cDNA clone	linear	EST 29-APR-2000
DEFINITION		IMAGE:30354121	5', mRNA	sequence.				
ACCESSION	CB959008							
VERSION	CB959008..1	GI:30215124						
KEYWORDS	EST.							
SOURCE	Homo sapiens (human)							
ORGANISM	Homo sapiens							

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished.

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

Plate: NDCM155 row: p column: 02
 High quality sequence stop: 549.

FEATURES

Location/Qualifiers

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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30354121"
 /lab_host="DH10B (TI phage-resistant)"
 /clone_lib="NIH MGC 184"
 /notes="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site 1: Sfil (ggccattatggcc); Site 2: Sfil (ggccgctcgcc); Library is oligo-dT primed and directionally cloned. cDNA was prepared from a glandular pool of tissues from thyroid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATATATGCCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGCGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH MGC Library."

BASE COUNT 188 a 205 c 179 g 150 t 2 others

Query Match 88.0%; Score 340.6; DB 14; Length 724;
 Best Local Similarity 92.5%; Pred. No. 5.6e-91;
 Matches 358; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 1 ATGACATGAGGTCCCGCTCAGCTCTGGGGCTCTTCTGCTCTGGCTCCAGGTGCC 60
 Db 24 ATGACATGAGGTCCCGCTCAGCTCTGGGGCTCTTCTGCTCTGGCTCCAGGTGCC 83
 Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGTCATCTGTAGGGGACAGA 120
 Db 84 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGTCATCTGTAGGGGACAGA 143
 Qy 121 GTACCATCATCTTGCAGGGCAAGTCAGGACATTAAGGTATTATTTAAATGGTATCAGCAG 180
 Db 144 GTCACTATCACTTCCCGGCAAGTCAGGACATTAACAGGTATTATTAATGGTATCAGCAG 203
 Qy 181 AAACCGAGAAAGCTCTTAAGTCTCTGATCTATGTTGATCCAGTTTGCATTTGCAAGTGGGGTC 240
 Db 204 AAACCGAGAAAGCTCTTAAGTCTCTGATCTATGCTGATCCAGTTTGCATTTGCAAGTGGGGTC 263
 Qy 241 CCATCAAGTTTCAGCGCAGTGGATCTGGGACAGATTCTACTCTCACCATCAGCAGCTG 300
 Db 264 CCATCAAGTTTCAGCGCAGTGGATCTGGGACAGATTCTACTCTCACCATCAGCAGCTG 323
 Qy 301 CAGCCTGAAGATTTTGGGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGCTC 360
 Db 324 CAACCTGAAGATTTTGGGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGCTC 387
 Qy 361 GGCCAAAGGACCAAGGTGGAAATCAAA 387
 Db 384 GGCCAAAGGACCAAGGTGGAAATCAAA 410

RESULT 4

BO882857
 LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BO882857

AGENCOURT_8616470 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6302159

5', mRNA sequence.

BO882857

BO882857.1 GI:2274865

EST.

BO882857

EST.

BO882857

EST.

BO882857

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BO882857

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BO882857

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BO882857

EST.

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Db      313 CAACCTGAAGATTTTGCACACTTACTGTCTCAACAGACTTACATTACCCCTCGGACGTC 372
Qy      361 GGCCAAAGGACCAAGGTGGAAATCAAA 387
Db      373 GGCCAAAGGACCAAGGTGGAAATCAAA 399

RESULT 5
LOCUS   CB984750
DEFINITION AGENCOURT 13574990 NIH MGC 184 Homo sapiens cDNA clone
IMAGE:30326373 5', mRNA sequence.
ACCESSION CB984750
VERSION   CB984750.1 GI:30279274
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 799)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM133 row: k column: 22
High quality sequence stop: 412.
FEATURES
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/db_xref="taxon:9606"
/clone="IMAGE:30326373"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 184"
/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
SfiI (ggccattatggcc); Site_2: SfiI (ggccgcttcggcc);
Library is oligo-dT primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyroid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGGAGCGGCGGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH MGC Library."
BASE COUNT 178 a 226 c 227 g 168 t
ORIGIN
Query Match 87.6%; Score 339; DB 14; Length 799;
Best Local Similarity 92.2%; Pred. No. 1.8e-90;
Matches 357; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy      1 ATGGACATGAGGGTCCCGCTCAGCTCTCGGGGCTCTTCTGCTCTGCTCCCGAGTGCC 60
Db      28 ATGGACATGAGGGTCCCGCTCAGCTCTCGGGGCTCTTCTGCTCTGCTCCCGAGTGCC 87
Qy      61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGTCATCTGTAGGGACAGA 120
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Qy      181 AAACCGAGAAAGCTCCTAAGCTCTTGATCTATGTTGCATCCAGTTTGCAGAGTGGGTC 240
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Qy      241 CCATCAAGGTTTCAGCGGCACTGGATCTGGACAGAGTTCTCTACCGTCAGCAGCTG 300
Db      268 CCATCAAGGTTTCAGTGGCAGTGGATCTGGACAGAGTTCTCTACCGTCAGCAGCTG 327
Qy      301 CAGCTGAAGATTTTGGGACTTATTACTGTCTACAGTTTATAGTACCCCTCGGACGTC 360
Db      328 CAACCTGAAGATTTTGCACACTTACTGTCTCAACAGAGTTACAGTACCCCTCGGACGTC 387
Qy      361 GGCCAAAGGACCAAGGTGGAAATCAAA 387
Db      388 GGCCAAAGGACCAAGGTGGAAATCAAA 414

RESULT 6
LOCUS   BU99279
DEFINITION AGENCOURT_8532125 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279986
5', mRNA sequence.
ACCESSION BU99279
VERSION   BU99279.1 GI:24081192
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 969)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bs-x@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2470 row: h column: 03
High quality sequence stop: 640.
FEATURES
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1. 969
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6279986"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 113"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
BASE COUNT 234 a 288 c 229 g 218 t
ORIGIN
Query Match 87.6%; Score 339; DB 13; Length 969;
Best Local Similarity 92.2%; Pred. No. 2e-90;
Matches 357; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy      1 ATGGACATGAGGGTCCCGCTCAGCTCTCGGGGCTCTTCTGCTCTGCTCCCGAGTGCC 60
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74 AGATGTGCCATCCAGATGACCCAGTCTCCATCTCTCCCTGCTGTCATCTGTAGGAGACAGA 133
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134 GTACCATTAATCTTCCCGGCAAGTCAGGCAATTAAGCAATGATTTAGGCTGTGATCAGCAG 193
181 AAACACGAAAGCTCTCCTAGCTCCTGATCTATGTCATCCAGTTTGCAAGTGGGGTC 240
194 AAACACGAAAGCCCTTAACTCTGATCTATGCTGCATCCAGTTTACAAAGTGGGGTC 253
241 CCATCAAGTTTCAGCGGCAAGTCAGGACATTAAGTATTATTTAAATTCGTATCAGCAG 300
254 CCATCAAGTTTCAGCGGCAAGTCAGGACATTAAGTATTATTTAAATTCGTATCAGCAG 313
301 CAGCTGAAGTTTTCGCACTTATTAAGTCTTATGTCATCCAGTTTATAGTACCCCTCGGACGTC 360
314 CAGCTGAAGTTTTCGCACTTATTAAGTCTTATGTCATCCAGTTTATAGTACCCCTCGGACGTC 373
361 GGCCAAAGGACCAAGTGGAAATCAAA 387
374 GGCCAAAGGACCAAGTGGAAATCAAA 400

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RESULT 7
 CB986208 769 bp mRNA linear EST 01-MAY-2003
 LOCUS
 DEFINITION AGENCOURT_13632591 NIH_MGC_184 Homo sapiens cDNA clone
 IMAGE:30328747 5', mRNA sequence.

ACCESSION
 VERSION CB986208
 KEYWORDS
 SOURCE EST.
 ORGANISM Homo sapiens (human)
 HOMO sapiens
 HOMO sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 1 (bases 1 to 769)
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: NDCM139 row: n column: 20
 High quality sequence stop: 408.
 Location/Qualifiers

FEATURES

source

1. 769
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30328747"
 /lab_host="DH10B (TI phage-resistant)"
 /clone_lib="NIH_MGC_184"
 /note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site 1:
 SfiI (ggccgctcgcc); Site 2: SfiI (ggccgctcgcc);
 Library is oligo-dT primed and directionally cloned. cDNA
 parathyroid, adrenal, cortex and pineal gland. 5' and 3'
 adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
 5'-ATTTAGAGCCGAGGCGGCAGATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.38
 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH MGC Library."

BASE COUNT

192 a 231 c 178 g 168 t

ORIGIN

Query Match 87.2%; Score 337.4; DB 14; Length 769;
 Best Local Similarity 92.0%; Pred. No. 5.3e-90;
 Matches 356; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

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QY 1 ATGCACATGAGGTCCTCCGCTCAGCTCCTGGGGCTCTCTTCTGTGGTCCAGGTGCC 60
DB 24 ATGCACATGAGGTCCTCCGCTCAGCTCCTGGGGCTCTCTTCTGTGGTCCAGGTGCC 83
QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGACAGA 120
DB 84 AGTGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGACAGA 143
QY 121 GTCAACATCACTTTCGAGGGCAAGTCAGGACATTAAGTATTATTTAAATTCGTATCAGCAG 180
DB 144 GTCAACATCACTTTCGAGGGCAAGTCAGGACATTAAGTATTATTTAAATTCGTATCAGCAG 203
QY 181 AAACACGAAAGCTCTCCTAGCTCCTGATCTATGTCATCCAGTTTATAGTACCCCTCGGACGTC 240
DB 204 AAACACGAAAGCTCTCCTAGCTCCTGATCTATGTCATCCAGTTTATAGTACCCCTCGGACGTC 263
QY 241 CCATCAAGTTTCAGCGGCAAGTCAGGACATTAAGTATTATTTAAATTCGTATCAGCAG 300
DB 264 CCATCAAGTTTCAGCGGCAAGTCAGGACATTAAGTATTATTTAAATTCGTATCAGCAG 323
QY 301 CAGCTGAAGTTTTCGCACTTATTAAGTCTTATGTCATCCAGTTTATAGTACCCCTCGGACGTC 360
DB 324 CAGCTGAAGTTTTCGCACTTATTAAGTCTTATGTCATCCAGTTTATAGTACCCCTCGGACGTC 383
QY 361 GGCCAAAGGACCAAGTGGAAATCAAA 387
DB 384 GGCCAAAGGACCAAGTGGAAATCAAA 410

```

RESULT 8

CB956923

LOCUS

DEFINITION

AGENCOURT_13778921 NIH_MGC_184 Homo sapiens cDNA clone

IMAGE:30351494 5', mRNA sequence.

ACCESSION

VERSION CB956923

KEYWORDS

SOURCE EST.

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

NIH-MGC http://mgi.nci.nih.gov/
 1 (bases 1 to 708)

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

Plate: NDCM149 row: b column: 15

High quality sequence stop: 520.

Location/Qualifiers

1. 708

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:30351494"

/lab_host="DH10B (TI phage-resistant)"

/clone_lib="NIH_MGC_184"

/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site 1:
 SfiI (ggccgctcgcc); Site 2: SfiI (ggccgctcgcc);
 Library is oligo-dT primed and directionally cloned. cDNA
 parathyroid, adrenal, cortex and pineal gland. 5' and 3'
 adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
 5'-ATTTAGAGCCGAGGCGGCAGATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.38
 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH MGC Library."

FEATURES

source

1. 708
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30351494"
 /lab_host="DH10B (TI phage-resistant)"
 /clone_lib="NIH_MGC_184"
 /note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site 1:
 SfiI (ggccgctcgcc); Site 2: SfiI (ggccgctcgcc);
 Library is oligo-dT primed and directionally cloned. cDNA

was prepared from a glandular pool of tissues from thyroid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTTCAGAGCGCGGCGGCATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH MGC Library."

BASE COUNT 183 a 203 c 174 g 147 t 1 others

Query Match 86.8%; Score 335.8; DB 14; Length 708;

Best Local Similarity 91.7%; Pred. No. 1.5e-89; Mismatches 32; Indels 0; Gaps 0;

Matches 355; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 1 ATGACATGAGGGTCCCGCTCAGCTCTGGGGTCTCTTCTGCTCTGGCTCCCGAGTGCC 60
 |||||
 Db 31 ATGACATGAGGGTCCCGCTCAGCTCTGGGGTCTCTGCTCTGCTCTGGCTCCCGAGTGCC 90
 |||||

Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGAGAGA 120
 |||||
 Db 91 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGAGAGA 150
 |||||

Qy 121 GTCACCATCTCTGAGGCGAAGTCAGACATAGGTATTTAAATTTGTATCAGCAG 180
 |||||
 Db 151 GTCACCATCTCTGAGGCGAAGTCAGACATAGGTATTTAAATTTGTATCAGCAG 210
 |||||

Qy 181 AAACAGGAAAGCTCCTAAGCTCTGATCTATGTTGATCCAGTTTGCAAGTGGGTC 240
 |||||
 Db 211 AAACAGGAAAGCTCCTAAGCTCTGATCTATGTTGATCCAGTTTGCAAGTGGGTC 270
 |||||

Qy 241 CCATCAAGTTTCAGGCGAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGAGCCTG 300
 |||||
 Db 271 CCATCAAGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCTG 330
 |||||

Qy 301 CAGCTGAAGATTTTGGCACTTATCTGCTACAGTTTATAGTACCCCTCGACAGTTC 360
 |||||
 Db 331 CAACCTGAAGATTTTGGCACTTATCTGCTCAACAGACTTACAGTACCCCTCGACAGTTC 390
 |||||

Qy 361 GGCCAGGAGCAAGGTGGAATCAAA 387
 |||||
 Db 391 GGCCAGGAGCAAGGTGGAATCAAA 417
 |||||

RESULT 9

CB958128

LOCUS

DEFINITION AGENCOURT 13784991 NIH_MGC_184 Homo sapiens cDNA clone

IMAGE:30352433 5', mRNA sequence.

CB958128

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homosapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 745)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDCM151 row: 1 column: 18

High quality sequence stop: 557.

FEATURES
source

1..745

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:30352433"

/lab_host="DH10B (Ti phage-resistant)"

/clone_lib="NIH_MGC_184"

/notes="Organ: Pooled Glandular; Vector: pDNR-LIB; Site_1:

SfiI (ggccattatggcc); Site_2: SfiI (ggccgctccggcc);

Library is oligo-dr primed and directionally cloned. cDNA

was prepared from a glandular pool of tissues from thyroid,

parathyroid, adrenal, cortex and pineal gland. 5' and 3'

adaptors were used in cloning as follows: 5' adaptor

sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:

5'-ATTTCAGAGCGCGGCGGCATG-dt(30)BN-3' (where B = A,

C, or G and N = A, C, G, or T). Average insert size 1.38

kb (range 0.60-3.5 kb). 15/15 colonies contained inserts

by PCR. This library was enriched for full-length clones

and was constructed by Clontech Laboratories (Palo Alto,

CA). Note: this is a NIH_MGC Library."

BASE COUNT 192 a 215 c 187 g 151 t

Query Match 86.8%; Score 335.8; DB 14; Length 745;

Best Local Similarity 91.7%; Pred. No. 1.6e-89;

Matches 355; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 1 ATGACATGAGGGTCCCGCTCAGCTCTGGGGTCTCTTCTGCTCTGGCTCCCGAGTGCC 60
 |||||
 Db 29 ATGACATGAGGGTCCCGCTCAGCTCTGGGGTCTCTTCTGCTCTGGCTCCCGAGTGCC 88
 |||||

Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGAGAGA 120
 |||||
 Db 89 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGAGAGA 148
 |||||

Qy 121 GTCACCATCTCTGAGGCGAAGTCAGACATAGGTATTTAAATTTGTATCAGCAG 180
 |||||
 Db 149 GTCACCATCTCTGAGGCGAAGTCAGACATAGGTATTTAAATTTGTATCAGCAG 208
 |||||

Qy 181 AAACAGGAAAGCTCCTAAGCTCTGATCTATGTTGATCCAGTTTGCAAGTGGGTC 240
 |||||
 Db 209 AAACAGGAAAGCTCCTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAGTGGGTC 268
 |||||

Qy 241 CCATCAAGTTTCAGGCGAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGAGCCTG 300
 |||||
 Db 269 CCATCAAGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCGTCAGAGCCTG 328
 |||||

Qy 301 CAGCTGAAGATTTTGGCACTTATCTGCTACAGTTTATAGTACCCCTCGACAGTTC 360
 |||||
 Db 329 CAACCTGAAGATTTTGGCACTTATCTGCTCAACAGAGTTTCAATACCCCTCGACAGTTC 388
 |||||

Qy 361 GGCCAGGAGCAAGGTGGAATCAAA 387
 |||||
 Db 389 GGCCAGGAGCAAGGTGGAATCAAA 415
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RESULT 10

CB958128

LOCUS

DEFINITION AGENCOURT 13438717 NIH_MGC_184 Homo sapiens cDNA clone

IMAGE:30326564 5', mRNA sequence.

CB958128

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homosapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 763)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

CB958128 763 bp mRNA linear EST 01-MAY-2003

AGENCOURT 13438717 NIH_MGC_184 Homo sapiens cDNA clone

IMAGE:30326564 5', mRNA sequence.

CB958128

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homosapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 763)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM134 row: c column: 21
High quality sequence stop: 602.

FEATURES

Location/Qualifiers
1. 763
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30328564"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NIH_MGC_184"
/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site 1: SfiI (ggccattatgcc); Site 2: SfiI (ggccgctcgcc); Library is oligo-dT primed and directionally cloned. cDNA Library is oligo-dT primed and directionally cloned. cDNA parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGCGCCATTATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGGCGGCATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH MGC Library."
BASE COUNT 198 a 218 c 191 g 155 t 1 Others
ORIGIN

Query Match 86.4%; Score 334.2; DB 14; Length 763;
Best Local Similarity 91.5%; Pred. No. 4.8e-89;
Matches 354; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
Qy 1 ATGACATGAGGGTCCCGCTCAGCTCTGGGGCTCTTCTGCTCTGCTCCAGGTGCC 60
Db 29 ATGACATGAGGGTCCCGCTCAGCTCTGGGGCTCTTCTGCTCTGCTCCAGGTGCC 88
Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTCCCTGCTGCTATCTGTAGGAGCAGA 120
Db 89 AGATGTGACATCCAGATGACCCAGTCTCCATCTCCCTGCTGCTATCTGTAGGAGCAGA 148
Qy 121 GTACCATCATCTTCAGGCGCAAGTCAGGACATTAAGTATTATTAATTTGGTATCAGCAG 180
Db 149 GTACCATCATCTTCAGGCGCAAGTCAGGACATTAAGTATTATTAAGTATTATCAGCAG 208
Qy 181 AACACAGAAAGCTCTTAAGCTCTGATCTATGTTGATCCAGTTTGGCAAGTGGGGTC 240
Db 209 AAAGCAGGAAAGCCCTTAAGTCTGATCTATGTTGATCCAGTTTGGCAAGTGGGGTC 268
Qy 241 CCATCAGGTTTCAGGCGAGTGGTCTGGGACAGATTCATCTCAGCGTCAGCAGCTG 300
Db 269 CCATCAGGTTTCAGGCGAGTGGTCTGGGACAGATTCATCTCAGCGTCAGCAGCTG 328
Qy 301 CAGCTGAAGATTTCGACATTTATCTGCTACAGGTTTATAGTACCCCTCGGACGTTTC 360
Db 329 CAGCTGAAGATTTCGACATTTATCTGCTACAGGTTTATAGTACCCCTCGGACGTTTC 388
Qy 361 GGCCAAAGGACCAAGGTGGAAATCAAA 387
Db 389 GGCCAAAGGACCAAGGTGGAAATCAAA 415

RESULT 11
CB985395
LOCUS
DEFINITION AGNCOURT 13643437 NIH_MGC_184 Homo sapiens cDNA clone
IMAGE:30328513 5', mRNA sequence.

ACCESSION CB985395
VERSION CB985395.1
KEYWORDS GI:30279919
SOURCE EST
ORGANISM Homo sapiens (human)

REFERENCE

1 (bases 1 to 750)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM139 row: e column: 02
High quality sequence stop: 555.

FEATURES

Location/Qualifiers
1. 750
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30328513"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NIH_MGC_184"
/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site 1: SfiI (ggccattatgcc); Site 2: SfiI (ggccgctcgcc); Library is oligo-dT primed and directionally cloned. cDNA Library is oligo-dT primed and directionally cloned. cDNA parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGCGCCATTATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGGCGGCATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH MGC Library."
BASE COUNT 195 a 207 c 190 g 153 t 5 Others
ORIGIN

Query Match

Best Local Similarity 91.2%; Pred. No. 1.4e-88;
Matches 353; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 1 ATGACATGAGGGTCCCGCTCAGCTCTGGGGCTCTTCTGCTCTGCTCCAGGTGCC 60
Db 31 ATGACATGAGGGTCCCGCTCAGCTCTGGGGCTCTTCTGCTCTGCTCCAGGTGCC 90
Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTCCCTGCTGCTATCTGTAGGAGCAGA 120
Db 91 AGATGTGACATCCAGATGACCCAGTCTCCATCTCCCTGCTGCTATCTGTAGGAGCAGA 150
Qy 121 GTACCATCATCTTCAGGCGCAAGTCAGGACATTAAGTATTATTAATTTGGTATCAGCAG 180
Db 151 GTACCATCATCTTCAGGCGCAAGTCAGGACATTAAGTATTATTAATTTGGTATCAGCAG 210
Qy 181 AACACAGAAAGCTCTTAAGCTCTGATCTATGTTGATCCAGTTTGGCAAGTGGGGTC 240
Db 211 AACACAGAAAGCTCTTAAGCTCTGATCTATGTTGATCCAGTTTGGCAAGTGGGGTC 270
Qy 241 CCATCAGGTTTCAGGCGAGTGGTCTGGGACAGATTCATCTCAGCGTCAGCAGCTG 300
Db 271 CCATCAGGTTTCAGGCGAGTGGTCTGGGACAGATTCATCTCAGCGTCAGCAGCTG 330
Qy 301 CAGCTGAAGATTTCGACATTTATCTGCTACAGGTTTATAGTACCCCTCGGACGTTTC 360
Db 331 CAACCTGAAGATTTCGACATTTATCTGCTACAGGTTTATAGTACCCCTCGGACGTTTC 390

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QY 361 GGCCAGGGACCAAGTGGAAATCAAA 387
Db 391 GCGGAGGGACCAAGTGGAGATCAAA 417

RESULT 12
LOCUS BG540787 891 bp mRNA linear EST 03-APR-2001
DEFINITION 602570674F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4695114 5',
mRNA sequence.
ACCESSION BG540787
VERSION BG540787.1 GI:13533020
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 891)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM1520 row: c column: 19
High quality sequence stop: 577.
Location/Qualifiers
1. 891
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:4695114"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_77"
/note="Torgan; lung; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggcccctcgcc); Site 2: SfiI (ggccattatgcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGCGGCACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH MGC Library."
BASE COUNT 239 a 248 c 237 g 167 t
ORIGIN
Query Match 85.9%; Score 332.6; DB 10; Length 891;
Best Local Similarity 91.2%; Pred. No. 1.6e-88;
Matches 353; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 ATGGACATGAGGGTCCCGCTCAGCTCTGGGGCTCTCTGCTGTGGCTCCCGAGTGCC 60
Db 26 ATGGACATGAGGGTCCCGCTCAGCTCTGGGGCTCTCTGCTGTGGCTCCCGAGTGCC 85

QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGTGATCTGTAGGGGACAGA 120
Db 86 AGATGTGACATCCAGTTCACCCAGTCTCCATCTTCCCTGTCTGTGATCTGTAGGGGACAGA 145

QY 121 GTCACCATCTTGCCAGGCGAAGTCAGCATATTAGGTATTATTTAAATGGTATCAGCAG 180
Db 146 GTCACCATCTTGCCGGGCGAGTCAGGGCATATTAGCAATTATTTAGCTGTGATCAGCAA 205

QY 181 AAACAGGAAAGCTTCCTAAGCTCCTGATCTATGTGTGATCCAGTTTGCAAAGTGGGTC 240
Db 206 AAACAGGAAAGCCCTTAAGATTTCTATCTATGCTGATCCATCTTGCAAAGTGGGTC 265

QY 241 CCATCAAGGTTTCAGCGCAGTGGATCTGGACAGAGTTCTACTCTCACCGTCAGCAGCTG 300
Db 266 CCATCAAGGTTTCAGCGCAGTGGATCTGGACAGAGTTCTACTCTCACAAATCAGCAGCTG 325

QY 301 CAGCCTGAAGATTTTGGGACTTATTACTGTCTACAGGTTTATATACCCCTCGACGCTTC 360
Db 326 CAGCCTGAAGATTTTGGCAACGTATTACTGTCAACAGCTTAATACTATTATTCTCGGACGCTTC 385

QY 361 GGCCAGGGACCAAGTGGAAATCAAA 387
Db 386 GGCCAGGGACCAAGTGGAAATCAAA 412

RESULT 13
LOCUS BX336281 891 bp mRNA linear EST 02-MAY-2003
DEFINITION BX336281 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI026YL22 5-PRIME, mRNA sequence.
ACCESSION BX336281
VERSION BX336281.1 GI:30341499
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 891)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1696.r for
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODI026DF11QPI&cluster=1696.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CSODI026DF11QPI.
Location/Qualifiers
1. 891
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="CSODI026YL22"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 215 a 260 c 223 g 193 t
ORIGIN
Query Match 85.7%; Score 331.6; DB 13; Length 891;
Best Local Similarity 91.2%; Pred. No. 3.2e-88;
Matches 352; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 2 TGGACATGAGGGTCCCGCTCAGCTCTGGGGCTCTCTGCTGTGGCTCCCGAGTGCCA 61
Db 67 TGGACATGAGGGTCCCGCTCAGCTCTGGGGCTCTCTGCTGTGGCTCCCGAGTGCCA 126

QY 62 GATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGTGATCTGTAGGGGACAGAG 121
Db 127 GATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGTGATCTGTAGGGGACAGAG 186

QY 122 TCACCATCACTTGCCAGGCGAAGTCAGCATATTAGGTATTATTTAAATGGTATCAGCAGA 181
Db 187 TCACCATCACTTGCCGGGCGAGTCAGGGTATTAGCAGCTGGTATTAGCCTGGTATCAGCAGA 246

```


by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

BASE COUNT 192 a 214 c 203 g 151 t 4 others

ORIGIN

```
Query Match      85.5%; Score 331; DB 14; Length 764;
Best Local Similarity 91.0%; Pred. No. 4.4e-88;
Matches 352; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Qy 1 ATGACATGAGGTCCTCGGCTCAGCTCCTGGGGCTCCTCTGCTCTGCTCCCAAGTGCC 60
Db 27 ATGACATGAGGTCCTCGGCTCAGCTCCTGGGGCTCCTCTGCTCTGCTCCCAAGTGCC 86

Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
Db 87 AGGTGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 146

Qy 121 GTCACCATCACTTCGCGGCAAGTCAGGACATTAGGTATTATTAAATTGGTATCAGCAG 180
Db 147 GTCACCATCACTTCGCGGCAAGTCAGGACATTAGGTATTATTAAATTGGTATCAGCAG 206

Qy 181 AAACGAGGAAAGCTCCTAAGCTCCTGATCTATGTTCATCCAGTTTGCAAGTGGGTC 240
Db 207 ATACGAGGAGAGCCCTTAAGCGCTGATCTATGCTGCATCCACTTTGCAAGTGGGTC 266

Qy 241 CCATCAAGTTTCAGGGGAGTGGATCTGGGACAGATTCACTCTCACCGTCAGCAGCTG 300
Db 267 CCATCAAGTTTCAGGGGAGTGGATCTGGGACAGAAATTCACCTCTCAATCAGCAGCTG 326

Qy 301 CAGCTGAAGATTTTGGGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTT 360
Db 327 CAGCTGAAGATTTTGGGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTT 386

Qy 361 GGCCAAAGGACCAAGGTGGAATCAAA 387
Db 387 GGCCAAAGGACCAAGGTGGAATCAGA 413
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Search completed: December 29, 2003, 21:44:14
Job time : 1677.6 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 168.851 Seconds
(without alignment)
6187.013 Million cell updates/sec

Title: US-09-019-441-3

Perfect score: 387

Sequence: 1 ATGACATGAGGTCCCGC.....GGACCAAGGTGGAATCAAA 387

Scoring table: IDENTITY NUC

Gapop 10.0., Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq_19Jun03.*

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1: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
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22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	387	100.0	387	19 AAV33309	Anti-human CD23 5E
2	387	100.0	19035	19 AAV61794	Traget plasmid Man
3	342.2	88.4	729	21 AAA11630	Human immunoglobul
4	342.2	88.4	729	24 ABL46009	Humanised anti-Fas
5	339	87.6	1106	24 ABQ54241	Human ovarian anti
6	334.2	86.4	396	18 AAT75423	Human anti-tumour
7	334.2	86.4	438	22 AAH41157	Human coding seque
8	329.4	85.1	974	24 AAS99473	Anti-human AILIM m

9	326.2	84.3	714	21 AAA46899	DNA encoding the k
10	324.6	83.9	387	21 AAZ39327	Nucleotide sequenc
11	324.6	83.9	448	25 ABT31874	Anti-CD40 monoclon
12	323	83.5	728	25 ABT31882	Anti-CD40 monoclon
13	321.4	83.0	390	21 AAZ39340	Nucleotide sequenc
14	318.2	82.2	388	18 AAT73441	Human immunoglobul
15	318.2	82.2	388	19 AAV39239	Functional kappa t
16	318.2	82.2	388	20 AAZ21993	Partial nucleotide
17	316	82.2	936	21 AAA27390	Human IGFAM-10 imm
18	316.6	81.8	817	21 AAA27389	Human IGFAM-9 immu
19	316.6	81.8	1066	14 AAQ49943	Human anti-HBs lig
20	316.4	81.8	917	21 AAA27381	Human IGFAM-1 immu
21	313.4	81.0	427	25 ABT31868	Anti-CD40 monoclon
22	313.4	81.0	427	25 ABT31870	Anti-CD40 monoclon
23	311.8	80.6	565	24 ABQ58923	Human colon cancer
24	311.8	80.6	698	25 ABT31880	Anti-CD40 monoclon
25	311.8	80.6	944	22 AAF44892	Human breast cance
26	309.8	80.1	384	21 AAZ39320	Nucleotide sequenc
27	309.2	79.9	772	24 ABQ56247	Human ovarian anti
28	308.8	79.8	523	24 ABL37621	Human colon tumour
29	308.4	79.7	737	24 AAD31829	Human pancreatic t
30	307	79.3	387	16 AAQ82749	93KA9 anti-Varicel
31	307	79.3	409	19 AAV39241	Functional kappa c
32	307	79.3	439	18 AAT73443	Human immunoglobul
33	306	79.1	387	21 AAZ39325	Nucleotide sequenc
34	305.4	78.9	439	20 AAZ21995	Partial nucleotide
35	304.2	78.6	705	18 AAT61240	Human anti-RSV mon
36	303.8	78.5	389	15 AAQ67194	Humanized 1308F VL
37	303.8	78.5	389	17 AAT16181	Hul308 VL encoding
38	303.6	78.4	928	21 AAA27393	Human IGFAM-13 imm
39	302.6	78.2	424	25 ACC46511	Human dithp anti ge
40	302.4	78.1	372	21 AAZ39326	Nucleotide sequenc
41	302	78.0	420	18 AAT73445	Human immunoglobul
42	302	78.0	420	19 AAV39293	Synthetic kappa li
43	302	78.0	420	20 AAZ22047	Nucleotide sequenc
44	302	78.0	497	24 ABL38222	Human colon tumour
45	302	78.0	3819	18 AAT78825	Kappa light chain

ALIGNMENTS

RESULT 1	AAV33309	standard; DNA; 387 BP.
ID	AAV33309	standard; DNA; 387 BP.
XX	AAV33309;	
AC	AAV33309;	
DT	25-MAR-2003 (updated)	
DT	18-NOV-1998 (first entry)	
XX	Anti-human CD23 588 monoclonal antibody light chain variable region DNA.	
DE	Anti-human CD23 588 monoclonal antibody; light chain variable region; human CD23; IGE; PceRti/CD23; gamma-1 constant region; gamma-3 constant region; allergy; inflammation; autoimmune disease; allergic rhinitis; conjunctivitis; autoimmune haemolytic anaemia; ss.	
XX	Macaca fascicularis	
OS	Macaca fascicularis	
XX	Key	Location/Qualifiers
PH	Key	1..387
FT	CDS	/tag= a
FT		/product= "anti-human CD23 588 light chain variable region"
FT		/note= "CDS does not contain a stop codon"
FT	sig_peptide	1..66
FT		/tag= b
FT	mat_peptide	67..387
FT		/tag= c
FT	misc_feature	136..168
FT		/tag= d
FT		/note= "encodes CDR 1 region"

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FT misc_feature 214..234
FT /tag= e
FT /note= "encodes CDR 2 region"
FT misc_feature 331..357
FT /tag= f
FT /note= "encodes CDR 3 region"
XX
XX WO9837099-A1.
XX
XX PD
XX 27-AUG-1998.
XX
XX 17-FEB-1998; 98WO-US02253.
XX
XX 20-FEB-1997; 97US-0803085.
XX
XX 05-FEB-1998; 98US-0019441.
XX
XX (IDEC-) IDEC PHARM CORP.
XX PA
XX (SEK ) SEIKAGAKU CORP.
XX
XX PI Klotzer WS, Nakamura T, Reff ME;
XX
XX WPI; 1998-467495/40.
XX P-PSDB; AAW70379.
XX
XX New anti-human CD23 monoclonal antibody - used for inhibiting IgE
XX expression to treat or prevent allergic, inflammatory and
XX auto:immune conditions
XX
XX Example 1; Pages 106-108; 146pp; English.
XX
XX The present sequence represents a DNA sequence encoding the light
XX chain variable region of primate monoclonal antibody anti-human CD23 5E8.
XX The invention provides primate monoclonal antibodies which specifically
XX bind human CD23, the low affinity receptor for IgE (FcεRI/CD23),
XX and comprise either of a human gamma-1 or human gamma-3 constant region
XX that binds to human Fc gamma receptors and inhibits IgE expression.
XX The monoclonal antibodies of the invention are claimed to be useful
XX for inhibiting induced IgE production for treating or preventing
XX allergic, inflammatory and autoimmune conditions e.g. allergic rhinitis
XX conjunctivitis, autoimmune haemolytic anaemia, etc.
XX (Updated on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 387 BP; 92 A; 102 C; 98 G; 95 T; 0 other;
XX
XX Query Match 100.0%; Score 387; DB 19; Length 387;
XX Best Local Similarity 100.0%; Pred. No. 1.6e-108;
XX Matches 387; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 ATGGACATGAGGTCCTCCGCTCAGCTCCTGGGCTCCTTCTGCTGCTCCAGGTGCC 60
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCACTCTGTAGGGACAGA 120
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCACTCTGTAGGGACAGA 120
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 121 GTCACCATCACTTGCAGGCGAAGTCAGACATAGGTATTATTTAAATGGTATCAGCAG 180
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 121 GTCACCATCACTTGCAGGCGAAGTCAGACATAGGTATTATTTAAATGGTATCAGCAG 180
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 181 AAACAGGAAAGCTCCTTAAGCTCTGATGTATGTCATCCAGTTTGCAGGCGGTC 240
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 181 AAACAGGAAAGCTCCTTAAGCTCTGATGTATGTCATCCAGTTTGCAGGCGGTC 240
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 241 CCATCAAGGTTCCAGGCGAGTGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 241 CCATCAAGGTTCCAGGCGAGTGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 301 CAGCCTGAAGATTTTGCAGACTTATTTACTGTCTACAGGTTTATGATACCCCTCGGACGTTTC 360
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 301 CAGCCTGAAGATTTTGCAGACTTATTTACTGTCTACAGGTTTATGATACCCCTCGGACGTTTC 360
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 361 GGCCAAAGGACCAAGGTGGAAATCAA 387

```

```

Db 361 GGCCAAAGGACCAAGGTGGAAATCAA 387
RESULT 2
AAV61794
ID AAV61794 standard; DNA; 19035 BP.
XX
XX AC AAV61794;
XX
XX 07-JUN-1999 (first entry)
XX
XX Traget plasmid Mandy containing anti-CD23 gene.
XX
XX Mandy; target plasmid; gene integration; gene amplification;
XX homologous recombination; vector; neomycin phosphotransferase;
XX neo gene; selectable marker; immunoglobulin; CD23; 5E8; human; ss.
XX
XX Chimeric - Mus sp.
XX OS Chimeric - Escherichia coli.
XX OS Chimeric - Baculovirus.
XX OS Chimeric - Cytomegalovirus.
XX OS Chimeric - Rhesus macaque polyoma virus.
XX OS Chimeric - Photinus sp.
XX OS Chimeric - Salmonella typhimurium.
XX OS Chimeric - Homo sapiens.
XX
XX Key Location/Qualifiers
XX misc_feature 361
XX /tag= a
XX /note= "this base represents a nucleotide missing
XX from the sequence given in the
XX specification. It is included to
XX maintain the nucleotide numbering in the
XX specification for this sequence"
XX
XX misc_feature 721
XX /tag= b
XX /note= "this base represents a nucleotide missing
XX from the sequence given in the
XX specification. It is included to
XX maintain the nucleotide numbering in the
XX specification for this sequence"
XX
XX misc_feature 2941
XX /tag= c
XX /note= "this base represents a nucleotide missing
XX from the sequence given in the
XX specification. It is included to
XX maintain the nucleotide numbering in the
XX specification for this sequence"
XX
XX misc_feature 3301
XX /tag= d
XX /note= "this base represents a nucleotide missing
XX from the sequence given in the
XX specification. It is included to
XX maintain the nucleotide numbering in the
XX specification for this sequence"
XX
XX misc_feature 4261
XX /tag= e
XX /note= "this base represents a nucleotide missing
XX from the sequence given in the
XX specification. It is included to
XX maintain the nucleotide numbering in the
XX specification for this sequence"
XX
XX misc_feature 4621..4622
XX /tag= f
XX /note= "these bases represent nucleotides missing
XX from the sequence given in the
XX specification. They are included to
XX maintain the nucleotide numbering in the
XX specification for this sequence"
XX
XX misc_feature 8161
XX /tag= g
XX /note= "this base represents a nucleotide missing

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from the sequence given in the
 specification. It is included to
 maintain the nucleotide numbering in the
 specification for this sequence"
 8521..8522
 /*tag= h
 /note= "these bases represent nucleotides missing
 from the sequence given in the
 specification. They are included to
 maintain the nucleotide numbering in the
 specification for this sequence"
 12061
 /*tag= i
 /note= "this base represents a nucleotide missing
 from the sequence given in the
 specification. It is included to
 maintain the nucleotide numbering in the
 specification for this sequence"
 12421
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 from the sequence given in the
 specification. They are included to
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 specification for this sequence"
 13381
 /*tag= k
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 from the sequence given in the
 specification. It is included to
 maintain the nucleotide numbering in the
 specification for this sequence"
 14641..14642
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 /note= "these bases represent nucleotides missing
 from the sequence given in the
 specification. They are included to
 maintain the nucleotide numbering in the
 specification for this sequence"
 15001..15002
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 /note= "these bases represent nucleotides missing
 from the sequence given in the
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 maintain the nucleotide numbering in the
 specification for this sequence"
 15961..15962
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 from the sequence given in the
 specification. They are included to
 maintain the nucleotide numbering in the
 specification for this sequence"
 16321..16322
 /*tag= o
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 from the sequence given in the
 specification. They are included to
 maintain the nucleotide numbering in the
 specification for this sequence"
 98WO-US03935.
 98US-0023715.
 97US-0819866.
 (IDEC-) IDEC PHARM CORP.
 Barnett RS, McLachlan KR, Reff ME;

XX WPI; 1998-521229/44.
 DR
 XX
 PT Site specific integration of DNA in mammals for expressing, e.g.
 PT immunoglobulins - comprises homologous recombination using
 PT selectable marker and target plasmids.
 XX
 PS Example 1; Fig 10; 114pp; English.
 XX
 CC This is the nucleotide sequence of novel target plasmid Mandy.
 CC The plasmid includes an inactivated murine dihydrofolate reductase
 CC (DHFR) gene, the Escherichia coli beta-galactosidase gene,
 CC baculovirus DNA, a cassette comprising the promoter and enhancer
 CC elements from cytomegalovirus and SV40 virus, the E. coli
 CC beta-glucuronidase (GUS) gene, firefly luciferase gene, an
 CC inactivated Salmonella typhimurium histidinol dehydrogenase (HisD)
 CC gene and transposon Tn5 neomycin phosphotransferase (neo) gene
 CC sequences, in a pBR-derived backbone, and also an anti-human CD23
 CC IgE receptor human gamma-1 monoclonal antibody 5S8 gene. The
 CC invention provides a novel method for integrating a desired
 CC exogenous DNA at a target site within the genome of a mammalian
 CC cell via homologous recombination. This involves transfecting the
 CC cell with a 'marker plasmid' such as Desmond (see AAV61792), which
 CC contains a unique sequence that is foreign to the mammalian cell
 CC genome and which provides a substrate for homologous recombination,
 CC followed by transfection with a 'target plasmid', such as Mandy
 CC or Molly (see AAV61793), containing a sequence which provides for
 CC homologous recombination with the unique sequences contained in
 CC the marker plasmid, and further comprising a desired DNA that is
 CC to be integrated into the mammalian cells, typically an
 CC immunoglobulin or other secreted mammalian glycoprotein. The
 CC homologous recombination system utilises the neo gene as a
 CC dominant selectable marker. The neo gene is split into 3 exons.
 CC Exon 3 is present on the marker plasmid and becomes integrated
 CC into the host cell genome upon integration of the marker plasmid
 CC into the mammalian cells. Exons 1 and 2 are present on the
 CC targeting plasmid, and are separated by an intron into which at
 CC least one gene of interest is cloned. Homologous recombination
 CC of the targeting vector with the integrated marking vector results
 CC in correct splicing of all 3 exons of the neo gene and expression
 CC of a functional neo protein. The method is applicable to all
 CC mammalian cells, and can be used to express any type of recombinant
 CC protein. The use of a triply spliced selectable marker means that
 CC all selected colonies arise from homologous recombination. In
 CC addition, the number of colonies that need to be screened to
 CC identify high producer clones is reduced. An amplifiable gene can
 CC be inserted on integration of the marking vector, so that when a
 CC gene is targeted to this site, the gene is further enhanced by gene
 CC amplification.
 XX
 SQ Sequence 19035 BP; 4705 A; 4968 C; 4822 G; 4519 T; 21 other;
 Query Match 100.0%; Score 387; DB 19; Length 19035;
 Best Local Similarity 100.0%; Pred. No. 7.1e-108;
 Matches 387; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGCACATGAGGGTCCCGCTCAGCTCCCTGGGGCTCCTTCTGCTGGCTCCCGAGTGCC 60
 DB 7541 ATGCACATGAGGGTCCCGCTCAGCTCCCTGGGGCTCCTTCTGCTGGCTCCCGAGTGCC 7600
 QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTGCTGATCTGTAGGGGACAGA 120
 DB 7601 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTGCTGATCTGTAGGGGACAGA 7660
 QY 121 GTCCACATCACTTGCAGGGCAAGTCCAGGACATTTAGGTATTTTAAATTTGGTATCAGCAG 180
 DB 7661 GTCCACATCACTTGCAGGGCAAGTCCAGGACATTTAGGTATTTTAAATTTGGTATCAGCAG 7720
 QY 181 AAACAGGAAAGCTCTTAAGCTTCCTGATCTATGTTGCATCCAGTTTGCAGTGGGGTC 240
 DB 7721 AAACAGGAAAGCTCTTAAGCTTCCTGATCTATGTTGCATCCAGTTTGCAGTGGGGTC 7780
 QY 241 CCATCAAGGTTTCCAGCGGAGTGGATCTGGGACAGAGTTCACTCTCTACCGTCAGCAGCCTG 300

Db 7781 CCATCAAGTTTCAGCGCAGTGGATCTGGACAGAGTTCACTCTACCGTCAGCAGCTG 7840
 Qy 301 CAGCCTGAAGATTTTGGGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTT 360
 Db 7841 CAGCCTGAAGATTTTGGGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTT 7900
 Qy 361 GGCCAGGGACCAAGTGGAAATCAAA 387
 Db 7901 GGCCAGGGACCAAGTGGAAATCAAA 7927

RESULT 3

AAAL1630
 ID AAAL1630 standard; DNA; 729 BP.

XX AC AAAL1630;

DT 08-AUG-2000 (first entry)

XX Human immunoglobulin light chain kappa region subgroup type I DNA.

XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
 KW dermatological; immunosuppressive; thymimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antinfertility; neuroprotective; antirheumatic; anti-Fas;
 KW Hashimoto disease; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection; ss.

XX Homo sapiens.

XX EP990663-A2.

XX 05-APR-2000.

XX 29-SEP-1999; 99EP-0307711.

XX 30-SEP-1998; 98JP-0276881.

XX 30-SEP-1998; 98JP-0276882.

XX (SANY) SANKYO CO LTD.

XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;

XX WPI; 2000-258930/23.

XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems

XX Example 2; Page 154; 263pp; English.

XX This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thymimetic,
 CC antirheumatic, nephrotropic, antinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiac and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,

CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a human immunoglobulin light chain kappa variable region subgroup type I
 CC which is used in the construction of humanised anti-Fas antibody
 CC constructs described in the method of the invention.

XX SQ Sequence 729 BP; 192 A; 200 C; 182 G; 155 T; 0 other;

Query Match 88.4%; Score 342.2; DB 21; Length 729;

Best Local Similarity 92.8%; Pred. No. 1.1e-94;

Matches 359; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 1 ATGGACATGAGGTCCTCCGCTCAGCTCCCTGGGGCTCTTCTGCTCTGGCTCCCGAGTGCC 60

Db 7 ATGGACATGAGGTCCTCCGCTCAGCTCCCTGGGGCTCTTCTGCTCTGGCTCCCGAGTGCC 66

Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120

Db 67 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 126

Qy 121 GTCCACATCACTTTCAGGGCAAGTCAGGACATTAAGTATTAATTAATTCGATCAGCAG 180

Db 127 GTCCACATCACTTTCAGGGCAAGTCAGGACATTAAGTATTAATTAATTCGATCAGCAG 186

Qy 181 AAACAGGAAAGCTCTTAAGTCTTCCATCTATGTTGCATCCAGTTTGAAGTGGGTC 240

Db 187 AAACAGGAAAGCTCTTAAGTCTTCCATCTATGTTGCATCCAGTTTGAAGTGGGTC 246

Qy 241 CCATCAAGGTTTCAGCGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCGCTG 300

Db 247 CCATCAAGGTTTCAGCGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCGCTG 306

Qy 301 CAGCCTGAAGATTTTCGACTTATTACTGTCTACAGTTTATAGTACCCCTCGGACGTTT 360

Db 307 CAACTGAGATTTTGCACCTTACTACTGTCAACAGAGTTACAGTACCCCTCGAAGCGTTT 365

Qy 361 GGCCAGGGACCAAGTGGAAATCAAA 387

Db 367 GGCCAGGGACCAAGTGGAAATCAAA 393

RESULT 4

ABL46009
 ID ABL46009 standard; DNA; 729 BP.

XX ABL46009;

XX 26-APR-2002 (first entry)

XX Humanised anti-Fas antibody related PCR primer SEQ ID NO 76.

XX Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand;
 KW light chain subunit; apoptosis; immunosuppressive; antiallergic;
 KW autoimmune disease; allergy; atopic; PCR primer; ss.

XX Synthetic.

XX JP2001342148-A.

XX 11-DEC-2001.

XX 28-MAR-2001; 2001JP-0093106.

XX 29-MAR-2000; 2000JP-0090918.

XX (SANY) SANKYO CO LTD.

XX WPI; 2002-145113/19.
XX
XX Drug containing humanised anti-Fas antibody, used for preventing and
PT treating autoimmune diseases, allergy, and atopy -
XX
XX Example 15 (preparatory); Page 40; 194pp; Japanese.
XX
XX The invention relates to a preventive or treating agent for diseases
CC caused by abnormality in Fas/Fas ligand system containing as the active
CC component an antibody having as the light chain subunit a polypeptide
CC containing residues 1-218 of one of 3, 239 residue amino acid sequences,
CC or residues 1-451 of one of 3, 470 residue amino acid sequences, all
CC fully defined in the specification and having an activity of combining
CC specifically with mammalian Fas and an activity of inducing apoptosis
CC in a cell expressing Fas. The agent has immunosuppressive and
CC antiallergic activity and is used for preventing and treating autoimmune
CC diseases, allergy, atopy and others. The present sequence is that of a
CC PCR primer, useful to the invention.
XX
XX Sequence 729 BP; 192 A; 200 C; 182 G; 155 T; 0 other;
SQ
Query Match 88.4%; Score 342.2; DB 24; Length 729;
Best Local Similarity 92.8%; Pred. No. 1.1e-94;
Matches 359; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
QY 1 ATGGACATGAGGGTCCCGCTCAGCTCTGGGGCTCCTTCTGCTCTGGCTCCAGGTGCC 60
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
7 ATGGACATGAGGGTCCCGCTCAGCTCTGGGGCTCCTTCTGCTCTGGCTCCAGGTGCC 66
QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGTGATCTGTAGGGGACAGA 120
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
67 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGTGATCTGTAGGGGACAGA 126
QY 121 GTCACCATCTCTGACGGGCAAGTCAGGACATTAGGTATTATTTAAATGGTATCAGCAG 180
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
127 GTCACCATCTCTGACGGGCAAGTCAGGACATTAGGTATTATTTAAATGGTATCAGCAG 186
QY 181 AAACCCAGGAAGTCTTAGCTCTTATCTATCTATGTTTCATCCAGTTTGCAGTGGGTC 240
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
187 AAACCCAGGAAGTCTTAGCTCTTATCTATCTATGTTTCATCCAGTTTGCAGTGGGTC 246
QY 241 CCATCAAGTTTCAGCGCAGTGGATCTGGACAGATTTCACTCTCACCGTCAGCAGCTG 300
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
247 CCATCAAGTTTCAGCGCAGTGGATCTGGACAGATTTCACTCTCACCATCAGCAGCTG 306
QY 301 CAGCTGAAGATTTCGACTTATTAATCTGCTACAGGTTTATAGTACCCCTCGAGCTTC 360
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
307 CAACCTGAAGATTTCGAACTTACTACTGTCAACAGAGTTACAGTACCCCTCGAAGCTTC 366
QY 361 GGCCNAGGGACCAAGTGGAAATCAAA 387
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
367 GGCCNAGGGACCAAGTGGAAATCAAA 393
RESULT 5
ABQ54241
ID ABQ54241 standard; cDNA; 1106 BP.
XX
XX AC ABQ54241;
XX
XX 22-AUG-2002 (first entry)
XX
XX Human ovarian antigen HRACW30 cDNA, SEQ ID NO:121.
XX
XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;

KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive; chromosome 2p12;
KW gene; ss.
XX Homo sapiens.
OS
XX WO200200677-A1.
PN
XX 03-JAN-2002.
PD
XX 07-JUN-2001; 2001WO-US18569.
PF
XX 07-JUN-2000; 2000US-209467P.
PR
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX Birse CE, Rosen CA;
PI
XX WPI; 2002-147878/19.
DR
XX P-PSDB; ABP41164.
DR
XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
PT useful in the prevention, treatment and diagnosis of cancer (e.g.
PT ovarian cancer), immune disorders, cardiovascular disorders and
PT neurological diseases -
XX
XX Claim 1; SEQ ID NO 121; 2922pp; English.
PS
XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
CC encompasses polypeptides 90% identical and polynucleotides 95% identical
CC to the sequences of the invention. The invention additionally relates to
CC recombinant vectors and host cells comprising human ovarian antigen
CC polynucleotides, antibodies against human ovarian antigens, and the use
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC treating, prognosing or preventing various ovary and/or breast-related
CC disorders. Such conditions include ovarian cancer and breast cancer, and
CC metastatic tumours of ovarian or breast origin, reproductive system
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC vaginitis), immune disorders (e.g., congenital and acquired
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC respiratory disorders, neurological disorders, gastrointestinal disorders
CC and urinary system disorders. Ovarian antigen polypeptides and
CC polynucleotides may also be used in screening for compounds which
CC modulate ovarian antigen expression or activity. The polynucleotides may
CC further be used for gene therapy, chromosome mapping, in the
CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents a cDNA encoding a human ovarian antigen of the
CC invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 1106 BP; 321 A; 296 C; 247 G; 227 T; 15 other;
SQ
Query Match 87.6%; Score 339; DB 24; Length 1106;
Best Local Similarity 90.7%; Pred. No. 1.2e-93;
Matches 351; Conservative 7; Mismatches 29; Indels 0; Gaps 0;
QY 1 ATGCACATGAGGGTCCCGCTCAGCTCTGGGGCTCCTTCTGCTCTGGCTCCAGGTGCC 60
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
79 ATGCACATGAGGGTCCCGCTCAGCTCTGGGGCTCCTTCTGCTCTGGCTCCAGGTGCC 138
QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
139 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 198

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QY 121 GTACCATCACTTCGAGGCAAGTCAGACATTAAGGTATTATTTAAATTTGGTATCAGCAG 180
Db 199 GTACCATCACTTCGCGGGCAAGTCAGACATTAAGGTATTATTTAAATTTGGTATCAGCAG 258
QY 181 AAACAGGAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAGGAGTGGGTC 240
Db 259 AAACAGGAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAGGAGTGGGTC 318
QY 241 CCATCAAGTTTCAGGCGAGTGGATCTGGACAGAGTTCTACTCTCAGCGTCAGAGCTG 300
Db 319 CCATCAAGTTTCAGGCGAGTGGATCTGGACAGAGTTCTACTCTCAGCGTCAGAGCTG 378
QY 301 CAGCTCAAGATTTTCGAGCTTATTACTGTCACAGGTTTATAGTACCCCTCGGAGCTC 360
Db 379 CAGCTCAAGATTTTCGAGCTTATTACTGTCACAGGTTTATAGTACCCCTCGGAGCTC 438
QY 361 GGCCAAAGGACCAAGGTGGAAATCAAA 387
Db 439 GGCCAAAGGACCAAGGTGGAAATCAAA 465

RESULT 6
AAAT75423
ID AAT75423 standard; cDNA; 396 BP.
AC AAAT75423;
XX
XX
DT 12-SEP-1997 (first entry)
DE Human anti-tumour antigen antibody light chain variable region cDNA.
XX
XX
KW Human; tumour antigen; cancer; monoclonal; antibody; light chain;
KW variable region; medicine; pharmacology; biochemistry; ds.
XX
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT sig_peptide 1..66
FT FT /*tag= a
FT mat_peptide 67..396
FT FT /*tag= b
XX
XX
PN JP09100300-A.
XX
XX
PD 15-APR-1997.
XX
XX
PF 03-OCT-1995; 95JP-0278266.
XX
XX
PR 03-OCT-1995; 95JP-0278266.
XX
XX
PA (HAGI/) HAGIWARA Y.
XX
XX
XX WPI; 1997-276726/25.
DR DR P-PSDB; AAW22842.
XX
XX
PT Anticancer human monoclonal antibody variable region sequences - and
PT related DNA and RNA
XX
XX
PS Claim 12; Page 11; 14pp; Japanese.
XX
XX
CC The present sequence encodes a human anti-tumour antigen
CC monoclonal antibody (MAb) light chain variable region, useful in
CC medicine, pharmacology and biochemistry. The isotype of a MAb
CC secreted by the human/human hybridoma H7 was determined to be mu
CC and kappa. Human MAb was purified, and the antigen recognised by
CC human MAb CLN"-IgM identified by western blotting.
XX
XX
SQ Sequence 396 BP; 101 A; 107 C; 97 G; 91 T; 0 other;
Query Match 86.4%; Score 334.2; DB 18; Length 396;
Best Local Similarity 91.5%; Pred. NO. 2.4e-92;
Matches 354; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

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QY 1 ATGCACATGAGGTCCCTCCGCTCAGCTCCTGGGGCTCTTCTGCTCTGGCTCCAGGTGCC 60
Db 1 ATGCACATGAGGTCCCTCCGCTCAGCTCCTGGGGCTCTTCTGCTCTGGCTCCAGGTGCC 60
QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCGATCTGTAGGGACAGA 120
Db 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCGATCTGTAGGGACAGA 120
QY 121 GTACCATCACTTCGAGGCGAAGTCAGGACATTAAGGTATTATTTAAATTTGGTATCAGCAG 180
Db 121 GTACCATCACTTCGAGGCGAAGTCAGGACATTAAGGTATTATTTAAATTTGGTATCAGCAG 180
QY 181 AAACAGGAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAGGAGTGGGTC 240
Db 181 AAACAGGAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAGGAGTGGGTC 240
QY 241 CCATCAAGTTTCAGGCGAGTGGATCTGGACAGAGTTCTACTCTCAGCGTCAGAGCTG 300
Db 241 CCATCAAGTTTCAGTGGCAGTGGATCTGGACAGAGTTCTACTCTCAGCATCAGCAGTCTG 300
QY 301 CAGCTCAAGATTTTCGAGCTTATTACTGTCACAGGTTTATAGTACCCCTCGGAGCTTC 360
Db 301 CAACCTGAAGATTTTCGACTTACTACTGTCAACAGAGTTTACAGTACCCCTCAGACGTTT 360
QY 361 GGCCAAAGGACCAAGGTGGAAATCAAA 387
Db 361 GGCCAAAGGACCAAGGTGGAAATCAAA 387

RESULT 7
AAH41157
ID AAH41157 standard; DNA; 438 BP.
XX
XX
AC AAH41157;
XX
XX
DT 22-AUG-2001 (first entry)
DE Human coding sequence SEQ ID 11.
XX
XX
KW Human; antiarthritic; cardiant; monoclonal antibody; keloid; arthritis;
KW Tumour Growth Factor-beta II receptor; TGF-beta II receptor; atopy;
KW signal transduction inhibition; tissue fibrosis; atherosclerosis; ds.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200136642-A1.
XX
XX
PD 25-MAY-2001.
XX
XX
PF 17-NOV-2000; 2000WO-JP08129.
XX
XX
PR 18-NOV-1999; 99JP-0328681.
PR 08-NOV-2000; 2000JP-0340216.
XX
XX
PA (NIBS ) JAPAN TOBACCO INC.
XX
XX
PI Sakamoto S, Kamada M;
XX
XX
XX WPI; 2001-343825/36.
DR DR P-PSDB; AAB99115.
XX
XX
PT Human monoclonal antibodies recognizing human TGF-beta II receptor,
PT useful for treating TGF-beta associated diseases such as tissue
PT fibrosis -
XX
XX
PS Example.12; Page 103-104; 118pp; Japanese.
XX
XX
CC The present invention relates to novel human monoclonal antibodies. The
CC antibodies can bind to human Tumour Growth Factor-beta (TGF-beta) II
CC receptor, resulting in the inhibition of the signal transduction of human
CC TGF-beta into cells. The antibodies can be used for the prevention and
CC treatment of diseases associated with the production of TGF-beta, such as
CC tissue fibrosis in the lung, liver, skin, kidney or other tissues,

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CC atherosclerosis, atopy, keloid and arthritis. The present sequence was
 CC used in the present invention.
 XX
 SQ Sequence 438 BP; 103 A; 123 C; 111 G; 101 T; 0 other;
 Query Match 86.4%; Score 334.2; DB 22; Length 438;
 Best Local Similarity 91.5%; Pred. No. 2.5e-92;
 Matches 354; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
 QY 1 ATGGACATGAGGTCCTCCCGCTCAGCTCTGGGGCTCTCTGCTCTGGCTCCAGGTGCC 60
 DB 1 ATGGACATGAGGTCCTCCCGCTCAGCTCTGGGGCTCTCTGCTCTGGCTCCAGGTGCC 60
 QY 61 AGATGTGACATCCAGATGACCCAGCTCTCCATCTTCCCTGTCTGTCATCTGTAGGGGACAGA 120
 DB 61 AGGTGTGACATCCAGATGACCCAGCTCTCCATCTTCCCTGTCTGTCATCTGTAGGGGACAGA 120
 QY 121 GTCAACCATCACTTTCAGGGCAAGTCAGGACATTAAGGTATTATTTAAATTTGGTATCAGCAG 180
 DB 121 GTCAACCATCACTTTCAGGGCAAGTCAGGACATTAAGGTATTATTTAAATTTGGTATCAGCAG 180
 QY 181 AAACACAGAAAGCTCTAGCTCTCTGATCTATGTTTCATCCAGTTTGCAAGTGGGGTC 240
 DB 181 AAACACAGAAAGCTCTAGCTCTCTGATCTATGTTTCATCCAGTTTGCAAGTGGGGTC 240
 QY 241 CCATCAAGTTTCAGGGCAGTGGATCTGGGACAGATTCATCTCACCGTCAGCAGCCTG 300
 DB 241 CCATCAAGTTTCAGGGCAGTGGATCTGGGACAGATTCATCTCACAAATCAGCAGCCTG 300
 QY 301 CAGCTGAAGATTTTGGGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTTC 360
 DB 301 CAGCTGAAGATTTTGGCACTTATTACTGTCTACAGGATTAAGTAAACCGCTCACTTTC 360
 QY 361 GGCCAAAGGACCAAGGTGGAAATCAAA 387
 DB 361 GGCCGAGGACCAAGGTGGAGATCAAA 387
 RESULT 8
 AAS99473
 ID AAS99473 standard; cDNA; 974 BP.
 XX
 AC AAS99473;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Anti-human AILIM monoclonal antibody clone Jmab-136, light chain cDNA.
 XX
 KW Human; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
 KW antiallergic; antiulcer; neuroprotective; antithyroid; vasotropic;
 KW immunosuppressive; dermatological; antiinflammatory; hepatotropic;
 KW activation inducible lymphocyte immunomodulatory molecule; AILIM;
 KW monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus;
 KW multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis;
 KW allergic contact-type dermatitis; chronic inflammatory dermatosis;
 KW systemic lupus erythematosus; autoimmune disorder; inflammation; ss;
 KW graft versus host reaction; immune rejection; intestinal immunity;
 KW ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis.
 XX
 OS Homo sapiens.
 XX
 XN WO200187981-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 15-MAY-2001; 2001WO-JP04035.
 XX
 PR 18-MAY-2000; 2000JP-0147116.
 PR 30-MAR-2001; 2001JP-0099508.
 XX
 PA (NIBS) JAPAN TOBACCO INC.
 XX
 PI Tsuji T, Tezuka K, Hori N;

XX WPI; 2002-075313/10.
 DR P-PSDB; AAU74297.
 XX
 PT New human monoclonal antibody that binds to activation inducible
 PT lymphocyte immunomodulatory molecule, useful for treating rheumatoid
 PT arthritis, multiple sclerosis and inflammation
 XX
 PS Claim 45; Page 267-270; 300pp; English.
 XX
 CC The invention relates to a novel human antibody (I), preferably a human
 CC monoclonal antibody which binds to an activation inducible lymphocyte
 CC immunomodulatory molecule (AILIM). (I) is useful for modulating signal
 CC transduction into a cell mediated by AILIM, for modulating proliferation
 CC of AILIM-expressing cells, for modulating production of a cytokine from
 CC AILIM-expressing cells, and for inducing antibody-dependent cytotoxicity
 CC against AILIM-expressing cells and/or immune cytotoxicity or apoptosis of
 CC AILIM-expressing cells. (I) is useful for treating, preventing or
 CC prophylaxis of delayed type allergy. (I) is useful for treating and
 CC preventing various diseases associated with AILIM-mediated
 CC costimulatory transduction, and for inhibiting the onset and/or
 CC advancement of the diseases. (I) is useful for suppression,
 CC prevention and/or treatment of rheumatoid arthritis, multiple
 CC sclerosis, autoimmune thyroiditis, allergic contact-type dermatitis,
 CC chronic inflammatory dermatosis, systemic lupus erythematosus,
 CC insulin-dependent diabetes mellitus, psoriasis, autoimmune or allergic
 CC disorders, inflammation, graft versus host reaction, graft versus host
 CC disease, immune rejection, disorders caused by abnormal intestinal
 CC immunity, specifically inflammatory intestinal disorders such as
 CC ulcerative colitis, pneumonia, hepatitis, nephritis, vasculitis, and
 CC pancreatitis. (I) induces no serious immunorejection due to antigenicity
 CC to human, i.e., human anti-mouse antigenicity (HAMA) in a host.
 CC AAS99444-AAS99477 represent anti-human AILIM monoclonal antibody coding
 CC sequences and PCR primers of the invention.
 XX
 SQ Sequence 974 BP; 246 A; 282 C; 232 G; 214 T; 0 other;
 Query Match 85.1%; Score 329.4; DB 24; Length 974;
 Best Local Similarity 90.7%; Pred. No. 1e-90;
 Matches 351; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
 QY 1 ATGGACATGAGGTCCTCCCGCTCAGCTCTGGGGCTCTCTGCTCTGGCTCCAGGTGCC 60
 DB 39 ATGGACATGAGGTCCTCCCGCTCAGCTCTGGGGCTCTCTGCTCTGGCTCCAGGTGCC 98
 QY 61 AGATGTGACATCCAGATGACCCAGCTCTCCATCTTCCCTGTCTGTCATCTGTAGGGACAGA 120
 DB 99 AGATGTGACATCCAGATGACCCAGCTCTCCATCTTCCGTGTCTGTCATCTGTAGGGACAGA 158
 QY 121 GTCAACCATCACTTTCAGGGCAAGTCAGGACATTAAGGTATTATTTAAATTTGGTATCAGCAG 180
 DB 159 GTCAACCATCACTTTCAGGGCAAGTCAGGACATTAAGGTATTAGCCTGGTATCAGCAG 218
 QY 181 AAACACAGGAAAGCTCTTAAGCTCTCTGATCTATGTTGCATCCAGTTTGCAAGTGGGGTC 240
 DB 219 AAACACAGGAAAGCTCTTAAGCTCTCTGATCTATGTTGCATCCAGTTTGCAAGTGGGGTC 278
 QY 241 CCATCAAGGTTTCAGGGCAGTGGATCTGGGACAGATTTTCACTCTCACCATCAGCAGCCTG 300
 DB 279 CCATCAAGGTTTCAGGGCAGTGGATCTGGGACAGATTTTCACTCTCACCATCAGCAGCCTG 338
 QY 301 CAGCCTGAAGATTTTGGGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTTC 360
 DB 339 CAGCCTGAAGATTTTGGCACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTTC 398
 QY 361 GGCCAAAGGACCAAGGTGGAAATCAAA 387
 DB 399 GGCCAAAGGACCAAGGTGGAAATCAAA 425
 RESULT 9
 AAA46899
 ID AAA46899 standard; DNA; 714 BP.

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XX AC AAA46899;
XX DT 03-OCT-2000 (first entry)
XX DE DNA encoding the kappa chain of immunoglobulin clone 11.2.1.
XX KW Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
XX KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
XX KW proliferative disorder; cancer; immunodeficient disorder; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 67..714
XX FT /*tag= a
XX PN WO200037504-A2.
XX PD 29-JUN-2000.
XX PF 23-DEC-1999; 99WO-US0895.
XX PR 23-DEC-1998; 98US-0113647.
XX PA (PRIZ ) PFIZER INC.
XX PA (ABGE-) ABGENIX INC.
XX PI Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
XX PI Corvalan JR;
XX DR WPI; 2000-442647/38.
XX DR P-PSDB; AAY93735.
XX PT Novel antibodies capable of binding cytotoxic T-lymphocyte antigen
XX PT (CTLA)-4 containing specified heavy and light chain sequences, useful
XX PT for treating, e.g. immune disorders
XX PS Example 2; Fig 22r; 157pp; English.
XX CC The present sequence encodes a kappa chain of an antibody of the
XX CC invention. The antibody is directed cytotoxic T-lymphocyte antigen
XX CC (CTLA)-4. Antibodies of the invention are composed of a heavy chain
XX CC variable region, comprising a modified contiguous sequence from a
XX CC FRI-FR3 sequence encoded by a human VH3-33 family gene. The
XX CC modifications are contained in CDR1, CDR2 and/or framework regions.
XX CC The antibodies may be used to inhibit CTLA-4 and down-regulate the
XX CC immune system to treat hyperimmunity disorders (e.g. autoimmune
XX CC disease, diabetes and graft rejection) and proliferative disorders
XX CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate
XX CC immune system to up-regulate immunodeficient disorders.
XX SQ Sequence 714 BP; 188 A; 199 C; 173 G; 154 T; 0 other;

Query Match 84.3%; Score 326.2; DB 21; Length 714;
Best Local Similarity 90.2%; Pred. No. 8.6e-90;
Matches 349; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy 1 ATGGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCAGGTGCC 60
Db 1 ATGGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTGCTACTCTGGCTCCAGGTGCC 60

Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGATCTGTAGGGGACAGA 120
Db 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGATCTGTAGGGGACAGA 120

Qy 121 GTCACCATCACTTCAGGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAG 180
Db 121 GTCACCATCACTTCAGGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAG 180

Qy 181 AAACAGGAAAGCTCTCTAAGCTCCTGTATGTATGTGATCAGTCTTGCATTTGCAAGTGGGGTC 240
Db 181 AAACAGGAAAGCTCTCTAAGCTCCTGTATGTATGTGATCAGTCTTGCATTTGCAAGTGGGGTC 240

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Qy 241 CCATCAAGTTTCAGCGCAGTGGATCTGGCAGAGTTCACTCTCACCGTCAGCAGCTG 300
Db 241 CCATCAAGTTTCAGTGGCAGTGGATCTGGCAGAGTTCACTCTCACCATCAGCAGTCTG 300

Qy 301 CAGCCTGAAGATTTTGGCACTTATTACTGTCTACAGTTTATAGTACCCCTCGACGCTTC 360
Db 301 CAACCTGAAGATTTTGGCACTTATTACTGTCTACAGTATTACAGTACTCCATTCACTTTC 360

Qy 361 GGCAAGGGACCAAGGTGGAAATCAAA 387
Db 361 GGCCCTGGGACCAAGGTGGAAATCAAA 387

RESULT 10
AAZ39327
ID AAZ39327 standard; DNA; 387 BP.
XX AC AAZ39327;
XX DT 15-FEB-2000 (first entry)
XX DE Nucleotide sequence of chimpanzee V kappa cDNA clone 46-14.
XX KW Complementarity determining region; antibody; primate; immunogenicity;
XX KW Old World ape; Old World monkey; antigen-binding affinity; ss.
XX OS Pan troglodytes.
XX PN WO9955369-A1.
XX PD 04-NOV-1999.
XX PF 28-APR-1999; 99WO-US09131.
XX PR 28-APR-1998; 98US-0083367.
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX PI Taylor AH;
XX DR WPI; 2000-023265/02.
XX DR P-PSDB; AAY56659, AAY56724.
XX PT Antibodies containing donor complementarity determining regions and
XX PT non-human primate acceptor frameworks, having reduced immunogenicity in
XX PS humans
XX PS Example 2; Page 67-68; 123pp; English.
XX CC The invention provides an antibody (Ab) comprising donor CDRs
XX CC (complementarity determining regions) derived from a non-human antigen-
XX CC specific donor antibody, and an acceptor framework from a non-human
XX CC primate. The Abs are prepared by grafting CDRs from a non-human antigen-
XX CC specific donor antibody onto homologous Old World ape or monkey tolerated
XX CC frameworks. The Abs have reduced immunogenicity and are better tolerated
XX CC in humans (because of the close similarity between the human and primate
XX CC proteins), but retain the full antigen-binding affinity of the donor
XX CC antibody.
XX SQ Sequence 387 BP; 94 A; 104 C; 95 G; 94 T; 0 other;

Query Match 83.9%; Score 324.6; DB 21; Length 387;
Best Local Similarity 89.9%; Pred. No. 2.1e-89;
Matches 348; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy 1 ATGGACATGAGGTCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCAGGTGCC 60
Db 1 ATGGACATGAGGTCCCGCTCAGCTCCTGGGGCTCCTGCTCTGCTCTCAGGTACC 60

Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGATCTGTAGGGGACAGA 120
Db 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGATCTGTAGGGGACAGA 120

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QY 121 GTACCATCACTTGCAGGCAAGTCAGGACATTAGGTATTATTAAATTTGGTATCAGCAG 180
 DB 121 GTACCATCACTTGCAGGCAAGTCAGGACATTAGGTATTATTAAATTTGGTATCAGCAG 180
 QY 181 AAACAGGAAAGCTCTTAAGCTCCTGATCTATGTCATCCAGTTTGCAGGAGTGGGTC 240
 DB 181 AAACAGGAAAGCTCTTAAGCTCCTGATCTATGTCATCCAGTTTGCAGGAGTGGGTC 240
 QY 241 CCATCAAGGTTTCAGGCAAGTCAGGACATTAGGTATTATTAAATTTGGTATCAGCAG 300
 DB 241 CCATCAAGGTTTCAGGCAAGTCAGGACATTAGGTATTATTAAATTTGGTATCAGCAG 300
 QY 301 CAGCTGAAGATTTCAGGCAAGTCAGGACATTAGGTATTATTAAATTTGGTATCAGCAG 360
 DB 301 CAGCTGAAGATTTCAGGCAAGTCAGGACATTAGGTATTATTAAATTTGGTATCAGCAG 360
 QY 361 GGCAAGGACCAAGTGGGAAATCAAA 387
 DB 361 GGTGAGGACCAAGTGGGAAATCAAA 387

RESULT 11

ABT31874
 ID ABT31874 standard; DNA; 448 BP.

AC ABT31874;

DT 01-MAY-2003 (first entry)

XX Anti-CD40 monoclonal antibody related DNA SEQ ID No 49.

XX Antiallergic; haemostatic; immunomodulator; cytostatic; antibody;
 KW human CD40; IL-12; LPS; lipopolysaccharide; IFNgamma; interferon gamma;
 KW dendritic cell; high G28-5; CD95 expression; high G28-5; B cell line;
 KW immunoadactivator; anti-tumour agent; immunosuppressant; allergy;
 KW autoimmune disease; coagulation factor VIII inhibitor; anti-CD40; gene;
 KW ds.

XX Unidentified.

XX WO200288186-A1.

XX 07-NOV-2002.

XX 26-APR-2002; 2002WO-JP04292.

XX 27-APR-2001; 2001WO-US13672.

XX 11-MAY-2001; 2001JP-0142482.

XX 05-OCT-2001; 2001JP-0310535.

XX 26-OCT-2001; 2001US-0040244.

XX (KIRI) KIRIN BEER KK.

XX Mikayama T, Yoshida H, Force WR, Chen X, Takahashi N;

XX WPI; 2003-120463/11.

XX P-PSDB; ABJ36932.

XX Anti-CD40 monoclonal antibody with antagonist/agonist activity to CD40,
 PT or functional fragment, is useful in the treatment of e.g. autoimmune
 PT diseases or cancer

XX Claim 26; Page 52-53; 94pp; Japanese.

XX The invention relates to an antibody to human CD40, or its functional
 CC fragment, has at least one of the following properties: acting on
 CC dendritic cells to produce IL-12 in the presence of LPS
 CC (lipopolysaccharide) and IFNgamma (interferon gamma); acting on dendritic
 CC cells to activate maturation of the dendritic cells with high G28-5
 CC antibody; and activating CD95 expression with high G28-5 antibody against
 CC B cell line. Such antibodies or functional fragments can be used as
 CC immunoadactivators, anti-tumour agents, immunosuppressants, and as remedies

CC for autoimmune diseases, allergy or coagulation factor VIII inhibitors
 CC syndrome. This polynucleotide sequence represents a coding DNA sequence
 CC relating to the anti-CD40 monoclonal antibody of the invention.

XX Sequence 448 BP; 111 A; 123 C; 114 G; 100 T; 0 other;

Query Match 83.9%; Score 324.6; DB 25; Length 448;
 Best Local Similarity 91.7%; Pred. No. 2.2e-89;
 Matches 355; Conservative 0; Mismatches 29; Indels 3; Gaps 1;

QY 1 ATGGACATGAGGGTCCCGCTCAGCTCCTGAGCTCTGGGGCTCTTCTGCTCTGGCTCCCGAGTGC 60
 DB 59 ATGGACATGAGGGTCCCGCTCAGCTCCTGAGCTCTGGGGCTCTTCTGCTCTGGCTCCCGAGTGC 118
 QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
 DB 119 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 178
 QY 121 GTCACCATCACTTTCAGGGCAAGTCAAGGACATTAGGTATTATTAAATTTGGTATCAGCAG 180
 DB 179 GTCACCATCACTTTCAGGGCAAGTCAAGGACATTAGGTATTATTAGCTTGTATCAGCAG 238
 QY 181 AAACAGGAAAGCTCTTAAGCTCCTGATCTATGTCATCCAGTTTGCAGGAGTGGGTC 240
 DB 239 AAACAGGAAAGCTCTTAAGCTCCTGATCTATGTCATCCAGTTTGCAGGAGTGGGTC 298
 QY 241 CCATCAAGGTTTCAGGGCAAGTCTGGACAGAGTTCACCTCTCACCCTCAGCAGCCTG 300
 DB 299 CCATCAAGGTTTCAGGGCAAGTCTGGACAGAGTTCACCTCTCACCCTCAGCAGCCTG 358
 QY 301 CAGCTGAAGATTTCAGGCAAGTCTGATCTATGTCATCAGGTTTATAGTACCCCTCGGAGCTTC 360
 DB 359 CAGCTGAAGATTTCAGGCAAGTCTGATCTATGTCATCAGGTTTATAGTACCCCTCGGAGCTTC 415
 QY 361 GGCAAGGACCAAGTGGGAAATCAAA 387
 DB 416 GGCAAGGACCAAGTGGGAAATCAAA 442

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ABT31882
 ID ABT31882 standard; DNA; 728 BP.

AC ABT31882;

DT 01-MAY-2003 (first entry)

XX Anti-CD40 monoclonal antibody related DNA SEQ ID No 65;

XX Antiallergic; haemostatic; immunomodulator; cytostatic; antibody;
 KW human CD40; IL-12; LPS; lipopolysaccharide; IFNgamma; interferon gamma;
 KW dendritic cell; high G28-5; CD95 expression; high G28-5; B cell line;
 KW immunoadactivator; anti-tumour agent; immunosuppressant; allergy;
 KW autoimmune disease; coagulation factor VIII inhibitor; anti-CD40; gene;
 KW ds.

XX Unidentified.

XX WO200288186-A1.

XX 07-NOV-2002.

XX 26-APR-2002; 2002WO-JP04292.

XX 27-APR-2001; 2001WO-US13672.

XX 11-MAY-2001; 2001JP-0142482.

XX 05-OCT-2001; 2001JP-0310535.

XX 26-OCT-2001; 2001US-0040244.

XX (KIRI) KIRIN BEER KK.

XX Mikayama T, Yoshida H, Force WR, Chen X, Takahashi N;

XX Ig; affinity constant; human; antigen; hybridoma; B cell; transgene;
 KW transgenic; mouse; CD4; antibody; autoimmune; inflammatory;
 KW transplant rejection; ss.
 XX Homo sapiens.
 XX OS
 XX W09713852-A1.
 XX PN
 XX XX
 XX 17-APR-1997.
 XX PD
 XX XX
 XX 10-OCT-1996; 96WO-US16433.
 XX PF
 XX XX
 XX 10-OCT-1995; 95US-0544404.
 XX PR
 XX XX
 XX (GENP-) GENPHARM INT INC.
 XX PA
 XX XX
 XX Kay RM, Lonberg N;
 XX PI
 XX WPI; 1997-235888/21.
 XX DR
 XX XX
 XX Novel anti-CD4 antibody produced by transgenic mice - used in the
 PT treatment of auto-immune disease etc.
 XX PT
 XX XX
 XX Claim 44; Page 255; 396pp; English.
 XX XX
 CC A novel composition has been developed which comprises an immunoglobulin
 CC (Ig) having an affinity constant (Ka) of at least 2 multiply
 CC 100000000 M-1 for binding to a predetermined human antigen. The
 CC present sequence represents a human light chain variable region partial
 CC nucleotide sequence, 10C5 kappa, which encodes an amino acid sequence
 CC from a claimed immunoglobulin that specifically binds human CD4. The
 CC anti-CD4 antibodies may be used in therapeutic and diagnostic
 CC applications, especially for the treatment of human diseases. These
 CC antibodies reduce activity of CD4 cells and reduce undesirable
 CC autoimmune reactions, inflammatory response and transplant rejection.
 CC Transgenic animals are capable of producing heterologous antibodies
 CC of multiple isotypes by undergoing isotype switching. These animals
 CC produce a first Ig type that is necessary for antigen-stimulated B-cell
 CC maturation and can switch to encode and produce one or more subsequent
 CC heterologous isotypes.
 XX XX
 SQ Sequence 388 BP; 89 A; 107 C; 97 G; 95 T; 0 other;
 Query Match 82.2%; Score 318.2; DB 18; Length 388;
 Best Local Similarity 88.9%; Pred. No. 1.9e-87;
 Matches 344; Conservative 0; Mismatches 43; Indels 0; Gaps 0;
 QY 1 ATGGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCTTCTGCTCGCTCCAGGTGCC 60
 DB 1 ATGGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCTTCTGCTCGCTCCAGGTGCC 60
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 QY 121 GTACCATCATCTTCAGGGCAAGTCAGACATATAGGTATTTAAATGCTATCAGCAG 180
 DB 121 GTACCATCATCTTCTCGGGCGAGTCAGACATATAGCAGCTGGTTAGCTGATCAGCAT 180
 QY 181 AAACCCAGAAAGCTCTTAAGCTCTGATCTATGCTGATCTGATCTGATCTGATCTGATCTG 240
 DB 181 AAACCCAGAAAGCTCTTAAGCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 240
 QY 241 CCATCAAGAGTTTACGGCAGTGGATCTGGGACAGATTTCACTCTCACCGTCAGAGCCTG 300
 DB 241 CCATCAAGAGTTTACGGCAGTGGATCTGGGACAGATTTCACTCTCACCGTCAGAGCCTG 300
 QY 301 CAGCCTGAAGATTTTGGCAGCTTATTAATGCTTACAGGTTTATAGTACCCCTCGACGCTTC 360
 DB 301 CAGCCTGAAGATTTTGGCAGCTTATTAATGCTTACAGGTTTATAGTACCCCTCGACGCTTC 360
 QY 361 GGCCAGGGACCAAGGTGGAAATCAAA 387

Db 361 GGCCAGGGACCAAGGTGGAAATCAAA 387
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 ID AAV39239 standard; DNA; 388 BP.
 XX AAV39239;
 AC AAV39239;
 XX XX
 DT 18-DEC-1998 (first entry)
 DE XX
 DE Functional Kappa transcript isolated from transgenic cell line 10C5.
 XX KW
 KW Transgenic animal; human heterologous antibody; transgene;
 KW isotype switching; neutrophil efflux; reperfusion injury; CD4 binding;
 KW autoimmune reaction; inflammatory response; transplant rejection;
 KW acid induced lung injury; acute adult respiratory distress syndrome;
 KW ARDS; vasculitis; septic shock; allergic reaction; asthma;
 KW cystic fibrosis; ss.
 XX XX
 OS Synthetic.
 OS Homo sapiens.
 OS Mus sp.
 XX XX
 PN W09824884-A1.
 XX PD 11-JUN-1998.
 XX PF 01-DEC-1997; 97WO-US21803.
 XX PR 02-DEC-1996; 96US-0758417.
 XX XX
 XX (GENP-) GENPHARM INT.
 XX XX
 XX Kay RM, Lonberg N;
 XX PI
 XX WPI; 1998-333306/29.
 DR XX
 XX Hybridoma producing antibody specific for interleukin-8 - used to
 PT prevent efflux of neutrophils from vasculature, and treat
 PT reperfusion injury
 XX XX
 PS Example 41; Page 304; 452pp; English.
 XX XX
 CC AAV39232-41 represent functional transcripts of a human IgGkappa
 CC anti-CD4 antibody. The sequences are isolated from 5 different
 CC transgenic mouse hybridoma cell lines. The specification describes
 CC transgenic non-human animals, especially a mouse, which are capable of
 CC producing a human heterologous antibodies of multiple isotypes by
 CC undergoing isotype switching. The transgenic animals have human heavy and
 CC light chain transgenes. The transgenes are capable of functionally
 CC rearranging a heterologous diversity (D) gene in a
 CC variable-diversity-junction (V-D-J) recombination. The transgenes include
 CC a heavy chain transgene comprising at least one V, D and J gene segment,
 CC and one constant region gene segment. The immunoglobulin (Ig) light chain
 CC transgene comprises at least one V and J gene segment and one constant
 CC region gene segment. The gene segments are heterologous to the transgenic
 CC animal. The antibody can be used to prevent efflux of neutrophils from
 CC vasculature. It can also be used to treat reperfusion injury. CD4 binding
 CC antibodies are used to reduce undesirable autoimmune reactions.
 CC inflammatory responses and rejection of transplanted organs. The
 CC anti-IL-8 antibodies can reduce tissue damage and prolong survival in
 CC animal models of acute adult respiratory distress syndrome (ARDS) and
 CC acid induced lung injury. The anti-IL-8 antibodies can also be used for
 CC the treatment of vasculitis, septic shock, allergic reactions (e.g.
 CC asthma) and cystic fibrosis.
 XX XX
 SQ Sequence 388 BP; 89 A; 107 C; 97 G; 95 T; 0 other;
 Query Match 82.2%; Score 318.2; DB 19; Length 388;
 Best Local Similarity 88.9%; Pred. No. 1.9e-87;
 Matches 344; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 19:01:43 ; Search time 559.115 Seconds
(without alignments)
2371.523 Million cell updates/sec

Title: US-09-019-441-3

Perfect score: 387

Sequence: 1 ATGACATGAGGTCCCGC.....GGACCAAGGTGGAATCAAA 387

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2244575 seqs, 1713117285 residues

Total number of hits satisfying chosen parameters: 4489150

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	387	100.0	387	11	US-09-019-441-3
2	387	100.0	387	15	US-10-103-686-3
3	342.2	88.4	729	13	US-10-384-933-125
4	342.2	88.4	729	15	US-10-216-484-125
5	329.4	85.1	974	10	US-09-859-053-29
6	326.2	84.3	714	15	US-10-153-382-18
7	324.6	83.9	387	9	US-09-905-243-27
8	323	83.5	728	10	US-09-844-684-15
9	323	83.5	728	15	US-10-040-244-15
10	321.4	83.0	390	9	US-09-905-243-57
11	321.4	83.0	514	15	US-10-066-543-2025
12	321.4	83.0	537	15	US-10-066-543-186
13	321.4	83.0	716	10	US-09-844-684-13
14	321.4	83.0	716	15	US-10-040-244-13
15	311.8	80.6	698	10	US-09-844-684-11

16	311.8	80.6	698	15	US-10-040-244-11	Sequence 11, Appl
17	310	80.1	634	15	US-10-158-646-55	Sequence 55, Appl
18	309.8	80.1	384	9	US-09-905-243-20	Sequence 20, Appl
19	309.8	80.1	402	15	US-10-158-646-56	Sequence 56, Appl
C 20	308.8	79.8	520	10	US-09-878-178-1210	Sequence 1210, Ap
C 21	308.8	79.8	520	14	US-10-046-933-1210	Sequence 1210, Ap
C 22	308.8	79.8	520	15	US-10-146-502-1210	Sequence 1210, Ap
23	308.4	79.7	737	10	US-09-919-344-7	Sequence 7, Appl
24	306	79.1	387	9	US-09-905-243-25	Sequence 25, Appl
25	305.8	79.0	384	13	US-10-389-221-10	Sequence 10, Appl
26	304.2	78.6	705	9	US-09-740-002-16	Sequence 16, Appl
27	303.8	78.5	708	13	US-10-401-344-3	Sequence 3, Appl
28	303.4	78.1	372	9	US-09-905-243-26	Sequence 26, Appl
29	302	78.0	494	10	US-09-878-178-1811	Sequence 1811, Ap
30	302	78.0	494	14	US-10-046-933-1811	Sequence 1811, Ap
31	302	78.0	494	15	US-10-146-502-1811	Sequence 1811, Ap
32	299	77.3	490	11	US-09-918-995-37859	Sequence 37859, A
33	299	77.3	819	15	US-10-158-646-65	Sequence 65, Appl
34	298.8	77.2	583	15	US-10-198-846-8365	Sequence 8365, Ap
35	297.8	77.0	384	9	US-09-905-243-56	Sequence 56, Appl
36	295	76.2	372	9	US-09-905-243-22	Sequence 22, Appl
37	293.2	75.8	928	15	US-10-221-945-5	Sequence 5, Appl
38	292.6	75.6	330	9	US-09-905-243-53	Sequence 53, Appl
39	288.4	74.5	941	9	US-09-800-729-81	Sequence 81, Appl
40	287.8	74.4	387	9	US-09-905-243-24	Sequence 24, Appl
C 41	287.4	74.3	463	10	US-09-878-178-2039	Sequence 2039, Ap
C 42	287.4	74.3	463	14	US-10-046-933-2039	Sequence 2039, Ap
C 43	287.4	74.3	463	15	US-10-146-502-2039	Sequence 2039, Ap
44	285.8	73.9	990	9	US-09-800-729-79	Sequence 79, Appl
45	284	73.4	381	9	US-09-905-243-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1

US-09-019-441-3
; Sequence 3, Application US/09019441
; Publication No. US20030086921A1
; GENERAL INFORMATION:
; APPLICANT: REFF, Mitchell E.
; KLOETZER, William S.
; NAKAMURA, Takehiko
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE THEREOF AS THERAPEUTICS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/019,441
; FILING DATE: 05-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/803,085
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35, 030
; REFERENCE/DOCKET NUMBER: 012712-502
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 3:

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SEQUENCE CHARACTERISTICS:
LENGTH: 387 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..387
NAME/KEY: mat_peptide
LOCATION: 67..387
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-019-441-3

Query Match      100.0%; Score 387; DB 11; Length 387;
Best Local Similarity 100.0%; Pred. No. 6e-114;
Matches 387; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCACATGAGGTCCTCCGCTCAGCTCTCTGGGGCTCTCTGCTCTGGCTCCAGGTGCC 60
Db 1 ATGCACATGAGGTCCTCCGCTCAGCTCTCTGGGGCTCTCTGCTCTGGCTCCAGGTGCC 60

Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
Db 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120

Qy 121 GTCACCATCACTTCGAGGGCAAGTCAGGACATTAAGGTATTAATTTAAATTTGGTATCAGCAG 180
Db 121 GTCACCATCACTTCGAGGGCAAGTCAGGACATTAAGGTATTAATTTAAATTTGGTATCAGCAG 180

Qy 181 AAACGAGAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAGTGGGGTC 240
Db 181 AAACGAGAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAGTGGGGTC 240

Qy 241 CCATCAAGGTTTCAGGGCAGTGGATCTGGGACAGATTCACCTCTCACCGTCAGCAGCCTG 300
Db 241 CCATCAAGGTTTCAGGGCAGTGGATCTGGGACAGATTCACCTCTCACCGTCAGCAGCCTG 300

Qy 301 CAGCCTGAAGATTTTGGCACTTATTACTGTCTACAGGTTTATAGTACCCCTCGACGTTTC 360
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Qy 361 GGCCAGGGACCAAGTGGAAATCAA 387
Db 361 GGCCAGGGACCAAGTGGAAATCAA 387
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RESULT 2
US-10-103-686-3
; Sequence 3, Application US/10103686
; Publication No. US20030059424A1
; GENERAL INFORMATION:
; APPLICANT: REFF, Mitchell E.
; KLOETZER, William S.
; NAKAMURA, Takehiko
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
; ANTIBODIES AND USE THEREOF AS THERAPEUTICS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/103,686
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; FILING DATE: 25-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/803,085
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 387 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..387
; NAME/KEY: mat_peptide
; LOCATION: 67..387
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-103-686-3

Query Match      100.0%; Score 387; DB 15; Length 387;
Best Local Similarity 100.0%; Pred. No. 6e-114;
Matches 387; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCACATGAGGTCCTCCGCTCAGCTCTCTGGGGCTCTCTGCTCTGGCTCCAGGTGCC 60
Db 1 ATGCACATGAGGTCCTCCGCTCAGCTCTCTGGGGCTCTCTGCTCTGGCTCCAGGTGCC 60

Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
Db 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120

Qy 121 GTCACCATCACTTCGAGGGCAAGTCAGGACATTAAGGTATTAATTTAAATTTGGTATCAGCAG 180
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Qy 181 AAACGAGAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAGTGGGGTC 240
Db 181 AAACGAGAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAGTGGGGTC 240

Qy 241 CCATCAAGGTTTCAGGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
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Qy 301 CAGCCTGAAGATTTTGGCACTTATTACTGTCTACAGGTTTATAGTACCCCTCGACGTTTC 360
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RESULT 3
US-10-384-933-125
; Sequence 125, Application US/10384933
; Publication No. US20030170817A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030170817Alufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126Cip/HG
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; CURRENT APPLICATION NUMBER: US/10/384,933
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 125
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-384-933-125

Query Match      88.4%; Score 342.2; DB 13; Length 729;
Best Local Similarity 92.8%; Pred. No. 1.8e-99;
Matches 359; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 1 ATGGACATGAGGGTCCCGCTCAGCTCCTGGGGTCTCTTCTGCTCTGGCTCCAGGTGCC 60
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Db 127 GTCACCATCACTTCGAGGGCAAGTCAGACATTAGGTATTATTTAAATTTGATATCAGCAG 186

Qy 181 AAACCCAGGAAAGCTCTTAAGCTCCCTGATCTATGTTGTCATCCAGTTTGCAAGTGGGGTC 240
Db 187 AAACCCAGGAAAGCTCTTAAGCTCCCTGATCTATGTTGTCATCCAGTTTGCAAGTGGGGTC 246

Qy 241 CCATCAAGGTTTCAGCGGCAAGTGGATCTGGGACAGAGTTTCACTCTCAGCGTCAGCAGCTG 300
Db 247 CCATCAAGGTTTCAGCGGCAAGTGGATCTGGGACAGAGTTTCACTCTCAGCGTCAGCAGCTG 306

Qy 301 CAGCCTGAAGATTTGGGACTTATTACTCTCTACAGGTTTATAGTACCCCTCGACGCTTC 360
Db 307 CAACCTGAAGATTTGGGACTTATTACTCTCTACAGGTTTATAGTACCCCTCGACGCTTC 366

Qy 361 GGCCAAAGGACCAAGGTGGAAATCAAA 387
Db 367 GGCCAAAGGACCAAGGTGGAAATCAAA 393

RESULT 5
US-09-859-053-29
; Sequence 29, Application US/09859053
; Patent No. US20020102658A1
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Tezuka, Katsumari
; APPLICANT: Hori, No. US20020102658A1uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; FILE REFERENCE: PHARMACEUTICAL USE THEREOF
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 974
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)...(38)
; NAME/KEY: CDS
; LOCATION: (39)...(746)
; NAME/KEY: 3'UTR
; LOCATION: (750)...(974)
; NAME/KEY: sig_peptide
; LOCATION: (39)...(104)
US-09-859-053-29

Query Match      85.1%; Score 329.4; DB 10; Length 974;
Best Local Similarity 90.7%; Pred. No. 2.6e-95;
Matches 351; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 1 ATGGACATGAGGGTCCCGCTCAGCTCCTGGGGTCTCTTCTGCTCTGGCTCCAGGTGCC 60
Db 39 ATGGACATGAGGGTCCCGCTCAGCTCCTGGGGTCTCTTCTGCTCTGGCTCCAGGTGCC 98

; CURRENT APPLICATION NUMBER: US/10/384,933
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 125
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-384-933-125

Query Match      88.4%; Score 342.2; DB 13; Length 729;
Best Local Similarity 92.8%; Pred. No. 1.8e-99;
Matches 359; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 1 ATGGACATGAGGGTCCCGCTCAGCTCCTGGGGTCTCTTCTGCTCTGGCTCCAGGTGCC 60
Db 7 ATGGACATGAGGGTCCCGCTCAGCTCCTGGGGTCTCTTCTGCTCTGGCTCCAGGTGCC 66

Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGATCTGTAGGGGACAGA 120
Db 67 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGATCTGTAGGGGACAGA 126

Qy 121 GTCACCATCACTTCGAGGGCAAGTCAGACATTAGGTATTATTTAAATTTGATATCAGCAG 180
Db 127 GTCACCATCACTTCGAGGGCAAGTCAGACATTAGGTATTATTTAAATTTGATATCAGCAG 186

Qy 181 AAACCCAGGAAAGCTCTTAAGCTCCCTGATCTATGTTGTCATCCAGTTTGCAAGTGGGGTC 240
Db 187 AAACCCAGGAAAGCTCTTAAGCTCCCTGATCTATGTTGTCATCCAGTTTGCAAGTGGGGTC 246

Qy 241 CCATCAAGGTTTCAGCGGCAAGTGGATCTGGGACAGAGTTTCACTCTCAGCGTCAGCAGCTG 300
Db 247 CCATCAAGGTTTCAGCGGCAAGTGGATCTGGGACAGAGTTTCACTCTCAGCGTCAGCAGCTG 306

Qy 301 CAGCCTGAAGATTTGGGACTTATTACTCTCTACAGGTTTATAGTACCCCTCGACGCTTC 360
Db 307 CAACCTGAAGATTTGGGACTTATTACTCTCTACAGGTTTATAGTACCCCTCGACGCTTC 366

Qy 361 GGCCAAAGGACCAAGGTGGAAATCAAA 387
Db 367 GGCCAAAGGACCAAGGTGGAAATCAAA 393

RESULT 4
US-10-216-484-125
; Sequence 125, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 125
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-216-484-125

Query Match      88.4%; Score 342.2; DB 15; Length 729;
Best Local Similarity 92.8%; Pred. No. 1.8e-99;
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Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTCCCTGCTGTCATCTGTAGGGGACAGA 120
Db 99 AGATGCGACATCCAGATGACCCAGTCTCCATCTCCGCTGCTGTCATCTGTAGGGGACAGA 158
Qy 121 GTCACCATCACTTGCAGGGCAAGTCCAGACATTAAGTATTTAAATTTGGTATCAGCAG 180
Db 159 GTCACCATCACTTGCAGGGCAAGTCCAGACATTAAGTATTTAAATTTGGTATCAGCAG 218
Qy 181 AAACAGGAAAGTCTTAAGCTCTGATCTATGTTGATCCAGTTTGCAGGAGTGGGTC 240
Db 219 AAACAGGAAAGTCTTAAGCTCTGATCTATGTTGATCCAGTTTGCAGGAGTGGGTC 278
Qy 241 CCATCAAGTTTCAGGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCTG 300
Db 279 CCATCAAGTTTCAGGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCTG 338
Qy 301 CAGCTGAAGATTTTGCAGTCTTACTGCTACAGGTTTATAGTACCCCTCGGACGTTTC 360
Db 339 CAGCTGAAGATTTTGCAGTCTTACTGCTCAACAGGCTAACAGTTTCCCGTGACGTTTC 398
Qy 361 GGCCAAGGACCAAGGTGGAATCAAA 387
Db 399 GGCCAAGGACCAAGGTGGAATCAAA 425

RESULT 6

US-10-153-382-18

; Sequence 18, Application US/10153382

; Publication No. US20030086930A1

; GENERAL INFORMATION:

; APPLICANT: PFIZER PRODUCTS INC.

; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES

; FILE REFERENCE: PC23019A

; CURRENT APPLICATION NUMBER: US/10/153,382

; CURRENT FILING DATE: 2002-05-22

; PRIOR APPLICATION NUMBER: 60/293042

; PRIOR FILING DATE: 2001-05-23

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: Patent in Ver. 2.1

; SEQ ID NO 18

; LENGTH: 714

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-153-382-18

Query Match 84.3%; Score 326.2; DB 15; Length 714;
Best Local Similarity 90.2%; Pred. No. 2.5e-94;
Matches 349; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy 1 ATGACATGAGGGTCCCGCTCAGCTCCTGGGGTCTCTTCTGCTCTGCTCCAGGTGCC 60
Db 1 ATGACATGAGGGTCCCGCTCAGCTCCTGGGGTCTCTTCTGCTCTGCTCCAGGTGCC 60
Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTCCCTGCTGATCTGTAGGGGACAGA 120
Db 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTCCCTGCTGATCTGTAGGGGACAGA 120
Qy 121 GTCACCATCACTTGCAGGGCAAGTCCAGACATTAAGTATTTAAATTTGGTATCAGCAG 180
Db 121 GTCACCATCACTTGCAGGGCAAGTCCAGACATTAAGTATTTAAATTTGGTATCAGCAG 180
Qy 181 AAACAGGAAAGTCTTAAGCTCTGATCTATGTTGATCCAGTTTGCAGGAGTGGGTC 240
Db 181 AAACAGGAAAGTCTTAAGCTCTGATCTATGTTGATCCAGTTTGCAGGAGTGGGTC 240
Qy 241 CCATCAAGTTTCAGGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCTG 300
Db 241 CCATCAAGTTTCAGGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCTG 300
Qy 301 CAGCTGAAGATTTTGCAGTCTTACTGCTACAGGTTTATAGTACCCCTCGGACGTTTC 360
Db 301 CAACCTGAAGATTTTGCAGTCTTACTGCTCAACAGTATTACAGTACTCCATTCATTTTC 360

Qy 361 GGCCAAGGACCAAGGTGGAATCAAA 387
Db 361 GGCCCTGGGACCAAGGTGGAATCAAA 387

RESULT 7

US-09-905-243-27

; Sequence 27, Application US/09905243

; Patent No. US20020062009A1

; GENERAL INFORMATION:

; APPLICANT: Taylor, Alexander H

; TITLE OF INVENTION: Monoclonal Antibodies with Reduced

; FILE REFERENCE: P50770

; CURRENT APPLICATION NUMBER: US/09/905,243

; CURRENT FILING DATE: 2001-07-16

; PRIOR APPLICATION NUMBER: 09/300,970

; PRIOR FILING DATE: 1999-04-28

; NUMBER OF SEQ ID NOS: 97

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 27

; LENGTH: 387

; TYPE: DNA

; ORGANISM: Pan troglodytes

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(387)

US-09-905-243-27

Query Match 83.9%; Score 324.6; DB 9; Length 387;
Best Local Similarity 89.9%; Pred. No. 6.5e-94;
Matches 348; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy 1 ATGACATGAGGGTCCCGCTCAGCTCCTGGGGTCTCTTCTGCTCTGCTCCAGGTGCC 60
Db 1 ATGACATGAGGGTCCCGCTCAGCTCCTGGGGTCTCTTCTGCTCTGCTCCAGGTGCC 60
Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTCCCTGCTGATCTGTAGGGGACAGA 120
Db 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTCCCTGCTGATCTGTAGGGGACAGA 120
Qy 121 GTCACCATCACTTGCAGGGCAAGTCCAGACATTAAGTATTTAAATTTGGTATCAGCAG 180
Db 121 GTCACCATCACTTGCAGGGCAAGTCCAGACATTAAGTATTTAAATTTGGTATCAGCAG 180
Qy 181 AAACAGGAAAGTCTTAAGCTCTGATCTATGTTGATCCAGTTTGCAGGAGTGGGTC 240
Db 181 AAACAGGAAAGTCTTAAGCTCTGATCTATGTTGATCCAGTTTGCAGGAGTGGGTC 240
Qy 241 CCATCAAGTTTCAGGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCTG 300
Db 241 CCATCAAGTTTCAGGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCTG 300
Qy 301 CAGCTGAAGATTTTGCAGTCTTACTGCTACAGGTTTATAGTACCCCTCGGACGTTTC 360
Db 301 CAACCTGAAGATTTTGCAGTCTTACTGCTCAACAGTATTACAGTACTCCATTCATTTTC 360
Qy 361 GGCCAAGGACCAAGGTGGAATCAAA 387
Db 361 GGTGGAGGACCAAGGTGGAATCAAA 387

RESULT 8

US-09-844-684-15

; Sequence 15, Application US/09844684

; Patent No. US2002012358A1

; GENERAL INFORMATION:

; APPLICANT: GEMINI SCIENCE, INC.

; TITLE OF INVENTION: HUMAN ANTI-CD40 ANTIBODIES AND METHODS OF MAKING SAME

; FILE REFERENCE: 21286/0276339

; CURRENT APPLICATION NUMBER: US/09/844,684

```

; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/200,601
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 728
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-844-684-15

```

Query Match	83.5%;	Score 323;	DB 10;	Length 728;	
Best Local Similarity	89.7%;	Pred. No. 2.7e-93;			
Matches 347;	Conservative 0;	Mismatches 40;	Indels 0;	Gaps 0;	
Qy	1	ATGGACATGAGGGTCCCGCTCAGCTCCTGGGGTCTCTCTGCTCTGGCTCCAGGTGCC	60		
Db	59	ATGGACATGAGGGTCCCGCTCAGCTCCTGGGGTCTCTGCTCTGGTCCCAAGTTCC	118		
Qy	61	AGATGTGACATCCAGATGACCCAGTCTCCATCTTTCCCTGTGTCGATCTGTAGGGGACAGA	120		
Db	119	AGATGCGACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGGATCTGTAGGAGACAGA	178		
Qy	121	GTCAACCATCACTTGCAGGGCAAGTCAGACATTAGGTATTATTTAAATTTGTTATCAGCAG	180		
Db	179	GTCAACCATCACTTGTCCGGCGAGTCAGGGTATTAGCAGCTGGTTAGCTGTGTATCAGCAG	238		
Qy	181	AAACCCAGGAAAAGCTCTCAAGCTCCTGATCTATGTTTGATCCAGTTTGCAAAGTGGGGTC	240		
Db	239	AAACCCAGGAAAAGCCCTTAAGCTCCTGATCTATGCTGGATCCAGTTTGCAAAGTGGGGTC	298		
Qy	241	CCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGAGTTTCACTCTCACGGTCAGCAGCGTG	300		
Db	299	CCATCAAGGTTTCAGCGGCAGTGGGATTTGGGACAGATTTTCACTCTCCACATCAGCAGCGTG	358		
Qy	301	CAGCCTCAAGATTTTGGGACTTATTTACTGTCTACAGGTTTTATAGTACCCCTCGGACGTTTC	360		
Db	359	CAGCCTCAAGATTTTGGCACTTACTATTGTCAACAGGCTAGCAGTTTCCCTCGGACATTC	418		
Qy	361	GGCCAAAGGGACCAAGGTGGAAATCAAA	387		
Db	419	GGCCAAAGGGACCAAGGTGGAGATCAAA	445		

RESULT 9
 US-10-040-244-15
 ; Sequence 15, Application US/10040244
 ; Publication No. US20030059427A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
 ; APPLICANT: FORCE, WALKER F.
 ; APPLICANT: TAKAHASHI, NOBUAKI
 ; APPLICANT: MIKAYAMA, TOSHIFUMI
 ; TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANTI-CD40 ANTIBODIES
 ; FILE REFERENCE: 021286/0272501
 ; CURRENT APPLICATION NUMBER: US/10/040,244
 ; CURRENT FILING DATE: 2002-06-17
 ; PRIOR APPLICATION NUMBER: 60/200,601
 ; PRIOR FILING DATE: 2000-4-28
 ; PRIOR APPLICATION NUMBER: PCT/US01/13672
 ; PRIOR FILING DATE: 2001-04-27
 ; PRIOR APPLICATION NUMBER: 09/844,684
 ; PRIOR FILING DATE: 2001-04-27
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn Ver. 3.0
 ; SEQ ID NO 15
 ; LENGTH: 728
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-040-244-15

Query Match	83.5%;	Score 323;	DB 15;	Length 728;
Best Local Similarity	89.7%;	Pred. No. 2.7e-93;		

	Matches	347;	Conservative	0;	Mismatches	40;	Indels	0;	Gaps	0
Qy	1	ATGGACATGAGGGTCCCGCTCAGCTCCTGGGGTCTCTTCTGCTCTGGCTCCAGGTGCC	60							
Db	59	ATGGACATGAGGGTCCCGCTCAGCTCCTGGGGTCTCTGCTGCTCTGGTTCCCGAGGTTC	118							
Qy	61	AGATGTGCACATCCAGATGACCCAGTCCCAATCTTCCCTGTCTGCATCTGTAGGGGACAGA	120							
Db	119	AGATGGCAGACATCCAGATGACCCAGTCTCCATCTTCCGTGCTGGATCTGTAGGAGACAGA	178							
Qy	121	GTCAACATCACTTTCAGGGCAAGTCAGGACATTAAGTATTATTAAATTTGCTATCAGCAG	180							
Db	179	GTCAACATCACTTGTGGCGGAGTCAGGATTAAGCAGCTGGTTAGCCTGTATCAGCAG	238							
Qy	181	AAACCGAGAAAGTCTTAAGTCTCTGATCTATGTTGGATCCAGTTTGGCAAAGTGGGGTC	240							
Db	239	AAACCGAGAAAGCCCTTAAGTCTCTGATCTATGCTGGATCCAGTTTGGCAAAGTGGGGTC	298							
Qy	241	CCATCAGGTTTCAGCGCAGTGGATCTGGGACAGAGTTCACTTCACCGTCAGCAGCCGTG	300							
Db	299	CCATCAGGTTTCAGCGCAGTGGATTTGGGACAGATTTCACTCTCACCATCAGCAGCCGTG	358							
Qy	301	CAGCCTCAAGATTTTGGCAGCTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTTC	360							
Db	359	CAGCCTCAAGATTTTGGCACTTACTATTGTCAACAGGCTAGCAGTTTCCCTCGGACATTC	418							
Qy	361	GGCCAAAGGACCAAGGTGGAAATCAAA	387							
Db	419	GGCCAAAGGACCAAGGTGGAGATCAAA	445							

```

RESULT 10
US-09-905-243-57
; Sequence 57, Application US/09905243
; Patent No. US20020062009A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Alexander H
; TITLE OF INVENTION: Monoclonal Antibodies with Reduced
;   Immunogenicity
; TITLE OF INVENTION: Immunogenicity
; FILE REFERENCE: P50770
; CURRENT APPLICATION NUMBER: US/09/905,243
; PRIOR FILING DATE: 2001-07-16
; PRIORITY APPLICATION NUMBER: 09/300,970
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 57
; LENGTH: 390
; TYPE: DNA
; ORGANISM: Macaca cynomolgus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(390)
US-09-905-243-57

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	Query Match	83.0%;	Score 321.4;	DB 9;	Length 390;
	Best Local Similarity	89.4%;	Pred. No. 6.9e-93;		
	Matches 346;	Conservative 0;	Mismatches 41;	Indels 0;	Gaps 0
Qy	1	ATGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTTCGTCTCTGGCTCCCAAGTGCC	60		
Db	1	ATGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTGTGCTCTGGCTCTCCTAGTGCC	60		
Qy	61	AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGTCATCTGTAGGGACAGA	120		
Db	61	AGATGTGACATCCAGATGACCCAGTCTCTTCTTCTGTCGATCTGTAGGACAGA	120		
Qy	121	GTCAACATCACTTCGAGGGCAAGTCACGACATTAGGTTATTATTAAATGGTATCAGCAG	180		
Db	121	GTCAACATCACTTGCACCAAGCGAGTCAGGGTATTAGCACTGGTTAGCCTGGTATCAGCAG	180		
Qy	181	AAACCGAGGAAAGCTCCTTAAGCTCCTCATCTATGTTGCATCCAGTTTGCAAAAGTGGGTC	240		

Patent No. US20020142358A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: LA JOLLA INSTITUTE FOR ALLERGY AND IMMUNOLOGY
; TITLE OF INVENTION: HUMAN ANTI-CD40 ANTIBODIES AND METHODS OF MAKING SAME
; FILE REFERENCE: 21286/0276339
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 09/844,684
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 13
; LENGTH: 716
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-844-684-13

Query Match 83.0%; Score 321.4; DB 10; Length 716;
Best Local Similarity 89.4%; Pred. No. 8.7e-93;
Matches 346; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 1 ATGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAAGTGCC 60
Db 47 ATGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAAGTGCC 106

Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
Db 107 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 166

Qy 121 GTCACCATCACTTGCAGGGCAAGTCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 180
Db 167 GTCACCATCACTTGCAGGGCAAGTCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 226

Qy 181 AAACCAAGAAAGCTCTAAGCTCCTAGCTATGTTGATCCAGTTTGCAGAGTGGGGTC 240
Db 227 AAACCAAGAAAGCTCTAAGCTCCTAGCTATGTTGATCCAGTTTGCAGAGTGGGGTC 286

Qy 241 CCATCAAGTTTACCGGCGAGTGGATCTGGGACAGATTTCACTCTCACCATCGGCGCTG 300
Db 287 CCATCAAGTTTACCGGCGAGTGGATCTGGGACAGATTTCACTCTCACCATCGGCGCTG 346

Qy 301 CAGCTGAAGATTTGGCACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTTC 360
Db 347 CAGCTGAAGATTTGGCACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTTC 406

Qy 361 GGCCAAGGACCAAGTGGAAATCAAA 387
Db 407 GGCCAAGGACCAAGTGGAAATCAAA 433

RESULT 14
US-10-040-244-13
; Sequence 13, Application US/10040244
; Publication No. US20030059427A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; APPLICANT: FORCE, WALKER F.
; APPLICANT: TAKAHASHI, NOBUAKI
; APPLICANT: MIKAYAMA, TOSHIFUMI
; TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANTI-CD40 ANTIBODIES
; FILE REFERENCE: 021286/0272501
; CURRENT APPLICATION NUMBER: US/10/040,244
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/200,601
; PRIOR FILING DATE: 2000-4-28
; PRIOR APPLICATION NUMBER: PCT/US01/13672
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 09/844,684
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in Ver. 3.0
; SEQ ID NO 13

; LENGTH: 716
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-040-244-13

Query Match 83.0%; Score 321.4; DB 15; Length 716;
Best Local Similarity 89.4%; Pred. No. 8.7e-93;
Matches 346; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 1 ATGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAAGTGCC 60
Db 47 ATGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAAGTGCC 106

Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
Db 107 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 166

Qy 121 GTCACCATCACTTGCAGGGCAAGTCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 180
Db 167 GTCACCATCACTTGCAGGGCAAGTCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 226

Qy 181 AAACCAAGAAAGCTCTAAGCTCCTAGCTATGTTGATCCAGTTTGCAGAGTGGGGTC 240
Db 227 AAACCAAGAAAGCTCTAAGCTCCTAGCTATGTTGATCCAGTTTGCAGAGTGGGGTC 286

Qy 241 CCATCAAGTTTACCGGCGAGTGGATCTGGGACAGATTTCACTCTCACCATCGGCGCTG 300
Db 287 CCATCAAGTTTACCGGCGAGTGGATCTGGGACAGATTTCACTCTCACCATCGGCGCTG 346

Qy 301 CAGCTGAAGATTTGGCACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTTC 360
Db 347 CAGCTGAAGATTTGGCACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTTC 406

Qy 361 GGCCAAGGACCAAGTGGAAATCAAA 387
Db 407 GGCCAAGGACCAAGTGGAAATCAAA 433

RESULT 15
US-09-844-684-11
; Sequence 11, Application US/09844684
; Patent No. US20020142358A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: LA JOLLA INSTITUTE FOR ALLERGY AND IMMUNOLOGY
; TITLE OF INVENTION: HUMAN ANTI-CD40 ANTIBODIES AND METHODS OF MAKING SAME
; FILE REFERENCE: 21286/0276339
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 09/844,684
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 11
; LENGTH: 698
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-844-684-11

Query Match 80.6%; Score 311.8; DB 10; Length 698;
Best Local Similarity 87.9%; Pred. No. 1e-89;
Matches 340; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy 1 ATGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAAGTGCC 60
Db 29 ATGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAAGTGCC 88

Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
Db 89 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 148

Qy 121 GTCACCATCACTTGCAGGGCAAGTCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 180

Db 149 GTCACCATCACTTCCCGGCCAGTCAGAGTATTAGTAACCTGGTTGGCTGTATCAGCAG 208
Qy 181 AAACCCAGGAAAGCTCCTAAGCTCCTGATCTATGTCATCCAGTTTGCAAAAGTGGGTC 240
Db 209 AAACCCAGGAAAGCCCTAAGCTCCTGCTCTATAAGGCATCTGGTTTAGAAAGTGGGTC 268
Qy 241 CCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGAGTTTCACTCTCACCGTCAGCAGCTG 300
Db 269 CCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGAAATTCATCTCACCATCAACAGCTG 328
Qy 301 CAGCTGAAGATTTTGGCACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTT 360
Db 329 CAGCTGATGATTTTGGCACTTATTACTGTCCACAGTCTAATAGTTATTCGTGGACGTTT 388
Qy 361 GGCCAAAGGACCAAGGTGGAAATCAAA 387
Db 389 GGCCACGGGACCAAGGTGGAAATCAAA 415

Search completed: December 30, 2003, 03:42:14
Job time : 563.115 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 42.5992 Seconds
(without alignments)
4009.823 Million cell updates/sec

Title: US-09-019-441-3

Perfect score: 387

Sequence: 1 ATGCACATGAGGCTCCCGC.....GGACCAAGGTGGAATCAAA 387

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents NA:*

- 1: /cgn2_6/ptodata/2/ina/5A COMB.seq:*
- 2: /cgn2_6/ptodata/2/ina/5B COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/6A COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/6B COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/PTCUS COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	387	100.0	387	3	US-08-803-085-3
2	387	100.0	19040	4	US-09-343-485A-3
3	318.2	82.2	388	3	US-09-042-353-358
4	318.2	82.2	388	4	US-08-758-417A-206
5	316.6	81.8	1066	1	US-08-157-101A-4
6	308.6	79.7	387	1	US-08-217-918-1
7	307	79.3	439	3	US-09-042-353-360
8	307	79.3	439	4	US-08-758-417A-208
9	304.2	78.6	705	1	US-08-488-376-16
10	304.2	78.6	705	2	US-08-634-223-16
11	304.2	78.6	705	2	US-08-634-224-16
12	304.2	78.6	705	2	US-08-634-400-16
13	304.2	78.6	705	2	US-08-635-878-16
14	304.2	78.6	705	2	US-08-770-057-16
15	304.2	78.6	705	3	US-09-335-697B-16
16	304.2	78.6	705	4	US-09-335-697B-16
17	304.2	78.6	705	4	US-09-740-002-16
18	302	78.0	420	3	US-09-042-353-420
19	302	78.0	420	4	US-08-758-417A-220
20	302	78.0	3819	3	US-09-042-353-393
21	302	78.0	3819	4	US-08-758-417A-243
22	297.4	76.8	390	2	US-08-646-367-2
23	296.2	76.5	384	1	US-08-259-372A-13
24	296.2	76.5	384	1	US-08-468-671-13
25	279.4	72.2	324	2	US-08-378-939-23
26	278.2	71.9	708	1	US-08-488-376-18
27	278.2	71.9	708	2	US-08-634-223-18

Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 5, Appl
Sequence 18, Appl
Sequence 187, App
Sequence 187, App
Sequence 187, App
Sequence 187, App
Sequence 102, App
Sequence 218, App
Sequence 221, App
Sequence 222, App
Sequence 70, Appl

ALIGNMENTS

RESULT 1
US-08-803-085-3
; Sequence 3, Application US/08803085
; Patent No. 6011138
; GENERAL INFORMATION:
; APPLICANT: REFF, Mitchell E.
; APPLICANT: KLOETZER, William S.
; APPLICANT: NAKAMURA, Takehiko
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES AND USE THEREOF AS THERAPEUTICS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/803,085
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 387 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..387
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 67..387
; US-08-803-085-3

Query Match 100.0%; Score 387; DB 3; Length 387;

Best Local Similarity 100.0%; Pred. No. 8.8e-113;
Matches 387; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ATGACATGAGGGTCCCGCTCAGCTCTGGGGTCTCTTCTGCTCTGCTCCAGGTGCC 60
Db 1 ATGACATGAGGGTCCCGCTCAGCTCTGGGGTCTCTTCTGCTCTGCTCCAGGTGCC 60

Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCTATCTGTAGGGGACAGA 120
Db 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCTATCTGTAGGGGACAGA 120

Qy 121 GTCACCATCACTTGCAGGGCAAGTCAGGACATTAAGTATTAATTTAAATTTGGTATCAGCAG 180
Db 121 GTCACCATCACTTGCAGGGCAAGTCAGGACATTAAGTATTAATTTAAATTTGGTATCAGCAG 180

Qy 181 AAACAGGAAAGCTTCTTAAGCTCCTGATCTATGTCATCCAGTTTGCAAGTGGGGTC 240
Db 181 AAACAGGAAAGCTTCTTAAGCTCCTGATCTATGTCATCCAGTTTGCAAGTGGGGTC 240

Qy 241 CCATCAAGTTTCAGGGGAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGGAGCTG 300
Db 241 CCATCAAGTTTCAGGGGAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGGAGCTG 300

Qy 301 CAGCTGAAGATTTTGGCACTTATTACTGCTACAGGTTTATAGTACCCCTCGGACGTTT 360
Db 301 CAGCTGAAGATTTTGGCACTTATTACTGCTACAGGTTTATAGTACCCCTCGGACGTTT 360

Qy 361 GGCCAAAGGACCAAGGTGGAATCAAA 387
Db 361 GGCCAAAGGACCAAGGTGGAATCAAA 387
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RESULT 2

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US-09-343-485A-3
; Sequence 3, Application US/09343485A
; Patent No. 6413777
; GENERAL INFORMATION:
; APPLICANT: REFF, MITCHELL R.
; APPLICANT: BARNETT, RICHARD S.
; APPLICANT: MCLACHLAN, KAREN R.
; TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT SPECIFIC SITES IN
; TITLE OF INVENTION: MAMMALIAN CELLS VIA HOMOLOGOUS RECOMBINATION AND
; TITLE OF INVENTION: VECTORS FOR ACCOMPLISHING THE SAME
; FILE REFERENCE: 037003-0275807
; CURRENT APPLICATION NUMBER: US/09/343.485A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/023,715
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 08/819,866
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 19040
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; OTHER INFORMATION: referred to as "Mandy"
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US-09-343-485A-3

Query Match
Best Local Similarity 100.0%; Score 387; DB 4; Length 19040;
Matches 387; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ATGACATGAGGGTCCCGCTCAGCTCTGGGGTCTCTTCTGCTCTGCTCCAGGTGCC 60
Db 7545 ATGACATGAGGGTCCCGCTCAGCTCTGGGGTCTCTTCTGCTCTGCTCCAGGTGCC 7604

Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCTATCTGTAGGGGACAGA 120
Db 7605 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCTATCTGTAGGGGACAGA 7664
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Qy 121 GTCACCATCACTTGCAGGGCAAGTCAGGACATTAAGTATTAATTTAAATTTGGTATCAGCAG 180
Db 7665 GTCACCATCACTTGCAGGGCAAGTCAGGACATTAAGTATTAATTTAAATTTGGTATCAGCAG 7724

Qy 181 AAACAGGAAAGCTCCTTAAGCTCCTGATCTATGTCATCCAGTTTGCAAGTGGGGTC 240
Db 7725 AAACAGGAAAGCTCCTTAAGCTCCTGATCTATGTCATCCAGTTTGCAAGTGGGGTC 7784

Qy 241 CCATCAAGTTTCAGGGGAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGGAGCTG 300
Db 7785 CCATCAAGTTTCAGGGGAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGGAGCTG 7844

Qy 301 CAGCTGAAGATTTTGGCACTTATTACTGCTACAGGTTTATAGTACCCCTCGGACGTTT 360
Db 7845 CAGCTGAAGATTTTGGCACTTATTACTGCTACAGGTTTATAGTACCCCTCGGACGTTT 7904

Qy 361 GGCCAAAGGACCAAGGTGGAATCAAA 387
Db 7905 GGCCAAAGGACCAAGGTGGAATCAAA 7931
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RESULT 3

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US-09-042-353-358
; Sequence 358, Application US/09042353
; Patent No. 6255458
; GENERAL INFORMATION:
; APPLICANT: Lomborg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 421
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,353
; FILING DATE: 13-MAR-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/096,762
; FILING DATE: 22-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,301
; FILING DATE: 18-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/161,739
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/165,699
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FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA: US 08/209,741
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-009040US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 358:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-042-353-358

Query Match 82.2%; Score 318.2; DB 3; Length 388;
Best Local Similarity 88.9%; Pred. No. 4.6e-91;
Matches 344; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY	1	ATGGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCTCTGCTCTGGCTCCAGGTGCC	60
DB	1	ATGGACATGATGGTCCCGCTCAGCTCCTGGGGCTCTCTGCTCTGGTCCAGGTCC	60
QY	61	AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGTGATCTGTAGGGACAGA	120
DB	61	AGATGCGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGTGATCTGTAGGGACAGA	120
QY	121	GTACCATCATCTTGCAGGCAAGTCAGGACATTAGGTATTATTAAATTTGTTATCAGCAG	180
DB	121	GTACCATCATCTTGTCCGGGAGTCAGGATATTAGCAGCTGGTTAGCTGTGATTCAGCAT	180
QY	181	AAACGAGAAAGCTCCTAGCTCCTGATCTATGTTGCATCCAGTTTGCAAGTGGGGTC	240
DB	181	AAACGAGAAAGCTCCTAGCTCCTGATCTATGTTGCATCCAGTTTGCAAGTGGGGTC	240
QY	241	CCATCAAGGTTTCAGCGCAGTGGATCTGGACAGAGTTCACTCTCACCGTCAGCAGCTG	300
DB	241	CCATCAAGGTTTCAGCGCAGTGGATCTGGACAGAGTTCACTCTCACCATCAGCAGCTG	300
QY	301	CAGCTGAAGATTTGGGACTTATTACTGTCACAGTTTATAGTACCCCTCGAGCTTC	360
DB	301	CAGCTGAAGATTTGGGACTTATTACTGTCACAGTTTATAGTACCCCTCGAGCTTC	360
QY	361	GGCCAGGAGCAAGGTGGAAATCAAA	387
DB	361	GGCCAGGAGCAAGGTGGAGATCAAA	387

RESULT 4
US-08-758-417A-206

Sequence 206, Application US/08758417A
Patent No. 6300129
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 417
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-DEC-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 206:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 206:
US-08-758-417A-206

Query Match 82.2%; Score 318.2; DB 4; Length 388;
Best Local Similarity 88.9%; Pred. No. 4.6e-91;
Matches 344; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY	1	ATGGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCTCTGCTCTGGTCCAGGTGCC	60
DB	1	ATGGACATGATGGTCCCGCTCAGCTCCTGGGGCTCTCTGCTCTGGTCCAGGTGCC	60
QY	61	AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGTGATCTGTAGGGACAGA	120
DB	61	AGATGCGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGTGATCTGTAGGGACAGA	120

QY 121 GTACCATCACTTCAGCGGCAAGTCAGACATAGGTATTATTTAAATTGGTATCAGCAG 180
DB 121 GTACCATCACTTCAGCGGCAAGTCAGACATAGGTATTATTTAAATTGGTATCAGCAG 180
QY 181 AAACCCAGGAAAGCTCTAGCTCTGATCTATCTGATCCAGTCTTGGCAAGTGGGGTC 240
DB 181 AAACCCAGGAAAGCTCTAGCTCTGATCTATCTGATCCAGTCTTGGCAAGTGGGGTC 240
QY 241 CCATCAAGGTTTACGCGCAGTGGATCTGGACAGAGTTCACTCTCACCGTCAGCAGCTG 300
DB 241 CCATCAAGGTTTACGCGCAGTGGATCTGGACAGAGTTCACTCTCACCGTCAGCAGCTG 300
QY 301 CAGCCTGAAGATTTTGGCAACTTACTTGTCAACAGGCTAATAGTTTCCCGTACACTTTT 360
DB 301 CAGCCTGAAGATTTTGGCAACTTACTTGTCAACAGGCTAATAGTTTCCCGTACACTTTT 360
QY 361 GGCCCAAGGACCAAGTGGAAATCAAA 387
DB 361 GGCCCAAGGACCAAGTGGAAATCAAA 387

RESULT 5

US-08-157-101A-4
; Sequence 4, Application US/08157101A
; Patent No. 5808032
; GENERAL INFORMATION:
; APPLICANT: KURIHARA, TATSUYA
; APPLICANT: MATSUKURA, SHIGERAZU
; APPLICANT: TSURUOKA, NOBUO
; APPLICANT: ARIMA, KENJI
; APPLICANT: NISHIHARA, TATSURO
; TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION
; TITLE OF INVENTION: PLASMIDS THEREFOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/157,101A
; FILING DATE: 05-APR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: TITUS, MARLANA K
; REFERENCE/DOCKET NUMBER: 9437/204199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3711
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUCH
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1066 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-157-101A-4
Query Match 81.8%; Score 316.6; DB 1; Length 1066;
Best Local Similarity 88.6%; Pred. No. 2.2e-90;
Matches 343; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 1 ATGCACATGAGGGTCCCGCTCAGCTCTGGGGCTCTTCTGCTCTGGTCCCGAGTGCC 60

DB 33 ATGCACATGAGGGTCCCGCTCAGCTCTGGGGCTCTTCTGCTCTGGTCCCGAGTGCC 92
QY 61 AGATGTGACATCCAGATGACCCAGTCTCANTCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
DB 93 AGGTGTGACATCCAGATGACCCAGTCTCCATCTGCCATGCGTGCATCTGTAGGAGACAGA 152
QY 121 GTACCATCACTTCAGCGGCAAGTCAGACATAGGTATTATTTAAATTGGTATCAGCAG 180
DB 153 GTACCATCACTTCAGCGGCAAGTCAGACATAGGTATTATTTAAATTGGTATCAGCAG 212
QY 181 AAACCCAGGAAAGCTCTAGCTCTGATCTATCTGATCCAGTCTTGGCAAGTGGGGTC 240
DB 213 AAACCCAGGAAAGCTCTAGCTCTGATCTATCTGATCCAGTCTTGGCAAGTGGGGTC 272
QY 241 CCATCAAGGTTTACGCGCAGTGGATCTGGACAGAGTTCACTCTCACCGTCAGCAGCTG 300
DB 273 CCATCAAGGTTTACGCGCAGTGGATCTGGACAGAGTTCACTCTCACCGTCAGCAGCTG 332
QY 301 CAGCCTGAAGATTTTGGCAACTTACTTGTCAACAGGCTAATAGTTTCCCGTACACTTTT 360
DB 333 CAGCCTGAAGATTTTGGCAACTTACTTGTCAACAGGCTAATAGTTTCCCGTACACTTTT 392
QY 361 GGCCCAAGGACCAAGTGGAAATCAAA 387
DB 393 GGCCCAAGGACCAAGTGGAAATCAAA 419

RESULT 6

US-08-217-918-1
; Sequence 1, Application US/08217918
; Patent No. 5506132
; GENERAL INFORMATION:
; APPLICANT: LAKE, PHILIP
; APPLICANT: OSTBERG, LARS
; TITLE OF INVENTION: HUMAN ANTIBODIES AGAINST
; TITLE OF INVENTION: VARICELLA-ZOSTER VIRUS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,918
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 387 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..387
US-08-217-918-1

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Query Match 79.7%; Score 308.6; DB 1; Length 387;
Best Local Similarity 87.3%; Pred. No. 4.9e-88;
Matches 338; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Qy 1 ATGGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCTTCTGCTCTGGCTCCCGAGTGGCC 60
Db 1 ATGGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCTTCTGCTCTGGCTCCCGAGTGGCC 60

Qy 61 AGATGTGACATCCAGATGACCCAGTCCCATCTTCCCTGCTGCATCTGTAGGGGACAGA 120
Db 61 AGATGTGACATCCAGATGACCCAGTCCCATCTTCCCTGCTGCATCTGTAGGGGACAGA 120

Qy 121 GTACCATCACTTGCAGGCAAGTCAGGACATAGGTATTTAAATTTGGTATCAGCAG 180
Db 121 GTACCATCACTTGCAGGCAAGTCAGGACATAGGTATTTAAATTTGGTATCAGCAG 180

Qy 181 AAACAGGAAAGCTCCTTAAGCTCCCTGATCTATGTTGATCCAGTTTGCAAGTGGGTC 240
Db 181 AAACAGGAAAGCTCCTTAAGCTCCCTGATCTATGTTGATCCAGTTTGCAAGTGGGTC 240

Qy 241 CCATCAAGTTTCCAGGCGGAGTGGATCTGGGACAGAGTTCACTCTCACCCTGACGCGTG 300
Db 241 CCATCAAGTTTCCAGGCGGAGTGGATCTGGGACAGAGTTCACTCTCACCCTGACGCGTG 300

Qy 301 CAGCTCAAGATTTGGGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTT 360
Db 301 CAGCTCAAGATTTGGGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTT 360

Qy 361 GGCCAGGGACCAAGTGGGAAATCAAA 387
Db 361 GGCCAGGGACCAAGTGGGAAATCAAA 387

RESULT 7
US-09-042-353-360
Sequence 360, Application US/09042353
Patent No. 6255458
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/042,353
FILING DATE: 13-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
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Query Match 79.3%; Score 307; DB 3; Length 439;
Best Local Similarity 87.1%; Pred. No. 1.7e-87;
Matches 337; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy 1 ATGGACATGAGGGTCCCGCTCAGCTCCCTGGGGCTCTTCTGCTCTGGCTCCCGAGTGGCC 60
Db 1 ATGGACATGAGGGTCCCGCTCAGCTCCCTGGGGCTCTTCTGCTCTGGCTCCCGAGTGGCC 60

Qy 61 AGATGTGACATCCAGATGACCCAGTCCCATCTTCCCTGCTGCATCTGTAGGGGACAGA 120
Db 61 AGATGTGACATCCAGATGACCCAGTCCCATCTTCCCTGCTGCATCTGTAGGGGACAGA 120

Qy 121 GTACCATCACTTGCAGGCAAGTCAGGACATAGGTATTTAAATTTGGTATCAGCAG 180
Db 121 GTACCATCACTTGCAGGCAAGTCAGGACATAGGTATTTAAATTTGGTATCAGCAG 180

Qy 181 AAACAGGAAAGCTCCTTAAGCTCCCTGATCTATGTTGATCCAGTTTGCAAGTGGGTC 240
Db 181 AAACAGGAAAGCTCCTTAAGCTCCCTGATCTATGTTGATCCAGTTTGCAAGTGGGTC 240

Qy 241 CCATCAAGTTTCCAGGCGGAGTGGATCTGGGACAGAGTTCACTCTCACCCTGACGCGTG 300
Db 241 CCATCAAGTTTCCAGGCGGAGTGGATCTGGGACAGAGTTCACTCTCACCCTGACGCGTG 300
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Db 241 CCATCAAGGTTCCGCGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCGCTG 300
Qy 301 CAGCTGAAGATTTTGGCACTTATCTACTGTCTACAGGTTTATAGTACCCCTCGGACGCTTC 360
Db 301 CAGCTGAAGATTTTGGCACTTATCTACTGTCTACAGGTTTATAGTACCCCTCGGACGCTTC 360
Qy 361 GGCCAAAGGACCAAGGTCGGAATCAAA 387
Db 361 GGCCAGGGGACCAAGCTGGAGATCAAA 387

RESULT 8

US-08-758-417A-208
; Sequence 208, Application US/08/58417A
; Patent No. 6300129
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
; Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 417
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,417A.
; FILING DATE: 02-Dec-1996
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 208:

SEQUENCE CHARACTERISTICS:
LENGTH: 439 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 208:

US-08-758-417A-208

Query Match 79.3%; Score 307; DB 4; Length 439;
Best Local Similarity 87.1%; Pred. No. 1.7e-87;
Matches 337; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
Qy 1 ATGCACATGAGGTCGCCGCTCAGCTCCCTGGGGCTCTCTTCTGCTCTGGCTCCCGAGGTGCC 60
Db 1 ATGCACATGAGGTCGCCGCTCAGCTCCCTGGGGCTCTCTTCTGCTCTGGCTCCCGAGGTGCC 60
Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGTCATCTGTAGGGGACAGA 120
Db 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTCTCACTGTCTGTCATCTGTAGGGGACAGA 120
Qy 121 GTCACCATCACTTTCAGGGGCAAGTCCAGGATAGGTATTTAAATTCGTATCAGCAG 180
Db 121 GTCACCATCACTTTCAGGGGCAAGTCCAGGATAGGTATTTAAATTCGTATCAGCAG 180
Qy 181 AAACCCAGGAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAGGAGTGGGTC 240
Db 181 AAACCCAGGAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAGGAGTGGGTC 240
Qy 241 CCATCAAGGTTTACGCGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
Db 241 CCATCAAGGTTTACGCGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
Qy 301 CAGCCTGAAGATTTTGGGACTTATTAAGTCTCTACAGGTTTATAGTACCCCTCGGACGCTTC 360
Db 301 CAGCCTGAAGATTTTGGGACTTATTAAGTCTCTACAGGTTTATAGTACCCCTCGGACGCTTC 360
Qy 361 GGCCAAAGGACCAAGGTCGGAATCAAA 387
Db 361 GGCCAGGGGACCAAGCTGGAGATCAAA 387

RESULT 9

US-08-488-376-16
; Sequence 16, Application US/08488376
; Patent No. 5811524

GENERAL INFORMATION:

APPLICANT: BRAMS, Peter
APPLICANT: CHAMAT, Soulaime Salim
APPLICANT: PAN, Li-Zhen
APPLICANT: WALSH, Edward E.
APPLICANT: HEARD, Cheryl Janne
APPLICANT: NEWMAN, Roland Anthony
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,376
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-150
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 705 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..705
US-08-488-376-16

Query Match 78.6%; Score 304.2; DB 1; Length 705;
Best Local Similarity 87.4%; Pred. No. 1.5e-86;
Matches 333; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 7 ATGAGGTCCTCCGCTCAGCTCCCTGGGCTCTCTGCTCTGGCTCCAGTGCAGATGT 66
DB 1 ATGAGAGACCCCTGCTCAGCTCCTGGGCTCTCTGCTCTGGCTCCAGTGCAGATGT 60

QY 67 GACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCTCATCTGTAGGGGACAGATCA 126
DB 61 GACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCTCATCTGTGAGAGACAGATCA 120

QY 127 ATCACTTGCAGGGCAAGTCAGGACATAGGTATTATTTAAATTTGGTATCAGCAGAAACCA 186
DB 121 ATCACTTGCAGGGCAAGTCAGGACATAGGTATTATTTAAATTTGGTATCAGCAGAAACCA 180

QY 187 GGAAGAGCTCTTAAGCTCTGATCTATGTTGATCCAGTTTGAAAGTGGGGTCCCATCA 246
DB 181 GGAAGAGCTCTTAAGCTCTGATATATGTTGATCCAGTTTGAAAGTGGGGTCCCATCA 240

QY 247 AGTTTCAGGCGCAGTGTGAGACAGATCTCACTCTCACCCTGACGAGCTGCAGCT 306
DB 241 AGTTTCAGGCGGCTGATCTGGACAGATTTCACTCTCACCCTGACGAGCTGCAGCT 300

QY 307 GAAGATTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGAGCTTCGGCCAA 366
DB 301 GAAGATTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGAGCTTCGGCCAA 360

QY 367 GGGACCAAGTGGAAATCAAA 387
DB 361 GGGACCAAGTGGAAATCAAA 381

RESULT 10
US-08-634-223-16
Sequence 16, Application US/08634223
Patent No. 5840298
GENERAL INFORMATION:
APPLICANT: BRAMS, Peter
APPLICANT: CHAMAT, Soulaime Salim
APPLICANT: PAN, Li-Zhen
APPLICANT: WALSH, Edward E.
APPLICANT: HEARD, Cheryl Janne
APPLICANT: NEWMAN, Roland Anthony
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/634,223
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/488,376
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-150
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 705 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..705
US-08-634-223-16

Query Match 78.6%; Score 304.2; DB 2; Length 705;
Best Local Similarity 87.4%; Pred. No. 1.5e-86;
Matches 333; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 7 ATGAGGTCCTCCGCTCAGCTCCCTGGGCTCTCTGCTCTGGCTCCAGTGCAGATGT 66
DB 1 ATGAGAGACCCCTGCTCAGCTCCTGGGCTCTCTGCTCTGGCTCCAGTGCAGATGT 60

QY 67 GACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCTCATCTGTAGGGGACAGATCA 126
DB 61 GACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCTCATCTGTGAGAGACAGATCA 120

QY 127 ATCACTTGCAGGGCAAGTCAGGACATAGGTATTATTTAAATTTGGTATCAGCAGAAACCA 186
DB 121 ATCACTTGCAGGGCAAGTCAGGACATAGGTATTATTTAAATTTGGTATCAGCAGAAACCA 180

QY 187 GGAAGAGCTCTTAAGCTCTGATCTATGTTGATCCAGTTTGAAAGTGGGGTCCCATCA 246
DB 181 GGAAGAGCTCTTAAGCTCTGATATATGTTGATCCAGTTTGAAAGTGGGGTCCCATCA 240

QY 247 AGTTTCAGGCGCAGTGTGAGACAGATCTCACTCTCACCCTGACGAGCTGCAGCT 306
DB 241 AGTTTCAGGCGGCTGATCTGGACAGATTTCACTCTCACCCTGACGAGCTGCAGCT 300

QY 307 GAAGATTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGAGCTTCGGCCAA 366
DB 301 GAAGATTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGAGCTTCGGCCAA 360

QY 367 GGGACCAAGTGGAAATCAAA 387
DB 361 GGGACCAAGTGGAAATCAAA 381

RESULT 11
US-08-634-224-16
Sequence 16, Application US/08634224
Patent No. 5866125
GENERAL INFORMATION:
APPLICANT: BRAMS, Peter
APPLICANT: CHAMAT, Soulaime Salim
APPLICANT: PAN, Li-Zhen
APPLICANT: WALSH, Edward E.
APPLICANT: HEARD, Cheryl Janne
APPLICANT: NEWMAN, Roland Anthony
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 19

```
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Burns, Doane, Swecker & Mathis
;; STREET: P.O. Box 1404
;; CITY: Alexandria
;; STATE: Virginia
;; COUNTRY: United States
;; ZIP: 22313-1404
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/634,224
;; FILING DATE:
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/488,376
;; FILING DATE: 07-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Teskin, Robin L.
;; REGISTRATION NUMBER: 35,030
;; REFERENCE/DOCKET NUMBER: 012712-150
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 836-6620
;; TELEFAX: (703) 836-2021
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 705 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..705
;; US-08-634-224-16

Query Match 78.6%; Score 304.2; DB 2; Length 705;
Best Local Similarity 87.4%; Pred. No. 1.5e-86;
Matches 333; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Qy 7 ATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCGAGTGCAGATGT 66
Db 1 ATGAGAGCCCTGCTCAGCTCCTGGGGCTCCTGCTACTCTGGCTCCGAGTGCAGATGT 60

Qy 67 GACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGAGTCA 126
Db 61 GACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGAGTCA 120

Qy 127 ATCACTTGACGGGCAAGTCAGACATTTAGGTATTATTAAATTTGGTATCAGCAAAACCA 186
Db 121 ATCACTTGACGGGCAAGTCAGACATTTAGGTATTATTAAATTTGGTATCAGCAAAACCA 180

Qy 187 GGAAAGCTCTAAGCTCTCATCTATGTTGCATCCAGTTTGCAGAGTGGGGTCCCATCA 246
Db 181 GGGAAAGCCCTTACGCTCTCTATATATGCTGGATCCAAATTTGCACCGTGGGGTCCCGTCA 240

Qy 247 AGGTTTACGCGGAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCTGCAGCCT 306
Db 241 AGGTTTACGCGGAGTGGATCTGGGACAGAGTTCACTCTCACCATCAACAGTCTGCAAGCT 300

Qy 307 GAAGATTGCGACTTATTACTGTCTCAGAGTTTATAGTACCCCTCGGACGTTTCGGCCAA 366
Db 301 GAAGATTGCGAACTTACTATTGTCAACAGGCTTACAGTACCCCTCGGACGTTTCGGCCAA 360

Qy 367 GGGACCAAGGTGGAAATCAAA 387
Db 361 GGGACCAAGGTGGAAATCAAA 381

RESULT 12
US-08-634-400-16

;; Sequence 16, Application US/08634400
;; Patent No. 5939068
;; GENERAL INFORMATION:
;; APPLICANT: BRAMS, Peter
;; APPLICANT: CHAWAT, Soulaïma Salim
;; APPLICANT: PAN, Li-Zhen
;; APPLICANT: WALSH, Edward E.
;; APPLICANT: HEARD, Cheryl Janne
;; APPLICANT: NEWMAN, Roland Anthony
;; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
;; TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
;; NUMBER OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
;; NUMBER OF SEQUENCES: 19
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Burns, Doane, Swecker & Mathis
;; STREET: P.O. Box 1404
;; CITY: Alexandria
;; STATE: Virginia
;; COUNTRY: United States
;; ZIP: 22313-1404
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/634,400
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/488,376
;; FILING DATE: 07-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Teskin, Robin L.
;; REGISTRATION NUMBER: 35,030
;; REFERENCE/DOCKET NUMBER: 012712-150
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 836-6620
;; TELEFAX: (703) 836-2021
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 705 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..705
;; US-08-634-400-16

Query Match 78.6%; Score 304.2; DB 2; Length 705;
Best Local Similarity 87.4%; Pred. No. 1.5e-86;
Matches 333; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Qy 7 ATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCGAGTGCAGATGT 66
Db 1 ATGAGAGCCCTGCTCAGCTCCTGGGGCTCCTGCTACTCTGGCTCCGAGTGCAGATGT 60

Qy 67 GACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGAGTCA 126
Db 61 GACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGAGTCA 120

Qy 127 ATCACTTGACGGGCAAGTCAGACATTTAGGTATTATTAAATTTGGTATCAGCAAAACCA 186
Db 121 ATCACTTGACGGGCAAGTCAGACATTTAGGTATTATTAAATTTGGTATCAGCAAAACCA 180

Qy 187 GGAAAGCTCTAAGCTCTCATCTATGTTGCATCCAGTTTGCAGAGTGGGGTCCCATCA 246
Db 181 GGGAAAGCCCTTACGCTCTCTATATATGCTGGATCCAAATTTGCACCGTGGGGTCCCGTCA 240

Qy 247 AGGTTTACGCGGAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCTGCAGCCT 306
Db 241 AGGTTTACGCGGAGTGGATCTGGGACAGAGTTCACTCTCACCATCAACAGTCTGCAAGCT 300

Qy 307 GAAGATTGCGACTTATTACTGTCTCAGAGTTTATAGTACCCCTCGGACGTTTCGGCCAA 366
Db 301 GAAGATTGCGAACTTACTATTGTCAACAGGCTTACAGTACCCCTCGGACGTTTCGGCCAA 360

Qy 367 GGGACCAAGGTGGAAATCAAA 387
Db 361 GGGACCAAGGTGGAAATCAAA 381

RESULT 12
US-08-634-400-16
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Db 241 AGGTTGAGTGGCGGTGAGTCTGGGACAGATTTCACTCTCACCATCAACAGCTCTGCAACCT 300
QY 307 GAAGATTTTCGAGCTTATTACTGTCTACAGTTTATAGTACCCTCGGACGTTTCGGCCAA 366
Db 301 GAGATTTTGCACCTTACTATTGTCAACAGCTTACAGTACCCCTCGGACCTTTTCGGCCCA 360
QY 367 GGGACCAAGGTGGAAATCAAA 387
Db 361 GGGACCAAGGTGGAAATCAAA 381

RESULT 13

US-08-635-878-16
; Sequence 16, Application US/08635878
; Patent No. 5953164
; GENERAL INFORMATION:
; APPLICANT: BRAMS, Peter
; APPLICANT: CHAMAT, Soulaïma Salim
; APPLICANT: PAN, Li-Zhen
; APPLICANT: WALSH, Edward E.
; APPLICANT: HEARD, Cheryl Janne
; APPLICANT: NEWMAN, Roland Anthony
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
; TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/635,878
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: 08/488,376
; APPLICATION NUMBER: 08/488,376
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-150
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 705 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..705
; US-08-635-878-16

Query Match 78.6%; Score 304.2; DB 2; Length 705;
Best Local Similarity 87.4%; Pred. No. 1.5e-86;
Matches 333; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
QY 7 ATGAGGTCCCGCTCAGCTCTCGGGGCTCTTCTGCTCGGCTCCAGGTGCCAGATGT 66
Db 1 ATGGAGACCCCTGCTCAGCTCTCGGGGCTCTGCTACTCTGCTCGGCTCCAGGTGCCAGATGT 60
QY 67 GACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGATCTGAGGGACAGAGTCAACC 126

Db 61 GACATCCAGATGACCCAGTCTCCATCTCCTCGTCTGCACTCTGTCGGACAGAGTCAACC 120
QY 127 ATCACTTCGAGGGCAAGTCAGGACATTAGGTATTATTTAAATTTGGTATCAGCAGAAACCA 186
Db 121 ATCACTTCGAGGGCAAGTCAGGACATTAGGTATTATTTAAATTTGGTATCAGCAGAAACCA 180
QY 187 GGAAGAGCTCTAAGCTCTCTGATCTATGTTGCATCCAGTTTGCAGAGTGGGGTCCCATCA 246
Db 181 GGAAGAGCTCTAAGCTCTCTGATCTATGTTGCATCCAGTTTGCAGAGTGGGGTCCCATCA 240
QY 247 AGGTTGAGGCGGACGTGGGACAGAGTTTCACTCTCACCCTGAGCAGCTTGCAGCCT 306
Db 241 AGGTTGAGTGGCGGTGGATCTGGGACAGATTTCACTCTCACCATCAACAGTCTGCAACCT 300
QY 307 GAAGATTTTGGCACTTATTACTGTCTACAGTTTATAGTACCCTCGGACGTTTCGGCCAA 366
Db 301 GAAGATTTTGGCACTTATTACTGTCTACAGTTTATAGTACCCTCGGACGTTTCGGCCCA 360
QY 367 GGGACCAAGGTGGAAATCAAA 387
Db 361 GGGACCAAGGTGGAAATCAAA 381

RESULT 14

US-08-770-057-16
; Sequence 16, Application US/08770057
; Patent No. 5958765
; GENERAL INFORMATION:
; APPLICANT: BRAMS, Peter
; APPLICANT: CHAMAT, Soulaïma Salim
; APPLICANT: PAN, Li-Zhen
; APPLICANT: WALSH, Edward E.
; APPLICANT: HEARD, Cheryl Janne
; APPLICANT: NEWMAN, Roland Anthony
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
; TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/770,057
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: 08/488,376
; APPLICATION NUMBER: 08/488,376
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-150
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 16:
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:

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; LOCATION: 1..705
US-08-770-057-16

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RESULT 15
US-09-335-697B-16
; Sequence 16, Application US/09335697B
; Patent No. 620804
; GENERAL INFORMATION:
; APPLICANT: BRAMS, Peter
; CHAMAT, Soulaime Salim
; PAN, Li-Zhen
; WALSH, Edward E.
; HEARD, Cheryl Janne
; NEWMAN, Roland Anthony
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
; MONOCLONAL ANTIBODIES SPECIFIC TO RSV P-PROTEIN AND
; METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/335,697B
; FILING DATE: 06-Jul-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/770,057
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
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; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-150
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 705 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..705
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-335-697B-16

Query Match      78.6%; Score 304.2; DB 3; Length 705;
Best Local Similarity 87.4%; Pred. No. 1.5e-86;
Matches 333; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Qy 7 ATGAGGTCCTCCGCTCAGCTCTCGGGCTCTCTGCTCTGGCTCCCGAGTGCAGATGT 66
Db 1 ATGGAGACCCCTGCTCAGCTCTCGGGCTCTCTGCTCTGGCTCCCGAGTGCAGATGT 60

Qy 67 GACATCCAGATGACCCAGTCTCCATCTCCCTGCTGATCTGTAGGAGTGCAGATGCACC 126
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Title: US-09-019-441-1_COPY_58_390

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	293	88.0	806	9	AB064155	AB064155 Homo sapi
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4	291.4	87.5	435	9	HS285033	Z85033 H.sapiens I
5	291.4	87.5	473	9	HUMIGLDS	M75282 Human Ig la
6	291.4	87.5	473	9	HUMIGLVDS	M75139 Human Ig re
7	291.4	87.5	808	9	AB064152	AB064152 Homo sapi
8	291.4	87.5	808	9	AB064164	AB064164 Homo sapi
9	289.8	87.0	333	9	AB064024	AB064024 Homo sapi
10	289.8	87.0	333	9	HS399863	AJ399863 Homo sapi
11	289.8	87.0	810	9	AB064163	AB064163 Homo sapi
12	288.2	86.5	333	9	AB064000	AB064000 Homo sapi
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14	288.2	86.5	435	9	HS285358	Z85358 H.sapiens I
15	288.2	86.5	433	9	HSU43772	U43772 Human immun
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25	286.6	86.1	809	9	AB064156	AB064156 Homo sapi
26	285.2	85.6	330	9	AF194579	AF194579 Homo sapi
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30	285.2	85.6	330	9	AF194605	AF194605 Homo sapi
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34	285	85.6	376	12	AF453127	AF453127 Synthetic
35	285	85.6	376	12	AF453182	AF453182 Synthetic
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37	285	85.6	435	9	HS285297	Z85297 H.sapiens I
38	285	85.6	331	9	HS249377	AJ249377 Homo sapi
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ALIGNMENTS

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(24-17TIIIIH34) rearranged; IG-Light-Lambda; VLambda.
435 bp DNA linear PRI 06-FEB-1997
ACCESSION Z85043
VERSION Z85043.1 GI:1834754
KEYWORDS antigen receptor; immunoglobulin; immunoglobulin light chain;
immunoglobulin superfamily; rearranged; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.

L03632
 L03632.1 GI:186090
 C-region; J-region; V-region; immunoglobulin lambda; immunoglobulin
 light chain; processed gene.
 SOURCE
 Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 409)
 Paul, E.; Iliev, A.; Livneh, A. and Diamond, B.
 The anti-DNA associated idiotype 8.12 is encoded by the V lambda II
 gene family and maps to the vicinity of L chain CDR1
 J. Immunol. (1992) In press
 COMMENT
 Original source text: Homo sapiens (individual isolate SLE patient
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 DEFINITION
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 (24-07ITIIB176) rearranged; Ig-Light-Lambda; VLambda.
 ACCESSION
 Z85033
 VERSION
 285033.1 GI:1834744
 KEYWORDS
 antigen receptor; immunoglobulin; immunoglobulin light chain;
 immunoglobulin superfamily; rearranged; variable region.
 SOURCE
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 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 Ignatovich, O., Tomlinson, I.M., Jones, P.T. and Winter, G.
 XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
 Repertoire
 J. Mol. Biol.
 2 (bases 1 to 435)
 Ignatovich, O.
 Direct Submission
 Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
 Engineering, Hills Road, Cambridge CB2 2QH, UK
 JOURNAL
 Location/Qualifiers
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Qy      301 TTCGAGAGAGGACCCGGTTGACGTCCTAGGT 333
Db      358 TTCGCGGAGGAGCAAGCTACCGTCTCTAGGT 390

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LOCUS   Human Ig lambda L chain subgroup II V-2.DS mRNA, VJ region, partial cds.
DEFINITION
ACCESSION M75282
VERSION M75282.1 GI:186134
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 473)
AUTHORS Paul, E., Livneh, A., Manheimer-Lory, A. and Diamond, B.
TITLE Characterization of the human immunoglobulin V-lambda-II gene family and analysis of V-lambda-II and C-lambda polymorphism in systemic lupus erythematosus
JOURNAL J. Immunol. (1991) In press
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Qy      1 CAGTCTGCCCGACTCAGCCTCCCTCTGTGTTATGTTCTCTGGTACAGTCCGTCACCATC 60
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ACCESSION M75139
VERSION M75139.1 GI:186154
KEYWORDS C-region; J-region; V-region; immunoglobulin; immunoglobulin lambda; immunoglobulin light chain; variable region subgroup II.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 473)
AUTHORS Paul, E., Livneh, A., Manheimer-Lory, A.J. and Diamond, B.
TITLE Characterization of the human Ig V lambda II gene family and analysis of V lambda II and C lambda polymorphism in systemic lupus erythematosus
JOURNAL J. Immunol. 147 (8), 2771-2776 (1991)
MEDLINE 92013092
PUBMED 1680918
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Matches 307; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy      1 CAGTCTGCCCGACTCAGCCTCCCTCTGTGTTATGTTCTCTGGTACAGTCCGTCACCATC 60

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RESULT 7
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LOCUS      808 bp      mRNA      linear.      PRI 02-JUL-2002
DEFINITION Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLIJ
AB064152
ACCESSION
VERSION    AB064152.1 GI:21669510
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE
AUTHORS    1 Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M.,
Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J.,
Miura, K. and Kurosawa, Y.
TITLE      Construction and characterization of antibody libraries: isolation
of therapeutic human antibodies and application to functional
genomics
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 808)
AUTHORS    Kurosawa, Y.
TITLE      Direct Submission
JOURNAL    Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
Comprehensive Medical Science, Fujita Health University;
Kutsukake-cho, Toyooka 470-1192, Japan
(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
COMMENT    Please visit our web site
URL:http://www.fujita-hu.ac.jp/immunity/
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gene
CDS

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Best Local Similarity 92.2%; Pred. No. 1.7e-74;
Matches 307; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
Qy      1  CAGTCTGCCCCGACTCAGCGCTCCCTCTGTGTCTGGGTCTCTCTGGACAGTCCGTCACCATC 60
Db      67  CAGTCTGCCCCGACTCAGCGCTCCCTCTGTGTCTGGGTCTCTCTGGACAGTCCGTCACCATC 126
Qy      61  TCTGCACTGGAACGACGATGACGTTGGTGTATTAATCTATCTCTCTGATCAACAC 120
Db      127  TCTGCACTGGAACGACGATGACGTTGGTGTATTAATCTATCTCTCTGATCAACAA 186
Qy      121  CACCCAGGCAAGCCCGGCTCATGATTTATGATGTCGTAAGCGGGCTCAGGGGTC 180
Db      187  CACCCAGGCAAGCCCGGCTCATGATTTATGATGTCAGTAAGCGGGCTCAGGGGTT 246
Qy      181  TCTGATCGCTTCTCTGGTCCAAAGTCTGGCAACACGGCTCCCTGACCATCTCTGGGTC 240
Db      247  TCTAATCGCTTCTCTGGTCCAAAGTCTGGCAACACGGCTCCCTGACCATCTCTGGGTC 306
Qy      241  CAGCTGAGGACGAGGCTGATTTATCTGTTGTTATATACACAGTACGACATTTGTTA 300
Db      307  CAGGCTAAGGACGAGGCTGATTTATCTGCGAGCTCATATACAGCAGACATTTGGTG 366
Qy      301  TTCGGAAGGAGGACCGGCTTACCGCTCTCTAGGT 333
Db      367  TTCGGGAGGAGGACCAAGCTGACCGTCTCTAGGT 399

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AB064164
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DEFINITION Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLIJ
AB064164
ACCESSION
VERSION    AB064164.1 GI:21669534
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SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE
AUTHORS    1 Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M.,
Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J.,
Miura, K. and Kurosawa, Y.
TITLE      Construction and characterization of antibody libraries: isolation
of therapeutic human antibodies and application to functional
genomics
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 808)
AUTHORS    Kurosawa, Y.
TITLE      Direct Submission
JOURNAL    Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
Comprehensive Medical Science, Fujita Health University;
Kutsukake-cho, Toyooka 470-1192, Japan
(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
COMMENT    Please visit our web site
URL:http://www.fujita-hu.ac.jp/immunity/
FEATURES   Location/Qualifiers
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TITLE
Bouanani,M. and Peraldi-Roux,S.
Thyroid peroxidase autoantibodies obtained from random single chain
FV libraries contain the same heavy/light chain combinations as
occur in vivo

JOURNAL
Endocrinology 142 (11), 4740-4750 (2001)

MEDLINE
21518466

PUBMED
11606439

REFERENCE
2 (bases 1 to 333)

AUTHORS
Chapal,N.

TITLE
Direct Submission

JOURNAL
Submitted (05-JAN-2000) Chapel N., Faculte de Pharmacie, CNRS

REFERENCE
UMR9921, 15 avenue Charles Flahault, Montpellier 34060, FRANCE

FEATURES

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/product="immunoglobulin lambda chain variable region"

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CDS

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ORIGIN

Query Match 87.0%; Score 289.8; DB 9; Length 333;
Best Local Similarity 91.9%; Pred. No. 5.1e-74;
Matches 306; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTGACAGTGGTCCACATC 60

Db 1 CAGTCTGCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTGACAGTGGTCCACATC 60

Qy 61 TCCTGCACCTGAACACGAGGATGAGTGGTGGTTTAACTATGTCCTCGTACCAACAC 120

Db 61 TCCTGCACCTGAACACGAGGATGAGTGGTGGTTTAACTATGTCCTCGTACCAACAC 120

Qy 121 CACCAGGCAAGCCCAAACTCATGATTTATGATGTCGTAAGCGGCGCTCAGGGGTC 180

Db 121 CACCAGGCAAGCCCAAACTCATGATTTATGATGTCGTAAGCGGCGCTCAGGGGTC 180

Qy 181 TCTGATCGTTCTCTGGCTCCAACTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC 240

Db 181 TCTAATCGTTCTCTGGCTCCAACTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC 240

Qy 241 CAGGCTGAGGACGAGGCTGATTTACTGTTGTTTATATACAAACAGTAGGACTTTGTTA 300

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Qy 301 TTCCGAGGAGGACCCCGGTTTCCACGCTCCTAGGT 333

Db 301 TTCCGAGGAGGACCCCGGTTTCCACGCTCCTAGGT 333

RESULT 11

AB064163

LOCUS
AB064163
Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
region, partial cds, clone:L23.

DEFINITION

ACCESSION
AB064163

VERSION
AB064163.1

KEYWORDS
GI:21669532

ORGANISM
Homo sapiens (human)

SOURCE
Homo sapiens

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE
1 Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirano,Y., Kakita,M.,

REFERENCE
Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,

AUTHORS
Miura,K. and Kurosawa,Y.

TITLE
Construction and characterization of antibody libraries: isolation

REFERENCE
of therapeutic human antibodies and application to functional

AUTHORS
genomics

TITLE
Unpublished

REFERENCE
2 (bases 1 to 810)

AUTHORS
Kurosawa,Y.

TITLE
Direct Submission

JOURNAL
Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for

REFERENCE
Comprehensive Medical Science, Fujita Health University;

AUTHORS
Kutsuke-cho, Toyake 470-1192, Japan

TITLE
(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)

COMMENT
Please visit our web site

REFERENCE
URL:http://www.fujita-hu.ac.jp/immunity/.

FEATURES
Location/Qualifiers

source

1. .810
/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="L23"

/clone_lib="AIMS4"

/notes="mixture of tissues:tonsils, umbilical cords,

peripheral blood and bone marrow"

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/codon_start=1

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Query Match 87.0%; Score 289.8; DB 9; Length 810;

Best Local Similarity 91.9%; Pred. No. 4.9e-74;

Matches 306; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTGACAGTGGTCCACATC 60

Db 67 CAGTCTGCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTGACAGTGGTCCACATC 126

Qy 61 TCCTGCACCTGAACACGAGGATGAGTGGTGGTTTAACTATGTCCTCGTACCAACAC 120

Db 127 TCCTGCACCTGAACACGAGGATGAGTGGTGGTTTAACTATGTCCTCGTACCAACAC 186

Qy 121 CACCAGGCAAGCCCAAACTCATGATTTATGATGTCGTAAGCGGCGCTCAGGGGTC 180

Db 187 CACCAGGCAAGCCCAAACTCATGATTTATGATGTCGTAAGCGGCGCTCAGGGGTC 246

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Db      307 CAGCGTAGGACGAGGCTGATTATTAATCTGCGAGCTCATATACAGCAGCTCTTGGGTG 366
Qy      301 TTCCGAGAGGAGCCCGGTTGACCGTCTCTAGGT 333
Db      367 TTCCGGGAGGAGGACCAAGCTGACCGTCTCTAGGT 399

RESULT 12
LOCUS   AB064000
DEFINITION Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
region, partial cds, clone:Li29.
ACCESSION AB064000
VERSION   AB064000.1 GI:21669206
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
Miura,K. and Kurosawa,Y.
TITLE Construction and characterization of antibody libraries: isolation
of therapeutic human antibodies and application to functional
genomics
JOURNAL Unpublished
REFERENCE 2. (bases 1 to 333)
AUTHORS Kurosawa,Y.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
Comprehensive Medical Science, Fujita Health University;
Kutsukake-cho, Toyosake 470-1192, Japan
(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
COMMENT Please visit our web site
URL:http://www.fujita-hu.ac.jp/immunity/.
FEATURES
source
1..333
/organism="Homo sapiens"
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/db_xref="taxon:9606"
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peripheral blood and bone marrow"
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BASE COUNT 72 a 102 c 79 g 80 t
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Best Local Similarity 91.6%; Pred. No. 1.5e-73;
Matches 305; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy      1 CAGTGTGCCCCGACTCAGCCTCCCTCTGTCTGGGTCTCTCGACAGTGGTACCATC 60
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Db      61 TCCTGCATCTGGAACACGAGGATGACCGTGGTGGTTAATACTATGTCTCTGGTACCAAC 120
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Qy      241 CAGGCTGAGGACGAGGCTGATTATTAATCTGTTGTTTCATATACACAGTAGACATTTGTTA 300
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Qy      301 TTCCGAGAGGAGCCCGGTTGACCGTCTCTAGGT 333
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DEFINITION H.sapiens Ig lambda light chain variable region gene (34-09SWIIC37)
rearranged; Ig-Light-Lambda; VLambda.
ACCESSION Z85382
VERSION   Z85382.1 GI:1835093
KEYWORDS antigen receptor; immunoglobulin; immunoglobulin light chain;
immunoglobulin superfamily; rearranged; variable region.
SOURCE   Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.
TITLE XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
Reertoire
JOURNAL J. Mol. Biol.
REFERENCE 2. (bases 1 to 375)
AUTHORS Ignatovich,O.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
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Qy      61 TCCTGCATCTGGAACACGAGGATGACCGTGGTGGTTAATACTATGTCTCTGGTACCAAC 120
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misc.

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misc feature /note="encodes CDR3" 358.390
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Qy 358 TTCGGGAGGAGGACCAAGCTGACCGTCTCAGGT 390
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Job time : 1380.44 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 1440.93 Seconds
(without alignments)
5616.780 Million cell updates/sec

Title: US-09-019-441-1_COPY_58_390
Perfect score: 333

Sequence: 1 CAGCTGCGCCGACTCAGCC.....CCCGTTGACGCTTAGGT 333

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hci:*
9: gb_est1:*
10: gb_est2:*
11: gb_est3:*
12: gb_est4:*
13: gb_est5:*
14: gb_estfun:*
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27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	291.4	87.5	880	10	BF975970 602246174
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4	281.8	84.6	716	9	AV693754 AV693754

5	281.8	84.6	767	9	AV697043
6	280.2	84.1	485	13	BX280395
7	280.2	84.1	751	9	AV699040
8	280.2	84.1	766	14	CD101742
9	280.2	84.1	768	9	AV685070
10	280.2	84.1	787	12	B1820758
11	280.2	84.1	829	10	BG685732
12	280.2	84.1	840	10	BG397282
13	280.2	84.1	843	10	BG756493
14	280.2	84.1	868	10	BG483745
15	279.9	83.8	417	9	AW406701
16	278.6	83.7	479	10	BG059377
17	278.6	83.7	487	9	AW404692
18	278.6	83.7	686	10	BG759257
19	278.6	83.7	786	10	BG758901
20	278.6	83.7	841	14	CB986194
21	278.6	83.7	889	10	BG756342
22	278.6	83.7	908	10	BG756874
23	278.6	83.7	953	10	BF976229
24	278.6	83.7	980	10	BG397302
25	278.4	83.6	1008	10	BG754756
26	277	83.2	536	10	BF674688
27	277	83.2	658	10	BG397577
28	277	83.2	684	9	AV686421
29	277	83.2	804	10	BG564971
30	276.8	83.1	611	10	BG566373
31	275.4	82.7	523	12	BM831030
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33	275.4	82.7	660	12	BM831125
34	275.4	82.7	890	10	BG342194
35	273.6	82.2	553	12	BM830982
36	273.6	82.2	554	12	BM830988
37	273.6	82.2	604	12	BM773502
38	273.6	82.2	710	12	BM769463
39	273.6	82.2	813	10	BF974961
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41	272.2	81.7	808	12	BM007694
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43	271.6	81.6	359	9	AW405058
44	270.8	81.3	824	10	BG536723
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ALIGNMENTS

RESULT 1

BF975970

LOCUS

DEFINITION

602246174F1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4337226 5',

mRNA sequence.

BF975970

VERSION

BF975970.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 880)

TITLE

NIH-MGC http://mgc.nci.nih.gov/.

JOURNAL

Unpublished

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L12CM1211 row: c column: 19

High quality sequence stop: 759.

BF975970 880 bp mRNA linear EST 22-JAN-2001

602246174F1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4337226 5',

mRNA sequence.

BF975970

VERSION

BF975970.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 880)

TITLE

NIH-MGC http://mgc.nci.nih.gov/.

JOURNAL

Unpublished

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L12CM1211 row: c column: 19

High quality sequence stop: 759.

FEATURES
source

Location/Qualifiers
1..880
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4337226"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site: 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
200 a 283 c 219 g 178 t

BASE COUNT
ORIGIN

Query Match 87.5%; Score 291.4; DB 10; Length 880;
Best Local Similarity 92.2%; Pred. No. 2.1e-71;
Matches 307; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCGACTCAGCCTCCCTCTGTCTGTGGTCTCTCGACAGTCGGTCACCATC 60
Db 90 CAGTCTGCCCTGACTCAGCCTGCCCTCGCTGTCTGGGTCTCTCGACAGTCGATCACCATC 149

Qy 61 TCCTGCACCTGGAACACGAGGACGCTGTGTGGTTTAACTATGTCTCTGGTACCAACAC 120
Db 150 TCCTGCACCTGGAACACGAGGACGCTGTGTGGTTTAACTATGTCTCTGGTACCAAC 209

Qy 121 CACCAGCAAGACCCCAAACTCATGATTATGATGTCGTAAGCGGGCTCTCAGGGGTC 180
Db 210 CACCAGCAAGACCCCAAACTCATGATTATGATGTCGTAATCGGCCCTCAGGGGTT 269

Qy 181 TCTGATCGCTTCTGTGGTCCAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGTC 240
Db 270 TCTAATCGCTTCTGTGGTCCAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGTC 329

Qy 241 CAGGCTGAGGACGAGGCTGATTATTACTTGTGTTTATATACAAACAGTAGCACTTTGTTA 300
Db 330 CAGGCTGAGGACGAGGCTGATTATTACTTGTGTTTATATACAAACAGTAGCACTTTGTTA 389

Qy 301 TTGGAAGAGGACCCGGTTGACCGTCTCTAGGT 333
Db 390 TTGCGGAGGAGGACCAAGGTGACCGTCTCTAGGT 422

RESULT 2
BM914350 1078 bp mRNA linear EST 12-MAR-2002
LOCUS AGENCOURT 6615290 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5480018
5', mRNA sequence.
BM914350
DEFINITION AGENCOURT 6615290 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5480018
5', mRNA sequence.
ACCESSION BM914350
VERSION BM914350.1 GI:19364729
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1078)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/ILLNL at:
<http://image.llnl.gov>
Plate: LLCM2002 row: d column: 03
High quality sequence stop: 538.

FEATURES
source

Location/Qualifiers
1..1078
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5480018"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site: 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
427 a -257 c 244 g 150 t

BASE COUNT
ORIGIN

Query Match 85.6%; Score 285; DB 12; Length 1078;
Best Local Similarity 91.0%; Pred. No. 1.5e-69;
Matches 303; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCGACTCAGCCTCCCTCTGTCTGTGGTCTCTCGACAGTCGGTCACCATC 60
Db 104 CAGTCTGCCCTGACTCAGCCTGCCCTCGCTGTCTGGGTCTCTCGACAGTCGATCACCATC 163

Qy 61 TCCTGCACCTGGAACACGAGGACGCTGTGTGGTTTAACTATGTCTCTGGTACCAACAC 120
Db 164 TCCTGCACCTGGAACACGAGGACGCTGTGTGGTTTAACTATGTCTCTGGTACCAACAG 223

Qy 121 CACCAGCAAGACCCCAAACTCATGATTATGATGTCGTAAGCGGGCTCTCAGGGGTC 180
Db 224 CACCAGCAAGACCCCAAACTCATGATTATGAGGTAGTAGTCGGCGCTCAGGGGTT 283

Qy 181 TCTGATCGCTTCTGTGGTCCAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGTC 240
Db 284 TCTAATCGCTTCTGTGGTCCAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGTC 343

Qy 241 CAGGCTGAGGACGAGGCTGATTATTACTTGTGTTTATATACAAACAGTAGCACTTTGTTA 300
Db 344 CAGGCTGAGGACGAGGCTGATTATTACTTGTGTTTATATACAAACAGTAGCACTTTGTTA 403

Qy 301 TTGGAAGAGGACCCGGTTGACCGTCTCTAGGT 333
Db 404 TTGCGGAGGAGGACCAAGCTGACCGTCTCTAGGT 436

RESULT 3
AV694861 710 bp mRNA linear EST 16-JAN-2002
LOCUS AV694861 GKC Homo sapiens cDNA clone GKCWE01 5', mRNA sequence.
DEFINITION AV694861
ACCESSION AV694861
VERSION AV694861.1 GI:10296724
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 710)
AUTHORS Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W., Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X., Hu, G., Gu, J., Chen, Z. and Han, Z.
TITLE Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
MEDLINE 21625106


```

PUBMED 11752456
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
Location/Qualifiers
1..710
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GKCGW05"
/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="GKC"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 147 a 239 c 182 g 142 t
ORIGIN
Query Match 84.6%; Score 281.8; DB 9; Length 710;
Best Local Similarity 90.4%; Pred. No. 9.9e-69;
Matches 301; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 1 CAGTCTCCCCGACTCAGCTCCCTCTGTGTCGGGTCTCTCGACAGTGGTCAACATC 60
DB 86 CAGTCTCCCTGACTCAGCTCCCTCGGTCTCTGGGTCTCTCGACAGTGGTCAACATC 145
QY 61 TCCTGCACTGGAACACGAGTGGTGGTATATATGCTCTCTCGTACCAACAC 120
DB 146 TCCTGCACTGGAACACGAGTGGTGGTATATATGCTCTCTCGTACCAACAA 205
QY 121 CACCCAGGCAAGCCCAAACTCATGATTTATGATGCTGCTAAGCGGGCTCAGGGGTC 180
DB 206 CACCCAGGCAAGCCCAAAAGTCATGATTTATGATGCTCAATATCGGCCCTCAGGGGTT 265
QY 181 TCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGCCCTCCCTGACCATCTCTGGGCTC 240
DB 266 TCTAATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGCCCTCCCTGACCATCTCTGGGCTC 325
QY 241 CAGCTGAGGACGAGGCTGATTTACTGTTTATATACACAGTACAGTACCTTTGTTA 300
DB 326 CAGCTGAGGACGAGGCTGATTTACTGTTTATATACACAGTACAGTACCTTTGTTA 385
QY 301 TTCGGAAGAGGAGCCCGTTGACCGTCTTAGGT 333
DB 386 TTCGGCGAGGAGCAAGCTGACCGTCTTAGGT 418

RESULT 4
LOCUS AV693754
DEFINITION AV693754 GKC Homo sapiens cDNA clone GKCGW05 5', mRNA sequence.
ACCESSION AV693754
VERSION AV693754.1 GI:10295617
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 716)
AUTHORS Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
Hu,G., Gu,J., Chen,Z. and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

PUBMED 21625106
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
Location/Qualifiers
1..716
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GKCGW05"
/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="GKC"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 148 a 240 c 183 g 144 t
ORIGIN
Query Match 84.6%; Score 281.8; DB 9; Length 716;
Best Local Similarity 90.4%; Pred. No. 9.9e-69;
Matches 301; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 1 CAGTCTCCCCGACTCAGCTCCCTCTGTGTCGGGTCTCTCGACAGTGGTCAACATC 60
DB 86 CAGTCTCCCTGACTCAGCTCCCTCGGTCTCTGGGTCTCTCGACAGTGGTCAACATC 145
QY 61 TCCTGCACTGGAACACGAGTGGTGGTATATATGCTCTCTCGTACCAACAC 120
DB 146 TCCTGCACTGGAACACGAGTGGTGGTATATATGCTCTCTCGTACCAACAA 205
QY 121 CACCCAGGCAAGCCCAAACTCATGATTTATGATGCTGCTAAGCGGGCTCAGGGGTC 180
DB 206 CACCCAGGCAAGCCCAAAAGTCATGATTTATGATGCTCAATATCGGCCCTCAGGGGTT 265
QY 181 TCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGCCCTCCCTGACCATCTCTGGGCTC 240
DB 266 TCTAATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGCCCTCCCTGACCATCTCTGGGCTC 325
QY 241 CAGCTGAGGACGAGGCTGATTTACTGTTTATATACACAGTACAGTACCTTTGTTA 300
DB 326 CAGCTGAGGACGAGGCTGATTTACTGTTTATATACACAGTACAGTACCTTTGTTA 385
QY 301 TTCGGAAGAGGAGCCCGTTGACCGTCTTAGGT 333
DB 386 TTCGGCGAGGAGCAAGCTGACCGTCTTAGGT 418

RESULT 5
LOCUS AV697043
DEFINITION AV697043 GKC Homo sapiens cDNA clone GKCGW01 5', mRNA sequence.
ACCESSION AV697043
VERSION AV697043.1 GI:10298906
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 767)
AUTHORS Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
Hu,G., Gu,J., Chen,Z. and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver

```

JOURNAL
MEDLINE
PUBMED
COMMENT

Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
21825106
11752456
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhongjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Tel: 86-21-50801922
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES

source

1. 767
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GKCGW01"
/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="GKC"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 165 a 249 c 198 g 154 t 1 others
ORIGIN

Query Match 84.6%; Score 281.8; DB 9; Length 767;
Best Local Similarity 90.4%; Pred. No. 1e-68;
Matches 301; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCGACTCAGCCCTCCCTCTGCTGGTCTCTGGACAGTCGGTCCACCATC 60
Db 86 CAGTCTGCCCGACTCAGCCCTCCCTCTGCTGGTCTCTGGACAGTCGGTCCACCATC 145
Qy 61 TCCTGCACTGGAACACGAGGATGACGTTGGTGGTTATTAATATATGTCCTCTGGTACCAACAC 120
Db 146 TCCTGCACTGGAACACGAGGATGACGTTGGTGGTTATTAATATATGTCCTCTGGTACCAACAA 205
Qy 121 CACCCAGGCAAGGCCCGCAAACTCATGTTATGATGTCGTTAGCGGGCTCTAGGGGTC 180
Db 206 CACCCAGGCAAGGCCCGCAAACTCATGTTATGATGTCGTTAGCGGGCTCTAGGGGTC 265
Qy 181 TCTGATCGCTCTCTGCTGCTCAAGTCTGCAACAGCGGCTCCCTGACCATCTCTGGGTC 240
Db 266 TCTAATCGCTCTCTGCTGCTCAAGTCTGCAACAGCGGCTCCCTGACCATCTCTGGGTC 325
Qy 241 CAGGCTGAGGACGAGGCTGATTATTAATGTTGTTTATATACAAACAGTAGCATTTTGTGA 300
Db 326 CAGGCTGAGGACGAGGCTGATTATTAATGTTGTTTATATACAAACAGTAGCATTTTGTGA 385
Qy 301 TTCGGAAGAGGACCCGGTTGACCGTCTCTAGGT 333
Db 386 TTCGCGCGAGGACCAAGCTGACCGTCTCTAGGT 418

RESULT 6

BX280395

LOCUS

DEFINITION BX280395 Soares multiple sclerosis 2NBHMSF Homo sapiens cDNA clone
IMAGp998E24628 ; IMAGE:283391, mRNA sequence.

ACCESSION

BX280395

VERSION

BX280395.1

KEYWORDS

EST.

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 485)

Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,

Radelof, U., Schneider, D. and Korn, B.

Human Unigeneset - RZPD3

Unpublished

Contact: Ina Rofls

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGp998E24628.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-bin/showlib.pl.cgi/response?libNo=972 Contact: Ina Rofls
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de

This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTACACAGGAACAGCTATGAC.

FEATURES

source

1. 485
Location/Qualifiers
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGp998E24628 ; IMAGE:283391"
/sex="male"
/tissue_type="multiple sclerosis lesions"
/dev_stage="Age 46"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares multiple sclerosis 2NBHMSF"
/note="Vector: p773D (Pharmacia) with a modified
polylinker V-TYPE; phagemid; Site_1: Not I; Site_2: Eco RI
; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5].
TGTTACCAATCTGAAGTGGAGCGCGCATTTTTTTTTTTTTTTT 3',
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p773 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldo. RNA from 4 multiple sclerosis
lesions from one patient was kindly provided by Dr. Kevin
G. Becker (NINDS/NIH)."

BASE COUNT 96 a 172 c 115 g 102 t
ORIGIN

Query Match 84.1%; Score 280.2; DB 13; Length 485;
Best Local Similarity 90.1%; Pred. No. 2.3e-68;
Matches 300; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCGACTCAGCCCTCCCTCTGCTGGTCTCTGGACAGTCGGTCCACCATC 60
Db 77 CAGTCTGCCCGACTCAGCCCTCCCTCTGCTGGTCTCTGGACAGTCAGTCCACCATC 136
Qy 61 TCCTGCACTGGAACACGAGGATGACGTTGGTGGTTATTAATATATGTCCTCTGGTACCAACAC 120
Db 137 TCCTGCACTGGAACACGAGGATGACGTTGGTGGTTATTAATATATGTCCTCTGGTACCAACAG 196
Qy 121 CACCCAGGCAAGGCCCGCAAACTCATGTTATGATGTCGTTAGCGGGCTCTAGGGGTC 180
Db 197 CACCCAGGCAAGGCCCGCAAACTCATGTTATGAGGTGAGTAAAGCGGCTCTAGGGGTC 256
Qy 181 TCTGATCGCTCTCTGCTGCTCAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGTC 240
Db 257 CCTGATCGCTCTCTGCTGCTCAAGTCTGGCAACAGCGGCTCCCTGACCGTCTCTGGGTC 316
Qy 241 CAGGCTGAGGACGAGGCTGATTATTAATGTTGTTTATATACAAACAGTAGCATTTTGTGA 300
Db 317 CAGGCTGAGGACGAGGCTGATTATTAATGTTGTTTATATACAAACAGTAGCATTTTGTGA 376
Qy 301 TTCGGAAGAGGACCCGGTTGACCGTCTCTAGGT 333
Db 377 TTCGGAAGAGGACCCGGTTGACCGTCTCTAGGT 409

RESULT 7

AV695040

LOCUS AV699040 751 bp mRNA linear EST 16-JAN-2002
 DEFINITION AV699040 GKC Homo sapiens cDNA clone GKGX07 5', mRNA sequence.
 ACCESSION AV699040
 VERSION AV699040.1 GI:10301011
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 1 (bases 1 to 751)
 Xu.X., Huang.J., Xu.Z., Qian.B., Zhu.Z., Yan.Q., Cai.T., Zhang.X.,
 Xie.H., Qu.J., Liu.F., Huang.Q., Cheng.Z., Li.N., Du.J., Hu.W.,
 Shen.K., Lu.G., Zhong.M., Xu.S., Gu.W., Huang.W., Zhao.X.,
 Hu.G., Gu.J., Chen.Z. and Han.Z.
 TITLE Insight into hepatocellular carcinogenesis at transcriptome level
 by comparing gene expression profiles of hepatocellular carcinoma
 with those of corresponding noncancerous liver
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
 MEDLINE 21625106
 PUBMED 11752456
 COMMENT Contact: Zequang Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919 (ex. 45)
 Fax: 86-21-50801922
 Email: hanzq@chgc.sh.cn
 This clone is available at CHGC in Shanghai.

FEATURES

Location/Qualifiers
 1..751
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="GKGX07"
 /tissue_type="hepatocellular carcinoma"
 /dev_stage="Adult"
 /lab_host="SOLR"
 /clone_lib="GKC"
 /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
 XhoI"

BASE COUNT 166 a 241 c 201 g 143 t

Query Match 84.1%; Score 280.2; DB 9; Length 751;
 Best Local Similarity 90.1%; Pred. No. 2.9e-68;
 Matches 300; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTGGACAGTCGGTCACCATC 60
 Db 68 CAGTCTGCCCTGACTCAGCCTCCCTCGTGTCTGGGTCTCTGGACAGTCGATCACCTTC 127
 Qy 61 TCCTGCACTGGAACACAGGATGAGTGGTGGTTATTAATATGTCTCTGTGATCAACAC 120
 Db 128 TCCTGCACTGGAACACAGGATGAGTGGTGGTTATTAATATGTCTCTGTGATCAACAA 187
 Qy 121 CACCCAGCAAGCCCAACTCATGATTTATGATGTCGCTAAGCGGCTCAGGGGTC 180
 Db 188 CACCCAGCAAGCCCAAGTATGATTTATGATGTCGCTAAGCGGCTCAGGGGTC 247
 Qy 181 TCTGATCGCTTCTCTGGTCTCAAGTCTGGCAACACAGCGCTCCCTGACCATCTCTGGGCTC 240
 Db 248 TCTAATCGCTTCTCTGGTCTCAAGTCTGGCAACACAGCGCTCCCTGACCATCTCTGGGCTC 307
 Qy 241 CAGGCTGAGGACGAGGCTGATTATTAATGTTGTTTATATACACACAGTAGCATTGTTA 300
 Db 308 CAGGCTGAGGACGAGGCTGATTATTAATGTTGTTTATATACACACAGTAGCATTGTTA 367
 Qy 301 TTCGAGAGGAGCCCGTTGACCGTCTTAGT 333
 Db 368 TTCGGCAGGAGCCCAAGCTGACCGTCTTAGT 400

RESULT 8

CD101742
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 SOURCE
 KEYWORDS
 ORGANISM

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

FEATURES

Location/Qualifiers
 1..766
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30347479"
 /tissue_type="Human Placenta"
 /lab_host="DH10B Tona"
 /clone_lib="NIH MGC 147"
 /note="Organ: placenta; Vector: pBluescriptR; Site_1:
 all-XhoI; Site_2: BamH; Oligo-dT primed using primer
 5'-TTTTTTTTTTTTTTVN-3', size-selected for average
 insert size 2.3 kb and normalized to ROT 5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIMH/NHGRI, National Institutes of Health). Note: This is
 a NIH_MGC library."

BASE COUNT 168 a 249 c 205 g 144 t

Query Match 84.1%; Score 280.2; DB 14; Length 766;
 Best Local Similarity 90.1%; Pred. No. 2.9e-68;
 Matches 300; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTGGACAGTCGGTCACCATC 60
 Db 126 CAGTCTGCCCTGACTCAGCCTCCCTCGTGTCTGGGTCTCTGGACAGTCGATCACCATC 185
 Qy 61 TCTGCACTGGAACACAGGATGAGTGGTGGTTATTAATATGTCTCTGTGATCAACAC 120
 Db 186 TCTGCACTGGAACACAGGATGAGTGGTGGTTATTAATATGTCTCTGTGATCAACAG 245
 Qy 121 CACCCAGCAAGCCCAACTCATGATTTATGATGTCGCTAAGCGGCTCAGGGGTC 180
 Db 246 CACCCAGGACACAGCCCAACTCATGATTTATGATGTCGCTAAGCGGCTCAGGGGTC 305
 Qy 181 TCTGATCGCTTCTCTGGTCTCAAGTCTGGCAACACAGCGCTCCCTGACCATCTCTGGGCTC 240
 Db 306 CCTGATCGCTTCTCTGGTCTCAAGTCTGGCAACACAGCGCTCCCTGACCATCTCTGGGCTC 365
 Qy 241 CAGGCTGAGGACGAGGCTGATTATTAATGTTGTTTATATACACACAGTAGCATTGTTA 300
 Db 366 CAGGCTGAGGACGAGGCTGATTATTAATGTTGTTTATATACACACAGTAGCATTGTTA 425
 Qy 301 TTCGGAAGAGGAGCCCGTTGACCGTCTTAGT 333

Qy	301	TTTCGGAAGAGGACCGGTTGACCGTCCTAGGT	333
Db	386	TTTCGGCGCAGGACCAAGCTGACCGTCCTAGGT	418
RESULT 10			
BI820758			
LOCUS	603034354F1	NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5175684 5',	linear EST 04-OCT-2001
DEFINITION		mRNA sequence.	
ACCESSION	BI820758		
VERSION	BI820758.1	GI:159322308	
KEYWORDS	EST.		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens (human)		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 787)		
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs@mail.nih.gov Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11437 row: k column: 13 High quality sequence start: 2 High quality sequence stop: 785.		
FEATURES			
source	1..787		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:5175684"		
	/lab_host="DH10B"		
	/clone_lib="NIH_MGC_115"		
	/notes="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH MGC Library."		
BASE COUNT	175 a 259 c 207 g 146 t		
ORIGIN			
Query Match	84.1%;	Score 280.2;	DB 12; Length 787;
Best Local Similarity	90.1%;	Pred. No. 2.9e-68;	
Matches	300; Conservative	0; Mismatches 33;	Indels 0; Gaps 0
Qy	1	CAGTCGTGCCCGACTGACGCTCCCTCTGTGTCTGGGTCTCTCTGCACAGTCGGTCACCATC	60
Db	89	CAGTCGTGCCCTGACTGACGCTCCCTCCGCGTCGCGGTCTCTCTGCACAGTCAGTCACCATC	148
Qy	61	TCTGTGCACGTGGACACGACGATGAGTTGGTGGTTTAACTATGTCCTCTGGTACCAACAC	120
Db	149	TCCTGTCACTGGAACACGACGATGAGTTGGTGGTTTAACTATGTCCTCTGGTACCAACA	208
Qy	121	CACCCAGGCAAAAGCCCCAAACTCATGATTTATGATGTGCGTAAAGCGGGCCTCAGGGGTC	180
Db	209	CTCCAGGCAAAAGCCCCAAACTCATGATTTATGAGGTCACTAAGCGGCCCTCAGGGGTC	268
Qy	181	TCTGATCGCTTCTCTGGCTCAAGTCATGGCAACACGGGCTCCCTGACCATCTCTGGGCTC	240
Db	269	CCTGATCGCTTCTCTGGCTCAAGTCATGGCAACACGGGCTCCCTGACCATCTCTGGGCTC	328

241 CAGGCTGAGGACGAGGCTGATTATTACTGTGTTTCATATACCAACAGTAGCACTTTGTTA 300
 329 CAGGCTGAGGATGAGGCTGATTATTACTGTGAGCTCATATGAGGAGCGACAATTAGTA 388
 301 TTCGGAAGAGGAGCCCGGTTGACCGTCTTAGGT 333
 389 TTCGGCGAGGAGCAACAGGTGACCGTCTTAGGT 421

RESULT 11
 BG685732 829 bp mRNA linear EST 01-MAY-2001
 LOCUS 602637827F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4765447 5',
 DEFINITION mRNA sequence.
 ACCESSION BG685732
 VERSION BG685732.1 GI:13917129
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 829)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LNCM1624 row: f column: 08
 High quality sequence stop: 821.
 Location/Qualifiers
 1..829
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4765447"
 /tissue_type="primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_48"
 /note="Organ: B-cells; Vector: pOTB7; Site: 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCAGGAG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."
 185 a 279 c 214 g 151 t

BASE COUNT
 ORIGIN

Query Match 84.1%; Score 280.2; DB 10; Length 829;
 Best Local Similarity 90.1%; Pred. No. 3e-68;
 Matches 300; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

1 CAGTCTGCCCGACTCAGCCTCCCTCTGTGTTCTCTGACAGTCGGTCAACATC 60
 89 CAGTCTGCCCGACTCAGCCTCCCTCCCGGTCCTCTGGACAGTCAGTCACCATC 148
 61 TCCTGCACTGGAACACAGGATGAGCTTGTTGTTATATGTTCTCTGTTACCAAC 120
 149 TCCTGCACTGGAACACAGGATGAGCTTGTTGTTATATGTTCTCTGTTACCAAG 208
 121 CACCCAGGCAAGCCCCCAAACTCATGATTTATGATGTCGTTAAGCGGGCCTCAGGGGTC 180
 209 CACCCAGGCAAGCCCCCAAACTCATGATTTATGAGGTTCAGTAAGCGGCGCTCAGGGGTC 268

181 TCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACAGCGCTCCCTGACCATCTCTGGGCTC 240
 269 CCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACAGCGCTCCCTGACCGTCTCTGGGCTC 328
 241 CAGGCTGAGGACGAGGCTGATTATTACTGTGTTTCATATACCAACAGTAGCACTTTGTTA 300
 329 CAGGCTGAGGATGAGGCTGATTATTACTGTGAGCTCATATGAGGAGCGACAATTAGTC 388
 301 TTCGGAAGAGGAGCCCGGTTGACCGTCTTAGGT 333
 389 TTCGGAAGTGGAGCAAGGTGACCGTCTTAGGT 421

RESULT 12
 BG397282 840 bp mRNA linear EST 12-MAR-2001
 LOCUS 602439065F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4565272 5',
 DEFINITION mRNA sequence.
 ACCESSION BG397282
 VERSION BG397282.1 GI:13290730
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 840)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LNCM1282 row: a column: 17
 High quality sequence stop: 840.
 Location/Qualifiers
 1..840
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4565272"
 /tissue_type="primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_48"
 /note="Organ: B-cells; Vector: pOTB7; Site: 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCAGGAG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."
 204 a 272 c 202 g 162 t

BASE COUNT
 ORIGIN

Query Match 84.1%; Score 280.2; DB 10; Length 840;
 Best Local Similarity 90.1%; Pred. No. 3e-68;
 Matches 300; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

1 CAGTCTGCCCGACTCAGCCTCCCTCTGTGTTCTCTGACAGTCGGTCAACATC 60
 49 CAGTCTGCCCGACTCAGCCTCCCTCTGTGTTCTCTGACAGTCAGTCACCATC 108
 61 TCCTGCACTGGAACACAGGATGAGCTTGTTGTTATATGTTCTCTGTTACCAAC 120
 109 TCCTGCACTGGAACACAGGATGAGCTTGTTGTTATATGTTCTCTGTTACCAAC 168

QY 121 CACCAGCAAGCCCAACTCATGATTTATGATCGCTACGCGGCTCAGGGTC 180
 DB 169 CACCAGCAATGCCCAACTCATGATTTATGATCGCTACGCGGCTCAGGGTT 228
 QY 181 TCTGATCGCTTCTGCGTCCAACTCTGCAACACGCGCTCCTGACCATCTCTGGGCTC 240
 DB 229 TCTGATCGCTTCTGCGTCCAACTCTGCAACACGCGCTCCTGACCATCTCTGGGCTC 288
 QY 241 CAGGCTGAGGACGAGGCTGATTTACTGTTGTTTCATATACACAGTAGCACTTTGTTA 300
 DB 289 CAGGCTGAGGACGAGGCTGATTTACTGTTGTTTCATATACACAGTAGCACTTTGTTA 348
 QY 301 TTCGAAAGAGGACCGGTTGACCGTCTAGGT 333
 DB 349 TTCGAAATGGGACCAAGGTCACCGTCTAGGT 381

RESULT 13
 LOCUS BG756493
 DEFINITION 602715633F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4855593 5',
 mRNA sequence.
 ACCESSION BG756493
 VERSION BG756493.1 GI:14067146
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 843)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-remail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLC1705 row: b column: 10
 High quality sequence stop: 838.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4855593"
 /tissue_type="primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 48"
 /note="Organ: B-cells; Vector: pORF7; Site 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Size-selected
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH MGC library."
 187 a 278 c 217 g 161 t

FEATURES

source
 1..843
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4855593"
 /tissue_type="primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 48"
 /note="Organ: B-cells; Vector: pORF7; Site 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Size-selected
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH MGC library."
 187 a 278 c 217 g 161 t

BASE COUNT

ORIGIN 187 a 278 c 217 g 161 t
 Query Match 84.1%; Score 280.2; DB 10; Length 843;
 Best Local Similarity 90.1%; Pred. No. 3e-68;
 Matches 300; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 1 CAGTCTGCCCGCACTCAGCGCTCCCTCTGTTGTTCTCTGGACAGTCGTCACCATC 60
 DB 91 CAGTCTGCCCGCACTCAGCGCTCCCTCTGTTGTTCTCTGGACAGTCGTCACCATC 150

QY 61 TCCTGCACTGGAACACGAGTACGTTGGTGGTTATAACTATGTCTCTGTTACCAAC 120
 DB 151 TCCTGCACTGGAACACGAGTACGTTGGTGGTTATAACTATGTCTCTGTTACCAAC 210
 QY 121 CACCAGCAAGCCCAACTCATGATTTATGATCGCTACGCGGCTCAGGGTC 180
 DB 211 CCCCCAGGACAGCCCAACTCATGATTTATGAGGTCTAGTTATCGGCCCTCAGGGTC 270
 QY 181 TCTGATCGCTTCTGCGTCCAACTCTGCAACACGCGCTCCTGACCATCTCTGGGCTC 240
 DB 271 CCTGATCGCTTCTGCGTCCAACTCTGCAACACGCGCTCCTGACCATCTCTGGGCTC 330
 QY 241 CAGGCTGAGGACGAGGCTGATTTACTGTTGTTTCATATACACAGTAGCACTTTGTTA 300
 DB 331 CAGGCTGAGGACGAGGCTGATTTACTGTTGTTTCATATACACAGTAGCACTTTGTTA 390
 QY 301 TTCGAAAGAGGACCGGTTGACCGTCTAGGT 333
 DB 391 TTCGCGGAGGACCAAGCTGACCGTCTAGGT 423

RESULT 14

LOCUS BG483745
 DEFINITION 602503383F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:461829 5',
 mRNA sequence.
 ACCESSION BG483745
 VERSION BG483745.1 GI:13415934
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 868)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-remail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLC1372 row: e column: 22
 High quality sequence stop: 834.
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
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 /clone_lib="NIH MGC 77"
 /note="Organ: lung; Vector: pNR-LIB (Clontech); Site 1:
 SfiI (ggccattatgcc); Site 2: SfiI (ggccattatgcc); 5' and
 3' adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CAGCGCCATTATGCC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCGCGGCGGCGACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.9
 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH MGC library."
 199 a 278 c 227 g 161 t

FEATURES

source
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:461829"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH MGC 77"
 /note="Organ: lung; Vector: pNR-LIB (Clontech); Site 1:
 SfiI (ggccattatgcc); Site 2: SfiI (ggccattatgcc); 5' and
 3' adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CAGCGCCATTATGCC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCGCGGCGGCGACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.9
 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH MGC library."
 199 a 278 c 227 g 161 t

BASE COUNT

ORIGIN 199 a 278 c 227 g 161 t
 Query Match 84.1%; Score 280.2; DB 10; Length 868;
 Best Local Similarity 90.1%; Pred. No. 3.1e-68;
 Matches 300; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTGTGACAGTGGTCCACCATC 60
 Db 97 CAGTCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTGTGACAGTGGTCCACCATC 156
 Qy 61 TCCTGCACTGAAACACAGGATGAGCTGGTGGTATTAATATGTCTCTGTGACCAACAC 120
 Db 157 TCCTGCACTGAAACACAGGATGAGCTGGTGGTATTAATATGTCTCTGTGACCAACAA 216
 Qy 121 CACCCAGCAAGCCCAACTCATGATTTATGATCTCGTAGCGGGCTCAGGGTC 180
 Db 217 CACCCAGCAAGCCCAACTCATGATTTATGATCTCGTAGTAATCGGCCCTCAGGGTT 276
 Qy 181 TCTGATCGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 Db 277 TCTAATCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 336
 Qy 241 CAGCTGAGGACGAGGCTGATTTATGATTTGTTTATATATATATATATATATATATAT 300
 Db 337 CAGCTGAGGACGAGGCTGATTTATGATTTGTTTATATATATATATATATATATATAT 396
 Qy 301 TTCGAGAGGACCCGGTTGACCGTCTTAGGT 333
 Db 397 TTCGGAACCTGGACCAAGGTACCGTCTTAGGT 429

RESULT 15
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 LOCUS UI-HF-BLO-ada-d-08-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
 DEFINITION IMAGE:3060903 5', mRNA sequence.
 ACCESSION AW406701
 VERSION AW406701.1 GI:6925758
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgaaba-remail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: M13 Forward.
 Location/Qualifiers
 1. 417
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3060903"
 /tissue_type="lymph"
 /cell_type="germinal center B cells"
 /cell_line="MGC85"
 /lab_host="DH10B (LTI)"
 /clone_lib="NIH_MGC_37"

FEATURES
 source
 1. 417
 /organism="Homo sapiens"
 /mol_type="mRNA"
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 /clone="IMAGE:3060903"
 /tissue_type="lymph"
 /cell_type="germinal center B cells"
 /cell_line="MGC85"
 /lab_host="DH10B (LTI)"
 /clone_lib="NIH_MGC_37"
 /note="Vector: p77T3-Pac; Site 1: NotI; Site 2: Eco RI;
 Constructed from size fractionated cytoplasmic mRNA
 (1.5-2.5kb). Directionally cloned. Cells provided by Louis
 M. Staudt, Ph.D. Library preparation by Maria de Fatima
 Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
 84 a 131 c 104 g 98 t

Query Match 83.8%; Score 279; DB 9; Length 417;

Best Local Similarity 90.8%; Pred. No. 4.7e-68;
 Matches 297; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
 Qy 7 GCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTGTGACAGTGGTCCACCATC 66
 Db 6 GGCCTGACTCAGCCTCCCTCCGCTGCTGGGTCTCTGTGACAGTGGTCCACCATC 65
 Qy 67 ACTGGAAACAGCGATGACGTTGGTGGTATTAATATGTCTCTGTGACCAACACCA 126
 Db 66 ACTGGAAACAGCGATGATGTTGGTGGTATTAATATGTCTCTGTGACCAACACCA 125
 Qy 127 GGCAAGAGCCCCAAACTCATGATTTATGATTCGCTAAGCGGCGCTCAGGGTCTCTGAT 186
 Db 126 GGCAAGAGCCCCAAACTCATGATTTATGATTCGCTAAGCGGCGCTCAGGGTCTCTAAT 185
 Qy 187 CGCTTCTCTGGCTCCAAAGTCTGSCAACACGGCTCCCTGACCATCTCTGGGCTCCAGGCT 246
 Db 186 CGCTTCTCTGGCTCCAAAGTCTGSCAACACGGCTCCCTGACCATCTCTGGGCTCCAGGCT 245
 Qy 247 GAGGACGAGGCTGATTTATGATTTGTTTATATATATATATATATATATATATAT 306
 Db 246 GAGGACGAGGCTGATTTATGATTTGTTTATATATATATATATATATATATATAT 305
 Qy 307 AGAGGACCGCGGTGACCGTCTTAGGT 333
 Db 306 GGAGGGACCAAGCTGACCGTCTTAGGT 332

Search completed: December 29, 2003, 21:44:06
 Job time : 1441.93 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 145.29 Seconds
(without alignments)
6187.013 Million cell updates/sec

Title: US-09-019-441-1_COPY_58_390

Perfect score: 333

Sequence: 1 CAGTCTGCCCGACTGACCC.....CCCGTTGACGTCCTAGGT 333

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 5: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
- 6: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
- 7: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
- 8: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
- 9: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
- 10: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
- 11: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
- 12: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
- 13: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
- 14: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
- 15: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
- 16: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
- 17: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
- 18: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
- 19: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
- 20: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
- 21: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*
- 25: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	333	100.0	390	19 AAV33307	Anti-human CD23 6G
2	285.6	85.1	605	24 ABK29738	Colon adenocarcino
3	284	85.3	5464	25 ABV77130	Nucleotide sequenc
4	284	85.3	6877	25 ABV77133	Nucleotide sequenc
5	283.4	85.1	726	25 ABZ25504	APRIL binding scFv
6	280.8	84.3	333	22 AAH42401	Nucleotide sequenc
7	280.8	84.3	333	22 AAH42407	Nucleotide sequenc
8	280.4	84.2	351	22 AAI68755	Human autoantibody

9	280.2	84.1	747	21 AAC67868	Recombinant human DNA encoding anti
10	280.2	84.1	816	24 ABK43226	Human ovarian spec
11	277	83.2	1460	25 ABX92194	DNA encoding singl
12	276.8	83.1	792	24 ABX00205	DNA encoding throm
13	276.8	83.1	792	24 ABK71411	DNA encoding singl
14	276.8	83.1	822	24 ABX00208	DNA encoding throm
15	276.8	83.1	822	24 ABK71414	Mouse DNA encoding
16	275.8	82.8	330	24 ABX00191	Thrombopoietin (TP
17	275.8	82.8	330	24 ABK71397	Mouse DNA encoding
18	275.8	82.8	387	24 ABX00199	DNA encoding throm
19	275.8	82.8	387	24 ABK71405	Human anti-Pseudom
20	275.4	82.7	333	17 AAT10327	Coding sequence fo
21	275.4	82.7	333	20 AAZ31655	Coding sequence fo
22	273.8	82.2	333	20 AAZ31654	MH4H7 MAb light ch
23	273.8	82.2	628	14 AQ36134	Human immune syste
24	273.8	82.2	891	22 AAC66528	Variable region of
25	273.8	82.2	1044	12 AQ12840	Human autoantibody
26	272.4	81.8	351	22 AAI68765	Antibody D lambda
27	272.2	81.7	902	14 AAQ35100	DNA encoding anti-
28	270.8	81.3	330	22 AAS03477	Anti-hSDRF antibod
29	270.4	81.2	729	22 AAH47763	DNA encoding anti-
30	269.2	80.8	330	22 AAS03520	DNA encoding a var
31	269	80.8	342	21 AAC62337	DNA encoding novel
32	267.4	80.3	889	23 AAS77073	Human U266 lambda
33	267.4	80.3	9071	13 AAQ22491	U266-Lambda gene a
34	267.4	80.3	9071	13 AAQ23370	DNA encoding novel
35	266.2	79.9	763	23 AAS83480	Monoclonal antibod
36	265.8	79.8	333	15 AAQ55859	DNA encoding novel
37	264.2	79.3	448	23 AAS77070	Human autoantibody
38	262.8	78.9	351	22 AAI68759	Human autoantibody
39	261.8	78.6	360	24 ABA94221	EBV transforming a
40	261	78.4	726	25 ABX12863	DNA encoding monoc
C 41	259.4	77.9	1636	23 ABV22585	Human prostate exp
C 42	259.4	77.9	1636	23 ABV28405	Human prostate exp
43	258.2	77.5	7528	22 AAF30316	Bicistronic idioty
44	258	77.5	336	22 AAS03509	DNA encoding anti-
45	257.8	77.4	453	23 AAS77071	DNA encoding novel

ALIGNMENTS

RESULT 1
AAV33307
ID AAV33307 standard; DNA; 390 BP.

XX AAV33307;

AC AAV33307;

DT 25-MAR-2003 (updated)

DT 18-NOV-1998 (first entry)

XX Anti-human CD23 6G5 monoclonal antibody light chain variable region DNA.

DE Anti-human CD23 6G5 monoclonal antibody; light chain variable region;

XX human CD23; IGE; FcεR1i/CD23; gamma-1 constant region;

KW gamma-3 constant region; allergy; inflammation; autoimmune disease;

KW allergic rhinitis; conjunctivitis; autoimmune haemolytic anaemia; ss.

XX Macaca fascicularis

OS Macaca fascicularis

XX Key Location/Qualifiers

PH Key Location/Qualifiers

FT CDS 1..390

FT /tag= a

FT /product= "anti-human CD23 6G5 light chain variable region"

FT /note= "CDS does not contain a stop codon"

FT sig_peptide 1..57

FT /tag= b

FT mat_peptide 58..390

FT /tag= c

FT misc_feature 124..165

FT /tag= d

FT /note= "encodes CDR 1 region"

```

FT misc_feature 211..231
FT /*tag= e
FT /note= "encodes CDR 2 region"
FT 328..357
FT /*tag= f
FT /note= "encodes CDR 3 region"
XX
XX
PN WO9837099-A1.
XX
XX 27-AUG-1998.
XX
XX 17-FEB-1998; 98WO-US02253.
XX
XX 20-FEB-1997; 97US-0803085.
PR 05-FEB-1998; 98US-0019441.
XX
XX (IDEC-) IDEC PHARM CORP.
PA (SEK) SEIKAGAKU CORP.
XX
XX Klotzer WS, Nakamura T, Reff ME;
XX
XX WPI; 1998-467495/40.
DR P-PSDB; AAW70377.
XX
XX New anti-human CD23 monoclonal antibody - used for inhibiting IgE
XX expression to treat or prevent allergic, inflammatory and
XX auto-immune conditions
XX
XX Example 1; Pages 102-104; 146pp; English.
XX
XX The present sequence represents a DNA sequence encoding the light
XX chain variable region of primate monoclonal antibody anti-human CD23 6G5.
XX The invention provides primate monoclonal antibodies which specifically
XX bind human CD23, the low affinity receptor for IgE (FcεRI/CD23),
XX and comprise either of a human gamma-1 or human gamma-3 constant region
XX that binds to human Fc gamma receptors and inhibits IgE expression.
XX The monoclonal antibodies of the invention are claimed to be useful
XX for inhibiting induced IgE production for treating or preventing
XX allergic, inflammatory and autoimmune conditions e.g. allergic rhinitis
XX conjunctivitis, autoimmune haemolytic anaemia, etc.
XX (Updated on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 390 BP; 74 A; 123 C; 96 G; 97 T; 0 other;
XX
XX Query Match 100.0%; Score 333; DB 19; Length 390;
XX Best Local Similarity 100.0%; Pred. No. 1.5e-94;
XX Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CAGTCTGCCCGACTCAGCCCTCCCTCTGTGCTGGTCTCTGGACATGCGTCACCATC 60
XX |||||||
XX 58 CAGTCTGCCCGACTCAGCCCTCCCTCTGTGCTGGTCTCTGGACATGCGTCACCATC 117
XX |||||||
XX 61 TCCTGCACTGGAACACGAGGATGAGTGTGGTGGTTATTAACATATGCTCTCTGGTACCAAC 120
XX |||||||
XX 118 TCCTGCACTGGAACACGAGGATGAGTGTGGTGGTTATTAACATATGCTCTCTGGTACCAAC 177
XX |||||||
XX 121 CACCAGGCAAGCCCCCAAACTCATGATTTATGATGTCGTAAGCGGGCTCAGGGGTC 180
XX |||||||
XX 178 CACCAGGCAAGCCCCCAAACTCATGATTTATGATGTCGTAAGCGGGCTCAGGGGTC 237
XX |||||||
XX 181 TCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGTC 240
XX |||||||
XX 238 TCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGTC 297
XX |||||||
XX 241 CAGGCTGAGGACGAGGCTGATTATTACTTGTGTTTATATACAAACAGTAGCATTGTTA 300
XX |||||||
XX 298 CAGGCTGAGGACGAGGCTGATTATTACTTGTGTTTATATACAAACAGTAGCATTGTTA 357
XX |||||||
XX 301 TTCGAAGAGGACCCCGTTGACCGTCTTAGT 333
XX |||||||
XX 358 TTCGAAGAGGACCCCGTTGACCGTCTTAGT 390
XX |||||||

```

RESULT 2

ABK29738

ID ABK29738 standard; cDNA; 605 BP.

XX AC ABK29738;

XX DT 23-APR-2002 (first entry)

XX DE Colon adenocarcinoma-specific cDNA #264.

XX KW Human; colon adenocarcinoma; colon cancer; tumour; gene; ss.

XX OS Homo sapiens.

XX PN W0200196389-A2.

XX PD 20-DEC-2001.

XX PF 07-JUN-2001; 2001WO-US18574.

XX PR 09-JUN-2000; 2000US-210667P.

XX PR 22-NOV-2000; 2000US-252614P.

XX PA (CORI-) CORIXA CORP.

XX PI Meagher MJ, King GE, Xu J, Secret H;

XX DR WPI; 2002-098052/13.

XX PT New isolated polynucleotide encoding a polypeptide comprising a portion of colon tumour protein, for detection, diagnosis and therapy of human colon cancer -

XX PS Claim 1; Page 181-182; 21pp; English.

XX CC The invention relates to an isolated polynucleotide (I) encoding a polypeptide (II) comprising a portion of a colon tumour protein. A new oligonucleotide (III) that hybridises to (I) is useful for determining the presence of a cancer in a patient. (II) or antigen presenting cells expressing (I) are useful for stimulating and/or expanding T cells specific for a tumour protein, by contacting T cells with (I), (II) or antigen-presenting cells that express (I), (II), or antigen presenting cells that express (II) and/or CD8+ T cells isolated from a patient by incubating CD4+ and/or CD8+ T cells isolated from a patient with (I), (II), or antigen presenting cells that express (II), so that T cells proliferate, and administering to the patient an effective amount of the proliferated T cells, thus inhibiting the development of a cancer in the patient. A new composition is useful for stimulating an immune response in a patient. (I) or (II) is useful in vaccines and pharmaceutical compositions for prevention and treatment of colon cancer and for the diagnosis and monitoring of the cancers. (I), (II) or an antibody against (II) is useful for detection, diagnosis and/or therapy of human colon cancer. (I) is useful as a probe or primer for nucleic acid hybridisation, and in the design and preparation of ribozyme molecules for inhibiting expression of (II) in tumour cells. ABK29475-ABK29851 represent human colon adenocarcinoma-specific cDNA sequences of the invention.

XX Sequence 605 BP; 123 A; 198 C; 154 G; 128 T; 2 other;

Query Match 86.1%; Score 286.6; DB 24; Length 605;

Best Local Similarity 91.3%; Pred. No. 6.9e-80;

Matches 304; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCGACTCAGCCCTCCCTCTGTGCTGGTCTCTGGACATGCGTCACCATC 60

Db 90 CAGTCTGCCCTGACTCAGCCCTCCCTCGTCTCTGGTCTCTGGACATGCGTCACCATC 149

Qy 61 TCCTGCACTGGAACACGAGGATGAGTGTGGTGGTTATTAACATATGCTCTCTGGTACCAAC 120

Db 150 TCCTGCACTGGAACACGAGGATGAGTGTGGTGGTTATTAACATATGCTCTCTGGTACCAAC 209

Qy 121 CACCAGGCAAGCCCCCAAACTCATGATTTATGATGTCGTAAGCGGGCTCAGGGGTC 180

Db 210 CACCAGGCAAGCCCAAACTCATGATTATGATGTCACTAGTCGGCCCTCAGGGTT 269
 Qy 181 TCTGATCGCTTCTCTGGCTCCAACTCTGGCAACAGCGCTCCCTGACATCTCTGGGCTC 240
 Db 270 TCTAATCGCTTCTCTGGCTCCAACTCTGGCAACAGCGCTCCCTGACATCTCTGGGCTC 329
 Qy 241 CAGCTGAGGACGAGGCTGATTATTAATCTGTTTTCATATACAACAGTAGACATTTGTTA 300
 Db 330 CAGCTGAGGACGAGGCTGATTATTAATCTGTTTTCATATACAACAGTAGACATTTGTTA 389
 Qy 301 TTCGGAAGAGGACCCCGTTGACCGTCTTAGT 333
 Db 390 TTCGGGAGGACCAAGGTCACCGTCTTAGT 422

RESULT 3

ABV77130
 ID ABV77130 standard; DNA; 5464 BP.

AC ABV77130;

XX 28-MAR-2003 (first entry)

DT Nucleotide sequence of plasmid pScFv-ECFP2.

DE Intracellularly analysing or detecting the presence of a target
 KW molecule within a biological cell, by determining the presence or
 KW MUC1; mucin 1; pScFv-ECFP2; ss.

XX Synthetic.

XX WO200286505-A2.

PN 31-OCT-2002.

XX 02-APR-2002; 2002WO-GB01235.

XX 31-MAR-2001; 2001GB-0008165.

XX (UYMA-) UNIV VICTORIA MANCHESTER.

XX Roderick SPB;

XX WPI; 2003-103417/09.

XX Intracellularly analysing or detecting the presence of a target
 PT molecule within a biological cell, by determining the presence or
 PT signal representative of binding of polypeptide species to the target
 PT molecule

XX Example; Page 29-31; Slipp; English.

XX The specification describes a method for the intracellular analysis of a
 CC target molecule within a biological cell. The method comprises expressing
 CC within the cell a first polypeptide sequence comprised of a first binding
 CC species capable of binding to the target molecule and a first reporter
 CC moiety attached to the first binding species; expressing within the cell
 CC a second polypeptide sequence comprised of a second binding species
 CC capable of competing with the target molecule for binding species capable
 CC of competing with the target molecule for binding of the first binding
 CC species and a second reporter moiety, the first and second reporter
 CC moieties being such that on binding together of the first and second
 CC binding species the first and second reporter moieties interact so as to
 CC be capable of producing a signal that can be differentiated from one
 CC capable of being generated when the first and second reporter moieties
 CC do not interact; and effecting a measurement to determine the presence
 CC or signal representative of binding of the first and second binding
 CC species. The method is useful for the intracellular analysis of a target
 CC molecule, e.g. for detecting the presence and/or amount of target
 CC molecules in cells. The method is also useful for studying the
 CC interactions of intracellular molecules. The present sequence represents
 CC a plasmid used in an intracellular assay for the MUC1 epitope of
 CC human mucin1, demonstrating the method of the invention. In this assay,

CC the first polypeptide is an anti-MUC1 scFv, and the second polypeptide
 CC comprises the MUC1 epitope attached to yellow fluorescent protein.

XX Sequence 5464 BP; 1294 A; 1485 C; 1468 G; 1217 T; 0 other;

XX Query Match 85.3%; Score 284; DB 25; Length 5464;

XX Best Local Similarity 91.0%; Pred. No. 1e-78;

XX Matches 302; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCGACTCAGCCTCCCTCTGTCTCTGGGTCTCTGGACAGTGGTCACCATC 60

Db 1038 CAGTCTGTCTGACTCAGCCTCCCTCGTCTCGGGTCTCTGGACAGTGGTCACCATC 1097

Qy 61 TCCTGCACTGGAACACGACGATGACGTTGGTGGTTATAAATATATGTCTCTGGTACCAACAC 120

Db 1098 TCCTGCACTGGAACACGACGATGACGTTGGTGGTTATAAATATATGTCTCTGGTACCAACAG 1157

Qy 121 CACCCAGGCAAGCCCGCCAACTCATGATTTATGATGTCTCTAAGCGGGCTCAGGGGTC 180

Db 1158 CACCCAGGCAAGCCCGCCAACTCATGATTTATGAGGTCTAGTAAGCGGGCTCAGGGGTC 1217

Qy 181 TCTGATCGCTTCTCTGGCTCCAACTCTGGCAACAGCGCTCCCTGACATCTCTGGGCTC 240

Db 1218 CTTGATCGCTTCTCTGGCTCCAACTCTGGCAACAGCGCTCCCTGACATCTCTGGGCTC 1277

Qy 241 CAGGCTGAGGACGAGGCTGATTATTAATCTGTTTTCATATACAACAGTAGACATTTGTTA 300

Db 1278 CAGGCTGAGGACGAGGCTGATTATTAATCTGAGCTCATATAGAGCAGTAACACTTGGGTG 1337

Qy 301 TTCGGAAGGAGGACCCCGTTGACCGTCTTAGG 332

Db 1338 TTCGGGAGGAGGACCAAGGTCACCGTCTTAGG 1369

RESULT 4

ABV77133

ID ABV77133 standard; DNA; 6877 BP.

AC ABV77133;

XX 28-MAR-2003 (first entry)

DT Nucleotide sequence of plasmid pBudMUC-EYFPscFvECFP.

DE Intracellular analysis; intracellular interaction; intrabody; ScFv;

KW MUC1; mucin 1; pBudMUC-EYFPscFvECFP; ss.

XX Synthetic.

XX WO200286505-A2.

PN 31-OCT-2002.

XX 02-APR-2002; 2002WO-GB01235.

XX 31-MAR-2001; 2001GB-0008165.

XX (UYMA-) UNIV VICTORIA MANCHESTER.

XX Roderick SPB;

XX WPI; 2003-103417/09.

XX Intracellularly analysing or detecting the presence of a target
 PT molecule within a biological cell, by determining the presence or
 PT signal representative of binding of polypeptide species to the target
 PT molecule

XX Example; Page 37-40; Slipp; English.

XX The specification describes a method for the intracellular analysis of a
 CC target molecule within a biological cell. The method comprises expressing
 CC within the cell a first polypeptide sequence comprised of a first binding


```

Db 574 TCTAATCGCTTCTCTGGCTCCAGCTCTGGCAACACGGCTCCCTGACAATCTCTGGGCTC 633
Qy 241 CAGCTGAGGACGAGGCTGATTATTAATCTGTTTCATATACAAACAGTACGACTTTGTTA 300
Db 634 CAGCTGAGGACGAGGCTGATTATTAATCTGCTGAGCTCATATACAAACAGGACGACTCGAGTT 693
Qy 301 TTCGGAAGAGGACCCGGTTGACCGTCTCTAGGT 333
Db 694 TTCGGCGGAGGACCAAGCTGACCGTCTCTAGGT 726

RESULT 6
AAH42401
ID AAH42401 standard; DNA; 333 BP.
XX
AC AAH42401;
XX
DT 01-OCT-2001 (first entry)
XX
DE Nucleotide sequence of variable light chain fragment of clone G93.
XX
KW Antibody; light chain; VL; amyloid protein; blood brain barrier;
KW endothelial cell; brain cell antigen; inflammation; adhesion molecule;
KW transferrin receptor; neurological disease; Alzheimer's disease;
KW prion disease; AIDS-related dementia; epilepsy; brain injury; ss.
XX
OS Homo sapiens.
XX
XX WO200144300-A2.
XX
XX 21-JUN-2001.
XX
XX 27-NOV-2000; 2000WO-GB04501.
XX
XX 13-DEC-1999; 99US-0170599.
XX
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Webster C, Osbourn J, Ward G, Miller K;
XX
XX WPI; 2001-398131/42.
XX
XX P-PSDB; AAG62957.
XX
XX Mixture or panel of antibodies for selecting specific binding members
XX that cross the blood brain barrier, for use in delivering different
XX molecules and treating neurological diseases -
XX
XX Disclosure; Page 103; 109pp; English.
XX
XX The present sequence encodes an antibody variable light chain (VL)
XX fragment. The fragment is used to produce a mixture or panel of 5
XX different specific binding members, each comprising an antibody VH
XX and/or VL variable domain and capable, when displayed on the surface
XX of filamentous bacteriophage particles or in the case of a specific
XX binding member comprising the D5 VH and/or VL variable domain when
XX bound to human serum amyloid protein, to pass through a mammalian
XX blood brain barrier (BBB). The panel is useful for the selection of
XX specific binding members with a desired property such as ability to
XX cross BBB, ability to bind endothelial cells or other brain cell antigen,
XX ability to bind areas of inflammation in the brain or BBB breakdown or
XX ability to bind intracellular adhesion molecules and to bind transferrin
XX receptor. The antibodies are useful in diagnosis, prophylaxis and
XX treatment of human or animal body, including neurological diseases, such
XX as Alzheimer's disease, prion disease, AIDS-related dementia, epilepsy
XX and traumatic brain injury and any diseases involving inflammation
XX occurring within the brain or central nervous system.
XX
XX Sequence 333 BP; 71 A; 99 C; 87 G; 76 T; 0 other;
XX
XX Query Match 84.3%; Score 280.8; DB 22; Length 333;
XX Best Local Similarity 90.4%; Pred. No. 3.7e-78;
XX Matches 300; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

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Qy 1 CAGTCTGCCCGACTCAGCCTCCCTCTGTCTGTGGTCTCTCGACAGTCTGGTCAACATC 60
Db 1 CAGTCTGTGTGACTCAGCCTCGCTCGTGTCTGTGGTCTCTCGACAGTCTGGTCAACATC 60
Qy 61 TCTGTGACGTGAACACGAGGATGAGCTGTGTGGTTAATCTATGTCTCTGTGATCAACAC 120
Db 61 TCTGTGACGTGAACACGAGGATGAGCTGTGTGGTTAATCTATGTCTCTGTGATCAACAA 120
Qy 121 CACCCAGGCAAGCCGCCAACTCATGATTATGATGCTGCTAAGCGGGCTCAGGGGCTC 180
Db 121 CACCCAGGCAAGCCGCCAACTCATGATTATGAGGGAGTAAAGCGGCCCTCAGGGGTT 180
Qy 181 TCTGATCGCTTCTCTGGCTCCAAAGTCTTGCAACACGGCTCTCCCTGACCATCTCTGGGCTC 240
Db 181 TCTAATCGCTTCTCTGGCTCCAAAGTCTTGCAACACGGCTCTCCCTGACCAATCTCTGGGCTC 240
Qy 241 CAGCTGAGGACGAGGCTGATTATTAATCTGTTTCATATACAAACAGTACGACTTTGTTA 300
Db 241 CAGCTGAGGACGAGGCTGATTATTAATCTGAGCTCATATACAAACAGGCGACTCGAGTT 300
Qy 301 TTCGGAAGAGGACCCGGTTGACCGTCTCTAGG 332
Db 301 TTCGGCGGAGGACCAAGCTGACCGTCTCTAGG 332

RESULT 7
AAH42407
ID AAH42407 standard; DNA; 333 BP.
XX
AC AAH42407;
XX
DT 01-OCT-2001 (first entry)
XX
DE Nucleotide sequence of variable light chain fragment of clone G102.
XX
KW Antibody; light chain; VL; amyloid protein; blood brain barrier;
KW endothelial cell; brain cell antigen; inflammation; adhesion molecule;
KW transferrin receptor; neurological disease; Alzheimer's disease;
KW prion disease; AIDS-related dementia; epilepsy; brain injury; ss.
XX
OS Homo sapiens.
XX
XX WO200144300-A2.
XX
XX 21-JUN-2001.
XX
XX 27-NOV-2000; 2000WO-GB04501.
XX
XX 13-DEC-1999; 99US-0170599.
XX
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Webster C, Osbourn J, Ward G, Miller K;
XX
XX WPI; 2001-398131/42.
XX
XX P-PSDB; AAG62963.
XX
XX Mixture or panel of antibodies for selecting specific binding members
XX that cross the blood brain barrier, for use in delivering different
XX molecules and treating neurological diseases -
XX
XX Disclosure; Page 106; 109pp; English.
XX
XX The present sequence encodes an antibody variable light chain (VL)
XX fragment. The fragment is used to produce a mixture or panel of 5
XX different specific binding members, each comprising an antibody VH
XX and/or VL variable domain and capable, when displayed on the surface
XX of filamentous bacteriophage particles or in the case of a specific
XX binding member comprising the D5 VH and/or VL variable domain when
XX bound to human serum amyloid protein, to pass through a mammalian
XX blood brain barrier (BBB). The panel is useful for the selection of
XX specific binding members with a desired property such as ability to

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CC cross BBB, ability to bind endothelial cells or other brain cell antigen,
CC ability to bind areas of inflammation in the brain or BBB breakdown or
CC ability to bind intracellular adhesion molecules and to bind transferrin
CC receptor. The antibodies are useful in diagnosis, prophylaxis and
CC treatment of human or animal body, including neurological diseases, such
CC as Alzheimer's disease, prion disease, AIDS-related dementia, epilepsy
CC and traumatic brain injury and any diseases involving inflammation
CC occurring within the brain or central nervous system.
XX
SQ Sequence 333 BP; 72 A; 99 C; 86 G; 76 T; 0 other;
Query Match 84.3%; Score 280.8; DB 22; Length 333;
Best Local Similarity 90.4%; Pred. No. 3.7e-78;
Matches 300; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
Qy 1 CAGTCTGCCCCGACTCAGCCCTCCCTCTGTCTGGGTCTCTGGACAGTCGGTCACCATC 60
Db 1 CAGTCTGCTGACTCAGCCTGCCTCCGTCTCTGGGTCTCTGGGACATCGATCACCATC 60
Qy 61 TCCTGCACTGAACACGAGGATGAGTGGTGGTTTATAACTATGTCTCTGGTACCAAC 120
Db 61 TCCTGCACTGAACACGAGGATGAGTGGTGGTTTATAACTATGTCTCTGGTACCAAC 120
Qy 121 CACCGAGCAAGCCCAACTCATGATTTATGATGTCGCTAAGCGGCGCTCAGGGGTC 180
Db 121 CACCGAGCAAGCCCAACTCATGATTTATGATGTCGCTAAGCGGCGCTCAGGGGTC 180
Qy 181 TCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTC 240
Db 181 TCTAATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGGCTCCCTGACCAATCTCTGGGCTC 240
Qy 241 CAGCTGAGGACGAGGCTGATTTACTGTGTTTCATATACACAGTAGCACATTTGTTA 300
Db 241 CAGGCTGAGGACGAGGCTGATTTACTGTGCTCATATACACAGGAGCACTCGAGTT 300
Qy 301 TTCGGAAGGAGGACCCGGTTGACCGTCTCTAGG 332
Db 301 TTCGCGGAGGAGCAACAGCTGACCGTCTCTAGG 332
RESULT 8
AAI68755
ID AAI68755 standard; DNA; 351 BP.
XX
AC AAI68755;
XX
DT 22-JAN-2002 (first entry)
XX
DE Human autoantibody MICA-1 variable region heavy chain DNA.
XX
KW Autoantigen; fusion protein; islet cell antigen; MICA autoantibody;
KW glutamate decarboxylase; diabetes mellitus type I; stiff-man syndrome;
KW polyglandular autoimmune syndrome; autoimmune disorder; IA2; GAD65;
KW variable region; heavy chain; MICA-1; ds.
XX
OS Homo sapiens.
XX
FN EP1149914-A2.
XX
PD 31-OCT-2001.
XX
PF 29-MAR-2001; 2001EP-0107702.
XX
PR 10-APR-2000; 2000DE-1017782.
PR 25-MAY-2000; 2000DE-1025840.
XX
XX (LABO-) LABOR KOCH MERK GMBH.
XX
PI Richter W, Rickert M, Rapp I, Dangel W;
XX
DR WPI; 2001-640702/74.
DR P-PSDB; AAG80206.
XX

PT New fusion protein, useful for diagnosis of diabetes type I and other
PT metabolic diseases, is reactive with autoantibodies against both
PT glutamate decarboxylase and islet cell antigen -
XX
PS Disclosure; Page 22; 68pp; German.
XX
CC This invention describes a novel fusion protein (I) that has, at its
CC N-terminus, one or more epitopes that bind specifically to autoantibodies
CC (AAb) against the islet cell antigen IA2 and, at its C-terminus, one or
CC more epitopes that bind specifically to antibodies (Ab) directed against
CC the glutamate decarboxylase GAD65. (I), also nucleic acid (II) encoding
CC it, vectors containing (II) and transformed cells, are useful for
CC diagnosis and prognosis of diabetes mellitus type 1, stiff-man syndrome,
CC polyglandular autoimmune syndrome or other autoimmune conditions
CC associated with AAb against GAD65 or IA2. (I) provides a rapid and simple
CC diagnosis of high specificity and sensitivity, capable of recognizing
CC antibodies against both IA2 and GAD65, simultaneously. Unlike known
CC fusions, where the GAD65 component is at the N-terminus, (I) contains
CC correctly folded conformational epitopes that can react with most MICA
CC autoantibodies. This sequence encodes the human autoantibody MICA-1
CC variable region heavy chain used in the method of the invention.
XX
SQ Sequence 351 BP; 71 A; 106 C; 91 G; 83 T; 0 other;
Query Match 84.2%; Score 280.4; DB 22; Length 351;
Best Local Similarity 91.9%; Pred. No. 5e-78;
Matches 296; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
Qy 12 GACTCAGCCTCCCTCTCTGTCTGGGTCTCTGGACAGTCGGTCACCATCTCTGCACTGG 71
Db 30 GACTCAGCCTCCCTCTCTGTCTGGGTCTCTGGACAGTCGGTCACCATCTCTGCACTGG 89
Qy 72 AACGAGGATGAGTGGTGGTTATTAATATGTCCTCTGTACCAACACACCCAGGCAA 131
Db 90 AACGAGGATGAGTGGTGGTTATTAATATGTCCTCTGTACCAACACACCCAGGCAA 149
Qy 132 AGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGCGCTCAGGGGTCTCTGATCGCTT 191
Db 150 AGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGCGCTCAGGGGTCTCTGATCGCTT 209
Qy 192 CTCTGGCTCCAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGA 251
Db 210 CTCTGGCTCCAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGA 269
Qy 252 CGAGGCTGATTTACTGTGTTTCATATACACAGTAGCACATTTGTTATTCGGAAGG 311
Db 270 CGAGGCTGATTTACTGTGCTCATATACAGCAGCAGCACTCTGTGTTTCGCGGAGG 329
Qy 312 GACCCGGTTGACCGTCTCTAGGT 333
Db 330 GACCAAGCTGACCGTCTCTAGGT 351
RESULT 9
AAC67868
ID AAC67868 standard; DNA; 747 BP.
XX
AC AAC67868;
XX
DT 16-FEB-2001 (first entry)
XX
DE Recombinant human antibody scFv TN11 nucleotide sequence.
XX
KW Human; antibody scFv; TN11; Tenascin-C; TN-C; domain C-containing TNC;
KW CTN-C; ds.
XX
OS Homo sapiens.
XX
FN WO200063699-A1.
XX
PD 26-OCT-2000.
XX
PF 19-APR-2000; 2000WO-EP03550.

```
XX 20-APR-1999; 99IT-F100094.
XX (PHIL-) PHILOGEN SRL.
XX Zardi L;
XX PI
XX 2000-687225/67.
XX P-PSDB; AAB36083.
XX
XX Ligands used for diagnosis and treatment of human neoplasias, are
XX capable of identifying the tenascin-C isoform containing domain C of
XX tenascin-C
XX
XX Claim 8; Page 5-6; 31pp; English.
XX
XX The present sequence encodes a recombinant human antibody scFv. Antibody
XX TN11 reacts with the long form of human Tenascin-C (TN-C). The epitope
XX recognised by TN11 is located inside domain C of TN-C. TN11 is therefore
XX only capable of recognising TN-C isoforms containing domain C (ctn-C).
XX TN11 is useful for detecting the presence of TN-C isoforms in vitro or
XX in vivo for diagnosing pathologies expressing the ctn-C isoforms of TN-C.
XX It is useful for the preparation of formulations for the treatment of
XX human neoplasias.
XX
XX Sequence 747 BP; 157 A; 197 C; 231 G; 162 T; 0 other;
XX
XX Query Match 84.1%; Score 280.2; DB 21; Length 747;
XX Best Local Similarity 90.1%; Pred. No. 7.7e-78;
XX Matches 300; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
XX
XX 1 CAGCTGCGCCGACTCAGCCTCCCTCTGTGTCCTGGTCTCTGGTCTCTGGACAGTGGTCCACCATC 60
XX 415 CAGTCTGCTGATCAGCTGCTCCGTGCTCTGGTCTCTGGACAGTGGTCCACCATC 474
XX
XX 61 TCCTGCACTGGAACACGAGTACGCTTGGTGGTTTAACTATGCTCTCTGGTACCAACAC 120
XX 475 TCCTGCACTGGAACACGAGTACGCTTGGTGGTTTAACTATGCTCTCTGGTACCAACAA 534
XX
XX 121 CACCCAGCAAGCCGCCAACTCATGTTATGATGTCGTAAGCGGCTCAGGGGTC 180
XX 535 CACCCAGCAAGCCGCCAACTCATGTTATGATGTCGTAAGCGGCTCAGGGGTT 594
XX
XX 181 TCTGATCGTCTCTGGCTCCAACTCTGGCAACACGCGCTCCCTGACCATCTCTGGGCTC 240
XX 595 TCTAATGCTTCTCTGGCTCCAACTCTGGCAACACGCGCTCCCTGACCATCTCTGGGCTC 654
XX
XX 241 CAGGCTGAGGACGAGGCTGATTATTACTGTTTATATACAAACAGTAGCATTCTTTGTTA 300
XX 655 CAGGCTGAGGACGAGGCTGATTATTACTGTTTATATACAAACAGTAGCATTCTCGAGTT 714
XX
XX 301 TTCGGAAGAGGAGCCCGGTTGACCGTCTAGGT 333
XX 715 TTCGCGGAGGAGCAAGCTGACCGTCTAGGT 747
XX
XX RESULT 10
XX ABK43226
XX ID ABK43226 standard; DNA; 816 BP.
XX AC
XX AC ABK43226;
XX
XX 05-JUN-2002 (first entry)
XX
XX DNA encoding anti beta-galactosidase single chain Fv fragment.
XX
XX Modified virus; cytostatic; gene therapy; tumour cell;
XX proliferating cell; cancer; vascular disease; inflammatory disease;
XX infectious disease; human immunodeficiency virus; HIV;
XX immunoglobulin; beta-galactosidase; variable fragment; Fv;
XX gene; ds.
XX
XX Unidentified.
XX
```

```
XX WO200208263-A2.
XX
XX 31-JAN-2002.
XX
XX 19-JUL-2001; 2001WO-GH03252.
XX
XX 19-JUL-2000; 2000GB-0017720.
XX
XX (GOTA-) GOT-A-GENE AB.
XX (GARD/) GARDNER R.
XX
XX Lindholm L, Nord AK, Boulanger PA;
XX
XX WPI; 2002-217049/27.
XX
XX Novel modified virus comprising non-native polypeptides with stable
XX conformation and having framework moieties containing binding moieties
XX which confer upon the virus, an altered tropism, useful in gene therapy
XX
XX Example 10; Page 148; 163pp; English.
XX
XX The invention describes a modified virus comprising non-native
XX polypeptides which has framework moieties each containing binding
XX moieties, where the virus has altered tropism conferred by the binding
XX moieties. The polypeptides can be expressed in the cytoplasm and nucleus
XX of mammalian host cell in conformation which is maintained in absence of
XX ligands for the binding moieties, where the conformation allows the
XX binding moiety subsequently to bind with the ligand. The modified virus
XX is useful in therapy for the preparation of a medicament for treating
XX tumour cells, cancer, proliferating cells, vascular diseases,
XX inflammatory diseases and infectious diseases such as Human
XX immunodeficiency virus (HIV). The altered tropisms allow the virus to be
XX used in treatment of disease in human or animal subjects, either by in
XX vivo treatment of, or ex vivo treatment of cells of, the subject
XX requiring treatment. The problems associated with the expression of
XX functional non-native viral components in the nucleus and cytosol of
XX host cells is solved by using the modified virus for the purpose. This
XX sequence represents an anti beta-galactosidase immunoglobulin variable
XX fragment (Fv) used in the creation of the modified virus containing
XX non-native polypeptides.
XX
XX Sequence 816 BP; 181 A; 220 C; 238 G; 177 T; 0 other;
XX
XX Query Match 84.1%; Score 280.2; DB 24; Length 816;
XX Best Local Similarity 90.1%; Pred. No. 8e-78;
XX Matches 300; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
XX
XX 1 CAGTCTGCGCCGACTCAGCCTCCCTCTGTGTCCTGGTCTCTGGACAGTGGTCCACCATC 60
XX 415 CAGTCTGCTGATCAGCTGCTCCGTGCTCTGGTCTCTGGACAGTGGTCCACCATC 474
XX
XX 61 TCCTGCACTGGAACACGAGTACGCTTGGTGGTTTAACTATGCTCTCTGGTACCAACAC 120
XX 475 TCCTGCGCTGGAACACGAGTACGCTTGGTGGTTTAACTATGCTCTCTGGTACCAACAA 534
XX
XX 121 CACCCAGCAAGCCGCCAACTCATGTTATGATGTCGTAAGCGGCTCAGGGGTC 180
XX 475 TCCTGCGCTGGAACACGAGTACGCTTGGTGGTTTAACTATGCTCTCTGGTACCAACAA 534
XX
XX 121 CACCCAGCAAGCCGCCAACTCATGTTATGATGTCGTAAGCGGCTCAGGGGTC 180
XX 535 CACCCAGCAAGCCGCCAACTCATGTTATGATGTCGTAAGCGGCTCAGGGGTT 594
XX
XX 181 TCTGATCGTCTCTGGCTCCAACTCTGGCAACACGCGCTCCCTGACCATCTCTGGGCTC 240
XX 535 CACCCAGCAAGCCGCCAACTCATGTTATGATGTCGTAAGCGGCTCAGGGGTT 594
XX
XX 181 TCTGATCGTCTCTGGCTCCAACTCTGGCAACACGCGCTCCCTGACCATCTCTGGGCTC 240
XX 595 TCTAATGCTTCTCTGGCTCCAACTCTGGCAACACGCGCTCCCTGACCATCTCTGGGCTC 654
XX
XX 241 CAGGCTGAGGACGAGGCTGATTATTACTGTTTATATACAAACAGTAGCATTCTTTGTTA 300
XX 655 CAGGCTGAGGACGAGGCTGATTATTACTGTTTATATACAAACAGTAGCATTCTCGAGTT 714
XX
XX 301 TTCGGAAGAGGAGCCCGGTTGACCGTCTAGGT 333
XX 715 TTCGCGGAGGAGCAAGCTGACCGTCTAGGT 747
XX
XX RESULT 10
XX ABK43226
XX ID ABK43226 standard; DNA; 816 BP.
XX AC
XX AC ABK43226;
XX
XX 05-JUN-2002 (first entry)
XX
XX DNA encoding anti beta-galactosidase single chain Fv fragment.
XX
XX Modified virus; cytostatic; gene therapy; tumour cell;
XX proliferating cell; cancer; vascular disease; inflammatory disease;
XX infectious disease; human immunodeficiency virus; HIV;
XX immunoglobulin; beta-galactosidase; variable fragment; Fv;
XX gene; ds.
XX
XX Unidentified.
XX
```

RESULT 11
 ABX92194
 ID ABX92194 standard; cDNA; 1460 BP.
 XX
 AC ABX92194;
 XX
 DT 08-MAY-2003 (first entry)
 XX
 DE Human ovarian specific nucleic acid DEX0310_8.
 XX
 KW Human; gene; ss; ovarian specific nucleic acid; OSNA; ovarian cancer;
 KW non-cancerous ovarian disease; gene therapy; vaccine; cytostatic;
 KW gynaecological.
 XX
 OS Homo sapiens.
 XX
 PN WO200292785-A2.
 XX
 PD 21-NOV-2002.
 XX
 PF 13-FEB-2002; 2002WO-US22271.
 XX
 PR 13-FEB-2001; 2001US-268290P.
 XX
 PR 15-FEB-2001; 2001US-268834P.
 XX
 PA (DIAD-) DIADEXUS INC.
 XX
 XX Salceda S, Macina RA, Hu P, Recipon H, Karra K, Cafferkey R;
 PI Sun Y, Liu C;
 XX
 XX WPI; 2003-120677/11.
 DR P-PSDB; ABU61023.
 XX
 PT New isolated OSNA nucleic acid and encoded polypeptide, useful for
 PT identifying, diagnosing, monitoring, staging, imaging and treating
 PT ovarian cancer and non-cancerous diseases in ovarian tissues -
 XX
 PS Claim 1; Page 146; 224pp; English.
 XX
 CC The invention relates to a new isolated nucleic acid termed ovarian
 CC specific nucleic acid (OSNA) comprising: (a) a nucleic acid molecule that
 CC encodes any of 53 fully defined protein sequences appearing as
 CC ABU61018-ABU61070 (termed ovarian specific proteins OSP); (b) any of 76
 CC fully defined nucleotide sequences appearing as ABX92187-ABX92262; or
 CC (c) a sequence having at least 60% sequence identity to the nucleic
 CC acid molecule of (a) or (b). Also included are a method for determining
 CC the presence of an ovary specific nucleic acid (OSNA) in a sample,
 CC a vector comprising an OSNA, a host cell comprising the vector,
 CC an isolated OSP polypeptide, an anti-OSP antibody or fragment,
 CC a method for determining the presence of an ovary specific protein
 CC in a sample and a vaccine comprising an OSP or OSNA. The methods and
 CC compositions of the present invention are useful for identifying,
 CC diagnosing, monitoring, staging, imaging and treating ovarian cancer and
 CC non-cancerous disease in ovary tissue. The present sequence is an
 CC OSNA of the invention.
 XX
 SQ Sequence 1460 BP; 351 A; 466 C; 401 G; 241 T; 1 other;
 Query Match 83.2%; Score 277; DB 25; Length 1460;
 Best Local Similarity 89.5%; Pred No. 1e-76;
 Matches 298; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
 QY 1 CAGTCTGCCCGACTCAGCCCTCCCTCTGTGTGGTCTCTGGGACATCGGTACCATC 60
 DB 56 CAGTCTGCCCTGACTCAGTCTGCTCCGTGTGGTCTCTGGGACATCGATCACCATC 115
 QY 61 TCCTGCATGNAACGAGCATGCTGGTGTATTAATCTGCTCTGCTGACCAAC 120
 DB 116 TCCTGCATGNAACGAGCATGCTGGTGTATTAATCTGCTCTGCTGACCAAC 175
 QY 121 CACCAGGCAAGCCCAAACTCATGATTATGATGTCGTAAAGCGGCTCAGGGGTC 180
 |||||||

Db 176 CACCAGGCAAGCCCAAACTCATGATTATGAGGTCAATATCGGCCCTCAGGGGTT 235
 QY 181 TCTGATCGCTTCTCTGGCTCCAGTCTGGCAACACGGCTCCCTGACCATCTCTGGGCTC 240
 DB 236 TCTAATCGCTTCTCTGGCTCCAGTCTGGCAACACGGCTCCCTGACCATCTCTGGGCTC 295
 QY 241 CAGGCTGAGGACGAGGCTGATTATTACTGTGTTCATATACACAGTAGACATTTGTTA 300
 DB 296 CAGGCTGAGGACGAGGCTGATTATTACTGTGTTCATATACACAGTAGACTTCTCTGTC 355
 QY 301 TTGGAAGAGGAGCCCGGTTGACCGTCTTAGGT 333
 DB 356 TTGGAAGAGGAGCCCGGTTGACCGTCTTAGGT 388

RESULT 12
 ABX00205
 ID ABX00205 standard; DNA; 792 BP.
 XX
 AC ABX00205;
 XX
 DT 20-DEC-2002 (first entry)
 XX
 DE DNA encoding single chain antibody 12E10 Fv.
 XX
 KW ds; gene; monoclonal antibody; signal transduction agonist;
 KW cancer; inflammatory disease; dysendocrinism; blood disease; leukaemia;
 KW cytostatic; antinflammatory; immunosuppressive; immunostimulant;
 KW hormonal disorder; diabetes; autoimmune disease.
 XX
 OS Synthetic.
 XX
 PN WO200233073-A1.
 XX
 PD 25-APR-2002.
 XX
 PF 22-OCT-2001; 2001WO-JP09260.
 XX
 PR 20-OCT-2000; 2000JP-0321821.
 PR 20-OCT-2000; 2000JP-0321822.
 PR 12-MAR-2001; 2001WO-JP01912.
 PR 17-APR-2001; 2001WO-JP03288.
 PR 12-SEP-2001; 2001JP-0277314.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 XX Fukushima N, Teuchiya M, Uno S, Ohtomo T, Yabuta N, Tsunoda H;
 PI WPI; 2002-682599/73.
 XX P-PSDB; ABG97834.
 DR Modified single chain multimeric Fv antibody acting as a signal
 XX transduction agonist for treatment of inflammatory hormonal and blood
 XX disorders and cancer -
 PS Example 8; Page 208-210; 217pp; Japanese.
 XX
 CC The invention relates to a new modified single chain Fv antibody
 CC containing at least two Heavy chain variable domains and at least two
 CC Light chain variable domains from the same or different monoclonal
 CC antibodies and which is an agonist for crosslinking a molecule at the
 CC cell surface or within the cell and thereby transducing a signal into the
 CC cell. Also include are the DNA encoding the antibody, animal cells and
 CC microorganisms transformed by and expressing the antibody, the preparation of
 CC the antibodies by culture of the transformed cells, drug compositions
 CC containing the antibodies and an assay method for the agonist activity
 CC of the antibodies by contacting the antibodies with cells expressing the
 CC relevant cell surface or internal molecule. The antibodies are useful for
 CC treatment and prevention of cancer, inflammatory disease, hormonal
 CC dysendocrinism and blood disorders. The present sequence is a DNA
 CC sequence encoding an antibody of the invention or a fragment thereof.
 XX


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SQ Sequence 792 BP; 170 A; 231 C; 217 G; 174 T; 0 other;
Query Match 83.1%; Score 276.8; DB 24; Length 792;
Best Local Similarity 90.2%; Pred. No. 9.2e-77;
Matches 296; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 4 TCTGCCCGGACTCAGCCCTCCCTCTGTGTCCTGGGTCTCTCTGGACAGTGGGTCCACCATCTCC 63
DB 428 TATGTGCTGACTCAGCCACCTCGGTGTCAGGGTCTCTCTGGACAGTGCATCACCATCTCC 487
QY 64 TGCACCTGGAACACCGATGACGTTGGTGGTTTAACTATATGTCCTCTGGTACCAACACAC 123
DB 488 TGCACCTGGAACACCGATGACGTTGGTGGTTTAACTATATGTCCTCTGGTACCAACACAC 547
QY 124 CCAGGCAAGCCCCCAACTCATGATTTATGATGCTGCTAAGCGGGCTCAGGGGTCTCT 183
DB 548 CCAGGCAAGCCCCCAACTCATGATTTATGATGCTGCTAAGCGGGCTCAGGGGTCTCT 607
QY 184 GATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGCCCTCCCTGACCATCTCTGGGCTCCAG 243
DB 608 AATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGCCCTCCCTGACCATCTCTGGGCTCCAG 667
QY 244 GCTGAGGACGAGGCTGATTTACTGTTGTTTATATACACAGTACAGTACCTTTGTTATTC 303
DB 668 GCTGAGGACGAGGCTGATTTACTGAGCTCATATACACAGTACAGTACCTTTGTTATTC 727
QY 304 GGAAGAGGGACCCCGTTGACCGTCTCTAG 331
DB 728 GCGGAGGGACCAAGCTGACCGTCTCTAG 755

RESULT 13
ABK71411
ID ABK71411 standard; DNA; 792 BP.
XX AC ABK71411;
XX DT 30-JUL-2002 (first entry)
XX DE DNA encoding thrombopoietin agonist antibody associated protein #26.
XX KW Modified antibody; thrombopoietin; TPO; agonist;
XX KW TPO receptor; platelet reduction-associated blood disease;
XX KW thrombocytopenia; cancer chemotherapy; leukaemia; signal transduction;
XX KW gene; ds.
XX OS Synthetic.
XX PN WO200233072-A1.
XX XX 25-APR-2002.
XX PD 22-OCT-2001; 2001WO-JP09259.
XX PF 20-OCT-2000; 2000JP-0321821.
XX PR 17-APR-2001; 2001WO-JP03288.
XX PR 12-SEP-2001; 2001JP-0277314.
XX PA (CHUS ) CHUGAI SEIYAKU KK.
XX TS Tsuchiya M, Ohtomo T, Yabuta N, Taunoda H, Orita T;
XX WPI; 2002-383513/41.
XX DR P-PSDB; ABG35335.
XX PT Degraded thrombopoietin agonist antibodies containing H and L chain V
XX PT domains of monoclonal antibody, useful in preventives and/or remedies
XX PT for blood diseases, thrombocytopenia following cancer chemotherapy or
XX PT leukaemia
XX PS Example 8; Page 205-206; 213pp; Japanese.
XX CC The invention describes a modified antibody comprising at least 2 heavy
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CC chain variable domains and 2 or more light chain variable domains of an
CC antibody, and exhibits thrombopoietin (TPO) agonistic effect by causing
CC the TPO receptor to crosslink. The antibodies are useful in preventives
CC and/or remedies for platelet reduction-associated blood diseases,
CC thrombocytopenia following cancer chemotherapy or leukaemia. The
CC antibody can act as a TPO signal transduction agonist by transducing a
CC signal into cells by crosslinking a TPO receptor to exert TPO agonism.
CC This sequence encodes a thrombopoietin (TPO) agonist antibody associated
CC protein.
XX SQ Sequence 792 BP; 170 A; 231 C; 217 G; 174 T; 0 other;
Query Match 83.1%; Score 276.8; DB 24; Length 792;
Best Local Similarity 90.2%; Pred. No. 9.2e-77;
Matches 296; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 4 TCTGCCCGGACTCAGCCCTCCCTCTGTGTCCTGGGTCTCTCTGGACAGTGGGTCCACCATCTCC 63
DB 428 TATGTGCTGACTCAGCCACCTCGGTGTCAGGGTCTCTCTGGACAGTGCATCACCATCTCC 487
QY 64 TGCACCTGGAACACCGATGACGTTGGTGGTTTAACTATATGTCCTCTGGTACCAACACAC 123
DB 488 TGCACCTGGAACACCGATGACGTTGGTGGTTTAACTATATGTCCTCTGGTACCAACACAC 547
QY 124 CCAGGCAAGCCCCCAACTCATGATTTATGATGCTGCTAAGCGGGCTCAGGGGTCTCT 183
DB 548 CCAGGCAAGCCCCCAACTCATGATTTATGATGCTGCTAAGCGGGCTCAGGGGTCTCT 607
QY 184 GATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGCCCTCCCTGACCATCTCTGGGCTCCAG 243
DB 608 AATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGCCCTCCCTGACCATCTCTGGGCTCCAG 667
QY 244 GCTGAGGACGAGGCTGATTTACTGTTGTTTATATACACAGTACAGTACCTTTGTTATTC 303
DB 668 GCTGAGGACGAGGCTGATTTACTGAGCTCATATACACAGTACAGTACCTTTGTTATTC 727
QY 304 GGAAGAGGGACCCCGTTGACCGTCTCTAG 331
DB 728 GCGGAGGGACCAAGCTGACCGTCTCTAG 755

RESULT 14
ABX00208
ID ABX00208 standard; DNA; 822 BP.
XX AC ABX00208;
XX DT 20-DEC-2002 (first entry)
XX DE DNA encoding single chain antibody sc12E10 Fv.
XX KW ds; gene; monoclonal antibody; signal transduction agonist;
XX KW cancer; inflammatory disease; dysendocrinism; blood disease; leukaemia;
XX KW cytostatic; antiinflammatory; immunosuppressive; immunostimulant;
XX KW hormonal disorder; diabetes; autoimmune disease.
XX OS Synthetic.
XX PN WO200233073-A1.
XX XX 25-APR-2002.
XX PD 22-OCT-2001; 2001WO-JP09260.
XX PF 20-OCT-2000; 2000JP-0321821.
XX PR 12-MAR-2001; 2001WO-JP01912.
XX PR 17-APR-2001; 2001WO-JP03288.
XX PR 12-SEP-2001; 2001JP-0277314.
XX PA (CHUS ) CHUGAI SEIYAKU KK.
XX TS Fukushima N, Tsuchiya M, Uno S, Ohtomo T, Yabuta N, Taunoda H;
```

```
XX WPI; 2002-682599/73.
DR P-PSDB; ABG97835.
XX
XX Modified single chain multimeric Fv antibody acting as a signal
PT transduction agonist for treatment of inflammatory hormonal and blood
PT disorders and cancer -
XX
XX Example 8; Page 211-213; 217pp; Japanese.
XX
XX The invention relates to a new modified single chain Fv antibody
CC containing at least two Heavy chain variable domains and at least two
CC Light chain variable domains from the same or different monoclonal
CC antibodies and which is an agonist for crosslinking a molecule at the
CC cell surface or within the cell and thereby transducing a signal into the
CC cell. Also include are the DNA encoding the antibody, animal cells and
CC microorganisms transformed by and expressing the DNA, the preparation of
CC the antibodies by culture of the transformed cells, drug compositions
CC containing the antibodies and an assay method for the agonist activity
CC of the antibodies by contacting the antibodies with cells expressing the
CC relevant cell surface or internal molecule. The antibodies are useful for
CC treatment and prevention of cancer, inflammatory disease, hormonal
CC disorders including diabetes, autoimmune disease, leukaemia,
CC dysendocrinism and blood disorders. The present sequence is a DNA
CC sequence encoding an antibody of the invention or a fragment thereof.
XX
XX Sequence 822 BP; 169 A; 233 C; 235 G; 185 T; 0 other;
SQ
Query Match 83.1%; Score 276.8; DB 24; Length 822;
Best Local Similarity 90.2%; Pred. No. 9.3e-77;
Matches 296; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 4 TCTGCCCGACTCAGCCCTCCTCTGTCTGGGTCTCTCTGGACAGTCGGTCACCATCTCC 63
DB 458 TATGTGCTGACTCAGCCACCCCTCGGTGTCTGGACAGTCGATCACCATCTCC 517
QY 64 TGCACCTGAACCCAGGATGAGTGTGTTTATGATGTCGCTAAGCGGCTCAGGGGTCTCT 183
DB 518 TGCACCTGAACCCAGGATGAGTGTGTTTATGATGTCGCTAAGCGGCTCAGGGGTCTCT 577
QY 124 CCAGGCAAGCCCCCAAACTCATGATGTCGCTAAGCGGCTCAGGGGTCTCT 63
DB 578 CCAGGCAAGCCCCCAAACTCATGATGTCGCTAAGCGGCTCAGGGGTCTCT 637
QY 184 GATCGCTTCTCTGGCTCAGGCTCGGCAACAGCGGCTCCCTGACCATCTCTGGGCTCCAG 243
DB 638 AATCGCTTCTCTGGCTCAGGCTCGGCAACAGCGGCTCCCTGACCATCTCTGGGCTCCAG 697
QY 244 GCTGAGGAGGAGCCGGTTGACCGTCTCTAG 331
DB 698 GCTGAGGAGGAGCCGGTTGACCGTCTCTAG 785
RESULT 15
ABK71414
ID ABK71414 standard; DNA; 822 BP.
XX
XX AC ABK71414;
XX
XX 30-JUL-2002 (first entry)
XX
XX DNA encoding thrombopoietin agonist antibody associated protein #27.
XX
XX Modified antibody; thrombopoietin; TPO; agonist;
KW TPO receptor; platelet reduction-associated blood disease;
KW thrombocytopenia; cancer chemotherapy; leukaemia; signal transduction;
XX gene; ds.
XX
XX Synthetic.
OS
```

```
XX WO200233072-A1.
PN
XX
XX 25-APR-2002.
PD
XX
XX 22-OCT-2001; 2001WO-JP09259.
PF
XX
XX 20-OCT-2000; 2000JP-0321821.
PR
XX
XX 17-APR-2001; 2001WO-JP03288.
PR
XX
XX 12-SEP-2001; 2001JP-027314.
PR
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
PA
XX
XX Teuchiya M, Ohtomo T, Yabuta N, Tsunoda H, Orita T;
PI
XX
XX WPI; 2002-393513/41.
DR
XX
XX P-PSDB; ABG35336.
DR
XX
XX Degraded thrombopoietin agonist antibodies containing H and L chain V
PT domains of monoclonal antibody, useful in preventives and/or remedies
PT for blood diseases, thrombocytopenia following cancer chemotherapy or
PT leukaemia
XX
XX Example 8; Page 208-209; 213pp; Japanese.
PS
XX
XX The invention describes a modified antibody comprising at least 2 heavy
CC chain variable domains and 2 or more light chain variable domains of an
CC antibody, and exhibits thrombopoietin (TPO) agonistic effect by causing
CC the TPO receptor to crosslink. The antibodies are useful in preventives
CC and/or remedies for platelet reduction-associated blood diseases,
CC thrombocytopenia following cancer chemotherapy or leukaemia. The
CC antibody can act as a TPO signal transduction agonist by transducing a
CC signal into cells by crosslinking a TPO receptor to exert TPO agonism.
CC This sequence encodes a thrombopoietin (TPO) agonist antibody associated
CC protein.
XX
XX Sequence 822 BP; 169 A; 233 C; 235 G; 185 T; 0 other;
SQ
Query Match 83.1%; Score 276.8; DB 24; Length 822;
Best Local Similarity 90.2%; Pred. No. 9.3e-77;
Matches 296; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 4 TCTGCCCGACTCAGCCCTCCTCTGTCTGGGTCTCTCTGGACAGTCGGTCACCATCTCC 63
DB 458 TATGTGCTGACTCAGCCACCCCTCGGTGTCTGGACAGTCGATCACCATCTCC 517
QY 64 TGCACCTGAACCCAGGATGAGTGTGTTTATGATGTCGCTAAGCGGCTCAGGGGTCTCT 123
DB 518 TGCACCTGAACCCAGGATGAGTGTGTTTATGATGTCGCTAAGCGGCTCAGGGGTCTCT 577
QY 124 CCAGGCAAGCCCCCAAACTCATGATGTCGCTAAGCGGCTCAGGGGTCTCT 183
DB 578 CCAGGCAAGCCCCCAAACTCATGATGTCGCTAAGCGGCTCAGGGGTCTCT 637
QY 184 GATCGCTTCTCTGGCTCAGGCTCGGCAACAGCGGCTCCCTGACCATCTCTGGGCTCCAG 243
DB 638 AATCGCTTCTCTGGCTCAGGCTCGGCAACAGCGGCTCCCTGACCATCTCTGGGCTCCAG 697
QY 244 GCTGAGGAGGAGCCGGTTGACCGTCTCTAG 303
DB 698 GCTGAGGAGGAGCCGGTTGACCGTCTCTAG 757
QY 304 GGAAGAGGAGCCGGTTGACCGTCTCTAG 331
DB 758 GCGGAGGAGCCAAAGCTGACCGTCTCTAG 785
Search completed: December 29, 2003, 16:25:34
Job time : 146.29 sec
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 19:01:43 ; Search time 481.099 Seconds
(without alignments)
2371.523 Million cell updates/sec

Title: US-09-019-441-1_COPY_58_390

Perfect score: 333

Sequence: 1 CAGTCTCCCGACTACGCC.....CCCGTTGACCGTCTTAGGT 333

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2244575 seqs, 1713117285 residues

Total number of hits satisfying chosen parameters: 4489150

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	333	100.0	390	11	US-09-019-441-1
2	333	100.0	390	15	US-10-103-686-1
3	283.4	85.1	726	15	US-10-151-882-4
4	283.4	85.1	735	13	US-10-139-785-59
5	283.4	85.1	735	13	US-10-139-785-63
6	283.4	85.1	735	13	US-10-139-785-64
7	283.4	85.1	735	14	US-10-039-785-59
8	283.4	85.1	735	14	US-10-039-785-63
9	283.4	85.1	735	14	US-10-039-785-64
c 10	280.2	84.1	1597	15	US-10-138-846-13540
11	277	83.2	1460	13	US-10-076-747-8
12	275.4	82.7	408	11	US-09-918-995-36573
13	275.4	82.7	421	11	US-09-918-995-16692
c 14	275.4	82.7	1640	15	US-10-198-846-13206
15	273.8	82.2	735	13	US-10-139-785-54

16	273.8	82.2	735	14	US-10-039-785-54	Sequence 54, Appl
17	269	80.8	342	10	US-09-974-449-7	Sequence 7, Appl
18	267.4	80.3	735	13	US-10-139-785-57	Sequence 57, Appl
19	267.4	80.3	735	14	US-10-039-785-57	Sequence 57, Appl
20	265.8	79.8	735	13	US-10-139-785-60	Sequence 60, Appl
21	265.8	79.8	735	14	US-10-039-785-60	Sequence 60, Appl
22	264.2	79.3	420	11	US-09-918-995-16500	Sequence 16500, A
23	264.2	79.3	1597	15	US-10-198-846-13540	Sequence 13540, A
24	262.6	78.9	741	13	US-10-322-673-63	Sequence 63, Appl
25	261.8	78.6	358	13	US-10-010-729-18	Sequence 18, Appl
c 26	261	78.4	379	13	US-10-029-386-15053	Sequence 15053, A
c 27	261	78.4	552	13	US-10-029-386-1351	Sequence 1351, Ap
c 28	261	78.4	707	13	US-10-027-632-18093	Sequence 18093, A
c 29	261	78.4	707	14	US-10-027-632-18093	Sequence 13, Appl
c 30	261	78.4	726	13	US-10-225-108A-13	Sequence 59, Appl
31	261	78.4	765	13	US-10-360-828-59	Sequence 58, Appl
32	259.4	77.9	735	13	US-10-139-785-58	Sequence 61, Appl
33	259.4	77.9	735	13	US-10-139-785-61	Sequence 58, Appl
34	259.4	77.9	735	14	US-10-039-785-58	Sequence 61, Appl
35	259.4	77.9	735	14	US-10-039-785-61	Sequence 64, Appl
36	259.4	77.9	735	13	US-10-322-673-64	Sequence 55, Appl
37	256.2	76.9	735	13	US-10-139-785-55	Sequence 55, Appl
38	256.2	76.9	735	14	US-10-039-785-55	Sequence 55, Appl
c 39	256	76.9	883	15	US-10-158-646-73	Sequence 436, App
c 40	254.4	76.4	518	13	US-10-029-386-436	Sequence 436, App
c 41	252.2	75.7	543	10	US-09-736-457-970	Sequence 970, App
c 42	252.2	75.7	543	10	US-09-902-941-970	Sequence 970, App
c 43	252.2	75.7	543	10	US-09-849-626-970	Sequence 970, App
c 44	252.2	75.7	543	13	US-10-113-878-970	Sequence 970, App
c 45	252.2	75.7	543	15	US-10-017-754-970	Sequence 970, App

ALIGNMENTS

RESULT 1

US-09-019-441-1

Sequence 1, Application US/09019441

Publication No. US20030086921A1

GENERAL INFORMATION:

APPLICANT: REFF, Mitchell E.

KLOETZER, William S.

NAKAMURA, Takehiko

TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL

ANTIBODIES AND USE THEREOF AS THERAPEUTICS

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/019,441

FILING DATE: 05-Feb-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/803,085

FILING DATE: 20-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-502

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 1:

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;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 390 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 1..390
;   FEATURE:
;     NAME/KEY: mat_peptide
;     LOCATION: 58..390
;   SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-019-441-1

Query Match      100.0%; Score 333; DB 11; Length 390;
Best Local Similarity 100.0%; Pred. No. 7.2e-102;
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGTCTGCCCGACTCAGCTCCCTCTGTGTCTGGTCTCTGGACAGTCCGTCAACATC 60
DB 58 CAGTCTGCCCGACTCAGCTCCCTCTGTGTCTGGTCTCTGGACAGTCCGTCAACATC 117
QY 61 TCTCTGACTGGAACACAGGATGACGTTGGTGGTTATACTATGTCTCTGGTACCAACAC 120
DB 118 TCTCTGACTGGAACACAGGATGACGTTGGTGGTTATACTATGTCTCTGGTACCAACAC 177
QY 121 CACCAGGCAAGCCCAAACTCATGATTATGATGTCGCTAAAGCGGCTCAGGGGTC 180
DB 178 CACCAGGCAAGCCCAAACTCATGATTATGATGTCGCTAAAGCGGCTCAGGGGTC 237
QY 181 TCTGATCGCTTCTCTGGCTCCAGTCTGGACACGGCTCCCTGACCATCTCTGGGTC 240
DB 238 TCTGATCGCTTCTCTGGCTCCAGTCTGGACACGGCTCCCTGACCATCTCTGGGTC 297
QY 241 CAGGCTGAGGACGAGCTGATTATTACTTGTGTTTCATATACAAACAGTAGCACTTTGTTA 300
DB 298 CAGGCTGAGGACGAGCTGATTATTACTTGTGTTTCATATACAAACAGTAGCACTTTGTTA 357
QY 301 TTCGGAAGAGGACCGGTTGACCTCTAGGT 333
DB 358 TTCGGAAGAGGACCGGTTGACCTCTAGGT 390

RESULT 2
US-10-103-686-1
; Sequence 1, Application US/10103686
; Publication No. US20030059424A1
; GENERAL INFORMATION:
;   APPLICANT: REFF, Mitchell E.
;               KLOETZER, William S.
;               NAKAMURA, Takehiko
;   TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
;                   ANTIBODIES AND USE THEREOF AS THERAPEUTICS
;   NUMBER OF SEQUENCES: 35
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;     STREET: P.O. Box 1404
;     CITY: Alexandria
;     STATE: Virginia
;     COUNTRY: United States
;     ZIP: 22313-1404
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA: US/10/103,686
;   APPLICATION NUMBER: US/10/103,686
;   FILING DATE: 25-Mar-2002
;   CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/08/803,085
```

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;
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Teskin, Robin L.
;   REGISTRATION NUMBER: 35,030
;   REFERENCE/DOCKET NUMBER: 012712-353
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (703) 836-6620
;     TELEFAX: (703) 836-2021
;   INFORMATION FOR SEQ ID NO: 1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 390 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;     FEATURE:
;       NAME/KEY: CDS
;       LOCATION: 1..390
;     FEATURE:
;       NAME/KEY: mat_peptide
;       LOCATION: 58..390
;     SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-103-686-1

Query Match      100.0%; Score 333; DB 15; Length 390;
Best Local Similarity 100.0%; Pred. No. 7.2e-102;
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGTCTGCCCGACTCAGCTCCCTCTGTGTCTGGTCTCTGGACAGTCCGTCAACATC 60
DB 58 CAGTCTGCCCGACTCAGCTCCCTCTGTGTCTGGTCTCTGGACAGTCCGTCAACATC 117
QY 61 TCTCTGACTGGAACACAGGATGACGTTGGTGGTTATACTATGTCTCTGGTACCAACAC 120
DB 118 TCTCTGACTGGAACACAGGATGACGTTGGTGGTTATACTATGTCTCTGGTACCAACAC 177
QY 121 CACCAGGCAAGCCCAAACTCATGATTATGATGTCGCTAAAGCGGCTCAGGGGTC 180
DB 178 CACCAGGCAAGCCCAAACTCATGATTATGATGTCGCTAAAGCGGCTCAGGGGTC 237
QY 181 TCTGATCGCTTCTCTGGCTCCAGTCTGGCAACACGGCTCCCTGACCATCTCTGGGTC 240
DB 238 TCTGATCGCTTCTCTGGCTCCAGTCTGGCAACACGGCTCCCTGACCATCTCTGGGTC 297
QY 241 CAGGCTGAGGACGAGCTGATTATTACTTGTGTTTCATATACAAACAGTAGCACTTTGTTA 300
DB 298 CAGGCTGAGGACGAGCTGATTATTACTTGTGTTTCATATACAAACAGTAGCACTTTGTTA 357
QY 301 TTCGGAAGAGGACCGGTTGACCTCTAGGT 333
DB 358 TTCGGAAGAGGACCGGTTGACCTCTAGGT 390

RESULT 3
US-10-151-882-4
; Sequence 4, Application US/10151882
; Publication No. US20030059662A1
; GENERAL INFORMATION:
;   APPLICANT: Ruben, Steven M.
;   TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
;   FILE REFERENCE: PF554
;   CURRENT APPLICATION NUMBER: US/10/151,882
;   CURRENT FILING DATE: 2002-05-22
;   PRIOR APPLICATION NUMBER: 60/293,100
;   PRIOR FILING DATE: 2001-05-24
;   NUMBER OF SEQ ID NOS: 48
;   SOFTWARE: PatentIn version 3.0
;   SEQ ID NO 4
;   LENGTH: 726
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;     OTHER INFORMATION: DNA encoding A027A11 scFv
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US-10-151-882-4

Query Match	85.1%	Score 283.4	DB 15	Length 726
Best Local Similarity	90.7%	Pred. No. 4.7e-85		
Matches 302	Conservative 0	Mismatches 31	Indels 0	Gaps 0
Qy	1	CAGTCTCCCGAGCTCAGCCTCCCTCTGTGTCTGGTCTCTGGACAGTCTGGTACCACATC	60	
Db	394	CAGTCTGTGTAGCTCAGCCTGCCTCCGTGTCCTGGTCTCTGGACAGTCTGATCACCATC	453	
Qy	61	TCCTGCACTGGAAACAGCGAGTGGTGGTGTATTAATACTATGTCCTCTGGTACCAACAC	120	
Db	454	TCCTGCACTGGAAACAGCGAGTGGTGGTGTATTAATACTATGTCCTCTGGTACCAACA	513	
Qy	121	CACCCAGGCAAAAGCCCCAAACTCATGATTTATGATGTCGTAAAGCGGGCTCAGGGGTC	180	
Db	514	CACCCAGGCAAAAGCCCCAAACTCATGATTTATGAGGCGAGTAAGCGGCCCTCAGGGGTT	573	
Qy	181	TCGTATCGCTTCTCTGGCTCCAAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGGTC	240	
Db	574	TCATAATCGCTTCTCTGGCTCCAAAGTCTGGCAACAGCGGCTCCCTGACCAATCTCTGGGGTC	633	
Qy	241	CAGGCTCAGGACGAGGGTGATTATTACTGTGTTTCATATACAACAGTAGCACTTTGTGA	300	
Db	634	CAGGCTCAGGACGAGGGTGATTATTACTGTCAGCTCATATACAACAGGAGCACTCGAGTT	693	
Qy	301	TTCCGAAGAGGGAACCGGGTTGACCGTCTCTAGGT	333	
Db	694	TTCCGGCGAGGGAACCAAGCTCAGCGTCTCTAGGT	726	

RESULT 4

US-10-139-785-59

Sequence 59, Application US/10139785
Publication No. US20030190685A1
GENERAL INFORMATION:
APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
FILE REFERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/139,785
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/369,860
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/331,044
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 60/327,364
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/323,807
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/309,176
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/294,981
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/293,473
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 59
LENGTH: 735
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: DNA encoding T1014B11 scFv

US-10-139-785-59

Qy	1	CAGTCTGCCCGGACTCAGCCTCCCTCTGTGTCTGGGTCTCTCTGACACAGTCGGTCACCATC	60
Db	403	CAATCTGCCCTGACTCAGCCTGCCCTCGTGTCTGGGTCTCTCTGACACAGTCGATCACCATC	462
Qy	61	TCCTGCACTGGAAACCGACGATGAGTTGGTGGTTATAAATACTATGTCTCTCTGGTACCAACAC	120
Db	463	TCCTGCACTGGAAACCAACAGTGAGTTGGTGGTTACAACATATGTCTCTCTGGTACCAACNA	522
Qy	121	CACCCAGGCAAAAGCCCCCAAACTCATGATTTATGATGTGCTTAAGCGGGCCCTCAGGGGTC	180
Db	523	CACCCAGGCAAAAGCCCCCAAACTCATGATTTATGAGGTCAATATCGGCCCTCAGGGGTT	582
Qy	181	TCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACAACGGCCTCCCTGACCATCTCTGGGCTC	240
Db	583	TCTAAATCGCTTCTCTGGCTCCAAGTCTGGCAACAACGGCCTCCCTGACCATCTCTGGGCTC	642
Qy	241	CAGGCTGAGGACGAGGCTGATTTATCTGTTGTTTCATATACAACAGTAGACACTTTTGTTTA	300
Db	643	CAGGCTGAOCACGAGGCTGATTTATTACTGCAGCTCATATACAACAGCAACACTTGGGTG	702
Qy	301	TTCCGAAGAGGGACCCGGTTGACCGTCTTAGT	333
Db	703	TTCCGGGAGGGACCAAGCTGACCGTCTTAGT	735

RESULT 5

US-10-139-785-63
Sequence 63, Application US/10139785
Publication No. US20030190685A1
GENERAL INFORMATION:
APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
FILE REFERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/139,785
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/369,860
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/331,044
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 60/327,364
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/323,807
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/309,176
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/294,981
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/293,473
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 63
LENGTH: 735
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: DNA encoding T1015A07 scFv
US-10-139-785-63

Qy 61 TCCTGCACTGGAAACAGCGATGACGCTGGTGGTTATTAACCTATGCTCTCGGTACCAAC 120
Db |||||
Qy 463 TCCTGCACTGGAAACAGCAGTGAAGTGGTGGTTATTAACCTATGCTCTCGGTACCAAC 522
Db |||||
Qy 121 CACCCAGCAAGAGCCCAACTCATGATTTATGATGTCGTAAGCGGCTCTCAGGGGTC 180
Db |||||
Qy 523 CACCCAGCAAGAGCCCAACTCATGATTTATGCGGTCACTAATCGGCCCTCAGGGGTT 582
Db |||||
Qy 181 TCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGTC 240
Db |||||
Qy 583 TCTAATCGCTTCTCTGGCTCCAAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGTC 642
Db |||||
Qy 241 CAGGCTGAGGACGAGGCTGATTATTAACCTATGCTGGTCACTAATCAAGCAGACACTTGGTG 300
Db |||||
Qy 643 CAGGCTGAGGACGAGGCTGATTATTAACCTATGCTGGTCACTAATCAAGCAGACACTTGGTG 702
Db |||||
Qy 301 TTCGGAAGAGGAGCCCGGTTGACCGTCTCTAGGT 333
Db |||||
Qy 703 TTCGGGAGGAGGACCAAGGTCACCGTCTCTAGGT 735
Db |||||

RESULT 6

US-10-139-785-64
; Sequence 64, Application US/10139785
; Publication No. US20030190685A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/139,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 64

; LENGTH: 735
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding T1015E01 scFv
US-10-139-785-64
Query Match 85.1%; Score 283.4; DB 13; Length 735;
Best Local Similarity 90.7%; Pred. No. 4.7e-85;
Matches 302; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
Qy 1 CAGTCTGCCCGACTCAGCCTCCCTCTGTGCTGGGTCTCTCGGACAGTCGGTCACCAATC 60
Db |||||
Qy 403 CAGTCTGCCCGACTCAGCCTCCCTCATGCTGGGTCTCTCGGACAGTCGATCACCATC 462
Db |||||
Qy 61 TCCTGCACTGGAAACAGCGATGACGCTGGTGGTTATTAACCTATGCTCTCGGTACCAAC 120
Db |||||
Qy 463 TCCTGCACTGGAAACAGCGATGACGCTGGTGGTTATTAACCTATGCTCTCGGTACCAAC 522
Db |||||
Qy 121 CACCCAGCAAGAGCCCAACTCATGATTTATGATGTCGTAAGCGGCTCTCAGGGGTC 180
Db |||||

Db 523 CACCCAGCAAGAGCCCAACTCATGATTTATGCGGTCACTAATCGGCCCTCAGGGGTT 582
Qy |||||
Qy 181 TCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGTC 240
Db |||||
Qy 583 TCTAATCGCTTCTCTGGCTCCAAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGTC 642
Db |||||
Qy 241 CAGGCTGAGGACGAGGCTGATTATTAACCTATGCTGGTCACTAATCAAGCAGACACTTGGTG 300
Db |||||
Qy 643 CAGGCTGAGGACGAGGCTGATTATTAACCTATGCTGGTCACTAATCAAGCAGACACTTGGTG 702
Db |||||
Qy 301 TTCGGAAGAGGAGCCCGGTTGACCGTCTCTAGGT 333
Db |||||
Qy 703 TTCGGGAGGAGGACCAAGGTCACCGTCTCTAGGT 735
Db |||||

RESULT 7

US-10-039-785-59
; Sequence 59, Application US/10039785
; Publication No. US20020067646A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 59

; LENGTH: 735
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding T1014B11 scFv
US-10-039-785-59
Query Match 85.1%; Score 283.4; DB 14; Length 735;
Best Local Similarity 90.7%; Pred. No. 4.7e-85;
Matches 302; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
Qy 1 CAGTCTGCCCGACTCAGCCTCCCTCTGTGCTGGGTCTCTCGGACAGTCGGTCACCAATC 60
Db |||||
Qy 403 CAGTCTGCCCGACTCAGCCTCCCTCATGCTGGGTCTCTCGGACAGTCGATCACCATC 462
Db |||||
Qy 61 TCCTGCACTGGAAACAGCGATGACGCTGGTGGTTATTAACCTATGCTCTCGGTACCAAC 120
Db |||||
Qy 463 TCCTGCACTGGAAACAGCGATGACGCTGGTGGTTATTAACCTATGCTCTCGGTACCAAC 522
Db |||||
Qy 121 CACCCAGCAAGAGCCCAACTCATGATTTATGATGTCGTAAGCGGCTCTCAGGGGTC 180
Db |||||
Qy 523 CACCCAGCAAGAGCCCAACTCATGATTTATGAGGTCAATAATCGGCCCTCAGGGGTT 582
Db |||||
Qy 181 TCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGTC 240
Db |||||

Db 583 TCTAATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGCTCCCTGACCATCTCTGGGCTC 642
Qy 241 CAGGCTGAGGACGAGGCTGATTATTACTGTTGTTTCATATACAAACAGTAGCATTGTTA 300
Db 643 CAGGCTGAGGACGAGGCTGATTATTACTGAGCTCATATACAAACAGCACTTGGGTG 702
Qy 301 TTCGGAAGAGGACCCCGGTTGACCGTCTCTAGGT 333
Db 703 TTCGGCGGAGGACCAAGCTGACCGTCTCTAGGT 735

RESULT 8

US-10-039-785-63
; Sequence 63, Application US/10039785
; Publication No. US20020067646A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 63
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding T1015A07 scFv

US-10-039-785-63
Query Match 85.1%; Score 283.4; DB 14; Length 735;
Best Local Similarity 90.7%; Pred. No. 4.7e-85;
Matches 302; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCGGACTCAGCCTCCCTCTGCTGGTCTCTGGACAGTCGGTCACCATC 60
Db 403 CAGTCTGCCCTGACTCAGCCTGCCCTCCATGCTGGGTCTCTGGACAGTCGATCACCATC 462
Qy 61 TCCTGCACTGGAACACGAGGATGAGCTTGGTGTATATGCTCTCTGGTACCAAC 120
Db 463 TCCTGCACTGGAACACGAGTACGCTTGGTGTATATGCTCTCTGGTACCAACAG 522
Qy 121 CACCCAGCAAGGCCCAAACTCATGATTATGATGTCGCTAAGCGGGCTCTAGGGGTC 180
Db 523 CACCCAGCAAGGCCCAAACTCATGATTATGCGGTCACTAATCGGCCCTCAGGGGTT 582
Qy 181 TCTGATCGCTTCTCTGGCTCCAAAGTCTGCAACACGGCTCCCTGACCATCTCTGGGTC 240
Db 583 TCTAATCGCTTCTCTGCTCCAAAGTCTGCAACACGGCTCCCTGACCATCTCTGGGTC 642
Qy 241 CAGGCTGAGGACGAGGCTGATTATTACTGTTGTTTCATATACAAACAGTAGCATTGTTA 300
Db 643 CAGGCTGAGGACGAGGCTGATTATTACTGAGCTCATATACAGCAACACTTGGGTG 702

Qy 301 TTCGGAAGAGGACCCCGGTTGACCGTCTCTAGGT 333
Db 703 TTCGGCGGAGGACCAAGGTCAACGCTCTAGGT 735

RESULT 9

US-10-039-785-64
; Sequence 64, Application US/10039785
; Publication No. US20020067646A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 64
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding T1015E01 scFv

US-10-039-785-64
Query Match 85.1%; Score 283.4; DB 14; Length 735;
Best Local Similarity 90.7%; Pred. No. 4.7e-85;
Matches 302; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCGGACTCAGCCTCCCTCTGCTGGTCTCTGGACAGTCGGTCACCATC 60
Db 403 CAGTCTGCCCTGACTCAGCCTGCCCTCCATGCTGGGTCTCTGGACAGTCGATCACCATC 462
Qy 61 TCCTGCACTGGAACACGAGGATGAGCTTGGTGTATATGCTCTCTGGTACCAAC 120
Db 463 TCCTGCACTGGAACACGAGTACGCTTGGTGTATATGCTCTCTGGTACCAACAG 522
Qy 121 CACCCAGCAAGGCCCAAACTCATGATTATGATGTCGCTAAGCGGGCTCTAGGGGTC 180
Db 523 CACCCAGCAAGGCCCAAACTCATGATTATGCGGTCACTAATCGGCCCTCAGGGGTT 582
Qy 181 TCTGATCGCTTCTCTGGCTCCAAAGTCTGCAACACGGCTCCCTGACCATCTCTGGGTC 240
Db 583 TCTAATCGCTTCTCTGCTCCAAAGTCTGCAACACGGCTCCCTGACCATCTCTGGGTC 642
Qy 241 CAGGCTGAGGACGAGGCTGATTATTACTGTTGTTTCATATACAAACAGTAGCATTGTTA 300
Db 643 CAGGCTGAGGACGAGGCTGATTATTACTGAGCTCATATACAGCAACACTTGGGTG 702
Qy 301 TTCGGAAGAGGACCCCGGTTGACCGTCTCTAGGT 333
Db 703 TTCGGCGGAGGACCAAGGTCAACGCTCTAGGT 735

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RESULT 10
US-10-198-846-13540/c
; Sequence 13540, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13540
; LENGTH: 1597
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-198-846-13540

Query Match      84.1%; Score 280.2; DB 15; Length 1597;
Best Local Similarity 90.1%; Pred. No. 7.6e-84;
Matches 300; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCGACTCAGCCCTCTCTGTCTGGTCTCTGGAGTCTCGGTACCATC 60
Db 1473 CAGTCTGCCCGACTCAGCCCTCTCTGTCTGGTCTCTGGAGTCTCGGTACCATC 1414

Qy 61 TCCTGCACCTGGAACACGAGGATGACCTTGGTGGTTATTAATATGTTCTCTGGTACCAAC 120
Db 1413 TCCTGCATTGGAACCTTCAATGACATTGGTAGTTATTAATATGTTCTCTGGTACCAAC 1354

Qy 121 CACCAGGCAAGCCCAACTCATGATTATGATGTCGTAAGCGGGCTCAGGGGTC 180
Db 1353 CACCAGGCAAGCCCAACTCATGATTATGATGTCGTAAGTCGTAAGTCGAGGGTT 1294

Qy 181 TCTGATCGTCTCTCTGGTCTCAAGTCTGCAACACGGCTCCCTGACCATCTCTGGGCTC 240
Db 1293 TCTAATCGTCTCTCTGGTCTCAAGTCTGCAACACGGCTCCCTGACCATCTCTGGGCTC 1234

Qy 241 CAGGCTGAGGACGAGGCTGATTATTAATGTTTTCATATACACAGTAGCATTGTTA 300
Db 1233 CAGGCTGAGGACGAGGCTGATTATTAATGTTTTCATATACACAGTAGCATTGTTA 1174

Qy 301 TTCGGAAGAGGACCGGTTGACCGTCTTAGGT 333
Db 1173 TTCGGCGGAGGACCAAGCTGACCGTCTCTGGGT 1141

RESULT 11
US-10-076-747-8
; Sequence 8, Application US/10076747
; Publication No. US20030180726A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Hu, Ping
; APPLICANT: Recipon, Herve
; APPLICANT: Karra, Kalpana
; APPLICANT: Cafferkey, Robert
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Ovarian Specific Genes and E
; FILE REFERENCE: DEX-0315
; CURRENT APPLICATION NUMBER: US/10/076,747
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: 60/268,290
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; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/268,834
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 1460
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1022)..(1022)
; OTHER INFORMATION: a, c, g or t
US-10-076-747-8

Query Match      83.2%; Score 277; DB 13; Length 1460;
Best Local Similarity 89.5%; Pred. No. 8.8e-83;
Matches 298; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCGACTCAGCCCTCTCTGTCTGGTCTCTGGAGTCTCGGTACCATC 60
Db 56 CAGTCTGCCCGACTCAGCTTGCCTCCGTCTCTGGTCTCTGGAGTCTCGATCACCATC 115

Qy 61 TCCTGCACCTGGAACACGAGGATGACGTTGGTGGTTATAAATATGTTCTCTGGTACCAAC 120
Db 116 TCCTGCACCTGGAACACGAGGATGACGTTGGTGGTTATAAATATGTTCTCTGGTACCAAC 175

Qy 121 CACCAGGCAAGCCCAACTCATGATTATGATGTCGTAAGCGGGCTCAGGGGTC 180
Db 176 CACCAGGCAAGCCCAACTCATATTTATGAGGTTCAGTAATCGGCCCTCAGGGGTT 235

Qy 181 TCTGATCGTCTCTCTGGTCTCAAGTCTGGAACACGGCTCCCTGACCATCTCTGGGCTC 240
Db 236 TCTAATCGTCTCTCTGGTCTCAAGTCTGGAACACGGCTCCCTGACCATCTCTGGGCTC 295

Qy 241 CAGGCTGAGGACGAGGCTGATTATTAATGTTTTCATATACACAGTAGCATTGTTA 300
Db 296 CAGGCTGAGGACGAGGCTGATTATTAATGTTTTCATATACACAGTAGCATTGTTA 355

Qy 301 TTCGGAAGAGGACCGGTTGACCGTCTTAGGT 333
Db 356 TTCGGAACCTGGACCAAGGTCAACCGTCTTAGGT 388

RESULT 12
US-09-918-995-36573
; Sequence 36573, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36573
; LENGTH: 408
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-36573

Query Match      82.7%; Score 275.4; DB 11; Length 408;
Best Local Similarity 89.2%; Pred. No. 1.9e-82;
Matches 297; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCGACTCAGCCCTCTCTGTCTGGTCTCTGGAGTCTCGGTACCATC 60
Db 76 CAGTCTGCCCGACTCAGCCCTCTCTGTCTGGTCTCTGGAGTCTCGATCACCATC 135
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QY 61 TCCTGCACTGAACACGAGCGATGACGTTGGTGGTTATATACTATGTTCTCTGGTACCAACAC 120
Db 136 TCCTGCACTGAACACGAGCGATGACGTTGGTGGTTATATACTATGTTCTCTGGTACCAACAA 195
QY 121 CACCAGCAAGACCCCAAACTCATGTTATGATGTCGTAAGCGGGCTCAGGGGTC 180
Db 196 CACCAGCAAGACCCCAAACTCATGTTATGAGGTGAGTAATCGGCCCTCAGGGGTT 255
QY 181 TCTGATCGTTCTCTGGCTCAAGTCTCGCAACACGGCTCCCTGACCATCTCTGGGCTC 240
Db 256 TCTATCGCTTCTCTGGCTCAAGTCTCGCAACACGGCTCCCTGACCATCTCTGGGCTC 315
QY 241 CAGCTGAGGACGAGGCTGATTTACTGTTTTCATATACACAGGAGTACCTTTGTTA 300
Db 316 CAGCTGAGGACGAGGCTGATTTACTGAGTTTCATATACACAGGAGTACCTCTGTC 375
QY 301 TTCGGAAGAGGACCCGGTTGACCGTCTAGGT 333
Db 376 TTCGGAATGGGCAAGGTACCGTCTCTATGT 408

RESULT 13

US-09-918-995-16692

; Sequence 16692, Application US/09918995
; Publication No. US20030073623A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

FILE OF INVENTION: FROM VARIOUS CDNA LIBRARIES

FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 16692

LENGTH: 421

TYPE: DNA

ORGANISM: Homo sapiens

US-09-918-995-16692

Query Match 82.7%; Score 275.4; DB 11; Length 421;
Best Local Similarity 89.2%; Pred. No. 1.9e-82;
Matches 297; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 CAGTCTGCCCGACTCAGCCTCCCTCTGTGTTCTCTGGTCTCTGGACAGTCGGTCACCATC 60
Db 88 CAGTCTGCCCTGACTCAGCCTCCCTCTGTGTTCTCTGGTCTCTGGACAGTCGATCACCATC 147
QY 61 TCCTGCACTGAACACGAGCGATGACGTTGGTGGTTATATACTATGTTCTCTGGTACCAACAC 120
Db 148 TCCTGCACTGAACACGAGCGATGACGTTGGTGGTTATATACTATGTTCTCTGGTACCAACAA 207
QY 121 CACCAGCAAGACCCCAAACTCATGTTATGATGTCGTAAGCGGGCTCAGGGGTC 180
Db 208 CACCAGCAAGACCCCAAACTCATGTTATGAGTCAGTAATCGGCCCTCAGGGGTT 267
QY 181 TCTGATCGTTCTCTGGCTCAAGTCTCGCAACACGGCTCCCTGACCATCTCTGGGCTC 240
Db 268 TCTAATCGTTCTCTGGCTCAAGTCTCGCAACACGGCTCCCTGACCATCTCTGGGCTC 327
QY 241 CAGCTGAGGACGAGGCTGATTTACTGTTTTCATATACACAGGAGTACCTTTGTTA 300
Db 328 CAGCTGAGGACGAGGCTGATTTACTGAGCTCATATACAGGAGTACCTCTGGTG 387
QY 301 TTCGGAAGAGGACCCGGTTGACCGTCTAGGT 333
Db 388 GTCGGGAGGAGCAAGCTACCGTCTCTAGGT 420

RESULT 14

US-10-198-846-13206/c

; Sequence 13206, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steimann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13206
; LENGTH: 1640
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-198-846-13206

Query Match 82.7%; Score 275.4; DB 15; Length 1640;
Best Local Similarity 89.2%; Pred. No. 3.2e-82;
Matches 297; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 CAGTCTGCCCGACTCAGCCTCCCTCTGTGTTCTCTGGTCTCTGGACAGTCGGTCACCATC 60
Db 1512 CAGTCTGCCCTGACTCAGCCTCCCTCAGTCTCCGGGTCTCTGGACAGTCAGTCACCATC 1453
QY 61 TCCTGCACTGAACACGAGCGATGACGTTGGTGGTTATATACTATGTTCTCTGGTACCAACAC 120
Db 1452 TCCTGCACTGAACACGAGCGATGACGTTGGTGGTTATATACTATGTTCTCTGGTACCAACAA 1393
QY 121 CACCAGCAAGACCCCAAACTCATGTTATGATGTCGTAAGCGGGCTCAGGGGTC 180
Db 1392 CACCAGCAAGACCCCAAACTCATGTTATGATGTCGTAAGCGGGCTCAGGGGTC 1333
QY 181 TCCTGATCGTTCTCTGGCTCAAGTCTGGCAACACGGCTCCCTGACCATCTCTGGGCTC 240
Db 1332 TCTAATCGTTCTCTGGCTCAAGTCTGGCAACACGGCTCCCTGACCAATCTCTGGGCTC 1273
QY 241 CAGCTGAGGACGAGGCTGATTTACTGTTTTCATATACACAGTACGACTTTGTTA 300
Db 1272 CAGCTGAGGACGAGGCTGATTTACTGTTTTCATATGAGTATATAGACTTTGGTG 1213
QY 301 TTCGGAAGAGGACCCGGTTGACCGTCTAGGT 333
Db 1212 TTCGGGAGGAGCAAGCTGACCGTCTAGGT 1180

RESULT 15

US-10-139-785-54

Sequence 54, Application US/10139785

Publication No. US20030190685A1

GENERAL INFORMATION:

APPLICANT: Salcedo et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

TITLE OF INVENTION: Receptors

FILE REFERENCE: PF550

CURRENT APPLICATION NUMBER: US/10/139,785

PRIOR FILING DATE: 2002-05-07

PRIOR APPLICATION NUMBER: 60/369,860

PRIOR FILING DATE: 2002-04-05

PRIOR APPLICATION NUMBER: 60/341,237

PRIOR FILING DATE: 2001-12-20

PRIOR APPLICATION NUMBER: 60/331,310

PRIOR FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/331,044

PRIOR FILING DATE: 2001-11-07

PRIOR APPLICATION NUMBER: 60/327,364

PRIOR FILING DATE: 2001-10-09

; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54

; LENGTH: 735

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: DNA encoding T1014A04 scFv

US-10-139-785-54

Query Match 82.2%; Score 273.8; DB 13; Length 735;
Best Local Similarity 88.9%; Pred. No. 8.2e-82;
Matches 296; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Qy	1	CAGTCTGCCCGCCGACCTCCCTCTGTGCTGGGTCTCTGTGACAGTCGGTCAACCATC	60
Db	403		
Qy	61	TCCTGCACCTGNAACGAGCGATGACGTTGGTGGTTTAACTATGCTCCTGGTACCAACAC	120
Db	463		
Qy	121	CACCCAGCAAGCCCCCAACTCATGATTTATGATGCTGCTAAGCGGGCCTCAGGGGTC	180
Db	523		
Qy	181	TCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTC	240
Db	583		
Qy	241	CAGGCTGAGGAGCGGCTGATTATTACTGTTGTTTCATATACACAGTAGCACTTTGTTA	300
Db	643		
Qy	301	FTCGGAAGAGGACCCCGTTGACCGTCTCTAGGT	333
Db	703		

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Job time : 481.099 secs

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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 36.6551 Seconds
(without alignments)
4009.823 Million cell updates/sec

Title: US-09-019-441-1_COPY_58_390

Perfect score: 333

Sequence: 1 CAGTCGCCCGACTGACCC.....CCCGTTGACCGTCCTAGGT 333

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	333	100.0	390	3	US-08-803-085-1
2	283.4	85.1	735	4	US-10-039-785-59
3	283.4	85.1	735	4	US-10-039-785-63
4	283.4	85.1	735	4	US-10-039-785-64
5	275.4	82.7	333	2	US-08-958-201-13
6	273.8	82.2	333	2	US-08-958-201-11
7	273.8	82.2	735	4	US-10-039-785-54
8	273.8	82.2	891	3	US-09-049-672A-23
9	272.2	81.7	902	2	US-08-378-939-11
10	267.4	80.3	735	4	US-10-039-785-57
11	265.8	79.8	735	4	US-10-039-785-60
12	259.4	77.9	735	4	US-10-039-785-58
13	259.4	77.9	735	4	US-10-039-785-61
14	256.2	76.9	735	4	US-10-039-785-55
15	252.2	75.7	543	4	US-09-702-705-970
16	252.2	75.7	543	4	US-09-736-457-970
17	244.6	73.5	548	4	US-09-404-879A-267
18	244.6	73.5	548	4	US-09-338-933-267
19	244.6	73.5	548	4	US-09-215-681-267
20	239.6	72.0	324	3	US-09-240-274-137
21	225.8	67.8	771	3	US-08-991-789A-241
22	225.8	67.8	771	4	US-09-062-451-241
23	225.8	67.8	771	4	US-09-598-326-241
24	225.8	67.8	771	4	US-09-289-198-241
25	208.8	62.7	312	3	US-09-240-274-138
26	195.4	58.7	585	4	US-09-620-312D-551
27	193.6	58.1	935	3	US-09-049-672A-20

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Sequence 4, Appli
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Sequence 56, Appli
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ALIGNMENTS

RESULT 1

US-08-803-085-1

; Sequence 1, Application US/08803085

; Patent No. 6011138

; GENERAL INFORMATION:

; APPLICANT: REPF, Mitchell E.

; APPLICANT: KLOETZER, William S.

; TITLE OF INVENTION: NAKAMURA, Takehiko

; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL

; NUMBER OF SEQUENCES: 35

; CORRESPONDENCE ADDRESS:

; ADDRESS: BURNS, DOANE, SWECKER & MATHIS

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/803,085

; FILING DATE: 20-FEB-1997

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Teskin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/DOCKET NUMBER: 012712-353

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 390 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..390

; FEATURE:

; NAME/KEY: mat_peptide

; LOCATION: 58..390

; US-08-803-085-1

Query Match 100.0%; Score 333; DB 3; Length 390;

Best Local Similarity 100.0%; Pred. No. 2.2e-95; Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCGACTCAGCCCTCCCTCTGTCTGGGTCTCTGGACAGTCGGTCAACATC 60
Db 58 CAGTCTGCCGACTCAGCCCTCCCTCTGTCTGGGTCTCTGGACAGTCGGTCAACATC 117

Qy 61 TCCTGCACTGAAACCCAGGATGAGTGGTGTATTAATCTATGTTCTCTGGTACCAAC 120
Db 118 TCCTGCACTGAAACCCAGGATGAGTGGTGTATTAATCTATGTTCTCTGGTACCAAC 177

Qy 121 CACCAGCAAAAGCCCAAACTCATGATTTATGATGTCGTTAAGCGGGCTCAGGGGTC 180
Db 178 CACCAGCAAAAGCCCAAACTCATGATTTATGATGTCGTTAAGCGGGCTCAGGGGTC 237

Qy 181 TCTGATCGCTTCTCTGGTCCAAAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGTC 240
Db 238 TCTGATCGCTTCTCTGGTCCAAAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGTC 297

Qy 241 CAGGCTGAGGAGGAGGCTGATTTACTGTTTTCATATACACAGTAGCATTGTTA 300
Db 298 CAGGCTGAGGAGGAGGCTGATTTACTGTTTTCATATACACAGTAGCATTGTTA 357

Qy 301 TTCGGAAGAGGAGCCCGTTGACCGTCTTAGGT 333
Db 358 TTCGGAAGAGGAGCCCGTTGACCGTCTTAGGT 390

RESULT 2

US-10-039-785-59
; Sequence 59, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding T1014B11 scFv

US-10-039-785-59
Query Match 85.1%; Score 283.4; DB 4; Length 735;
Best Local Similarity 90.7%; Pred. No. 1.1e-79;
Matches 302; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCGACTCAGCCCTCCCTCTGTCTGGGTCTCTGGACAGTCGGTCAACATC 60
Db 58 CAGTCTGCCGACTCAGCCCTCCCTCTGTCTGGGTCTCTGGACAGTCGGTCAACATC 117

Qy 61 TCCTGCACTGAAACCCAGGATGAGTGGTGTATTAATCTATGTTCTCTGGTACCAAC 120
Db 118 TCCTGCACTGAAACCCAGGATGAGTGGTGTATTAATCTATGTTCTCTGGTACCAAC 177

Qy 121 CACCAGCAAAAGCCCAAACTCATGATTTATGATGTCGTTAAGCGGGCTCAGGGGTC 180
Db 178 CACCAGCAAAAGCCCAAACTCATGATTTATGATGTCGTTAAGCGGGCTCAGGGGTC 237

Qy 181 TCTGATCGCTTCTCTGGTCCAAAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGTC 240
Db 238 TCTGATCGCTTCTCTGGTCCAAAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGTC 297

Qy 241 CAGGCTGAGGAGGAGGCTGATTTACTGTTTTCATATACACAGTAGCATTGTTA 300
Db 298 CAGGCTGAGGAGGAGGCTGATTTACTGTTTTCATATACACAGTAGCATTGTTA 357

Db 403 CAATCTGCCCTGACTCAGCCCTGCTCGGTGTCTGGGTCTCTCGACAGTCGATCACCATC 462

Qy 61 TCCTGCACTGAAACCCAGGATGAGTGGTGTATTAATCTATGTTCTCTGGTACCAAC 120
Db 463 TCCTGCACTGAAACCCAGGATGAGTGGTGTATTAATCTATGTTCTCTGGTACCAAC 522

Qy 121 CACCAGCAAAAGCCCAAACTCATGATTTATGATGTCGTTAAGCGGGCTCAGGGGTC 180
Db 523 CACCAGCAAAAGCCCAAACTCATGATTTATGATGTCGTTAAGCGGGCTCAGGGGTC 582

Qy 181 TCTGATCGCTTCTCTGGTCCAAAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGTC 240
Db 583 TCTAATCGCTTCTCTGGTCCAAAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGTC 642

Qy 241 CAGGCTGAGGAGGAGGCTGATTTACTGTTTTCATATACACAGTAGCATTGTTA 300
Db 643 CAGGCTGAGGAGGAGGCTGATTTACTGAGCTCATATACACAGTAGCATTGTTA 702

Qy 301 TTCGGAAGAGGAGCCCGTTGACCGTCTTAGGT 333
Db 703 TTCGGAAGAGGAGCCCGTTGACCGTCTTAGGT 735

RESULT 3

US-10-039-785-63
; Sequence 63, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding T1015A07 scFv

US-10-039-785-63
Query Match 85.1%; Score 283.4; DB 4; Length 735;
Best Local Similarity 90.7%; Pred. No. 1.1e-79;
Matches 302; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCGACTCAGCCCTCCCTCTGTCTGGGTCTCTGGACAGTCGGTCAACATC 60
Db 403 CAGTCTGCCGACTCAGCCCTCCCTCTGTCTGGGTCTCTGGACAGTCGATCACCATC 462

Qy 61 TCCTGCACTGAAACCCAGGATGAGTGGTGTATTAATCTATGTTCTCTGGTACCAAC 120
Db 463 TCCTGCACTGAAACCCAGGATGAGTGGTGTATTAATCTATGTTCTCTGGTACCAAC 522

Qy 121 CACCCAGCAAGCCCAAACTCATGATTATGATGTGCTAAGCGGCTCAGGGTC 180
Db 523 CACCCAGCAAGCCCAAACTCATGATTATGCGGTCACTATCGGCCCTCAGGGTT 582
Qy 181 TCTGATCGCTTCTGCTCCAACTCTGCAACACGGCTCCCTGACCATCTCTGGGCTC 240
Db 583 TCTAATCGCTTCTGCTCCAACTCTGCAACACGGCTCCCTGACCATCTCTGGGCTC 642
Qy 241 CAGGCTGAGGACGAGGCTGATTATGTTTATGCTGAGCTCATATACAGCAACACTTGGGTG 300
Db 643 CAGGCTGAGGACGAGGCTGATTATGTTTATGCTGAGCTCATATACAGCAACACTTGGGTG 702
Qy 301 TTCGGAAGAGGAGCCCGGTTGACCGTCTTAGGT 333
Db 703 TTCGCGGAGGAGCAAGGTCAACGCTCTTAGGT 735

RESULT 4

US-10-039-785-64
; Sequence 64, Application US/10039785
; Patent No. 6538338
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PE550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding T1015E01 scFv
US-10-039-785-64

Query Match 85.1%; Score 283.4; DB 4; Length 735;
Best Local Similarity 90.7%; Pred. No. 1.1e-79;
Matches 302; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
Qy 1 CAGTCTGCCCGGACTCAGCCTCCCTCTGTGCTGGGTCTCCTGGACAGTCGGTCACCATC 60
Db 403 CAGTCTGCCCGGACTCAGCCTCCCTCTGTGCTGGGTCTCCTGGACAGTCGATCACCATT 462
Qy 61 TCCTGCACCTGAAACAGCGATGAGTGGTGGTTATTAACATATGCTCCTGGTACCAACAC 120
Db 463 TCCTGCACCTGAAACAGCGATGAGTGGTGGTTATTAACATATGCTCCTGGTACCAACAG 522
Qy 121 CACCCAGCAAGCCCAAACTCATGATTATGATGTGCTAAGCGGCTCAGGGTC 180
Db 523 CACCCAGCAAGCCCAAACTCATGATTATGCGGTCACTAATCGGCCCTCAGGGGT 582

Qy 181 TCTGATCGCTTCTCTGCTCCAACTCTGCAACACGGCTCCCTGACCATCTCTGGGCTC 240
Db 583 TCTAATCGCTTCTCTGCTCCAACTCTGCAACACGGCTCCCTGACCATCTCTGGGCTC 642
Qy 241 CAGGCTGAGGACGAGGCTGATTATGTTTATGCTGAGCTCATATACAGCAACACTTGGGTG 300
Db 643 CAGGCTGAGGACGAGGCTGATTATGTTTATGCTGAGCTCATATACAGCAACACTTGGGTG 702
Qy 301 TTCGGAAGAGGAGCCCGGTTGACCGTCTTAGGT 333
Db 703 TTCGCGGAGGAGCAAGGTCAACGCTCTTAGGT 735

RESULT 5

US-08-958-201-13
; Sequence 13, Application US/08958201
; Patent No. 5977319
; GENERAL INFORMATION:
; APPLICANT: Pope, Anthony R
; APPLICANT: Pritchard, Kevin
; APPLICANT: Williams, Andrew J
; APPLICANT: Johnson, Kevin S
; TITLE OF INVENTION: Specific binding members for estradiol;
; TITLE OF INVENTION: materials and methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/958,201
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,897
; FILING DATE: 21-OCT-1996
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 333 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: 1C/2D
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..333
US-08-958-201-13

Query Match 82.7%; Score 275.4; DB 2; Length 333;
Best Local Similarity 89.2%; Pred. No. 2.6e-77;
Matches 297; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
Qy 1 CAGTCTGCCCGGACTCAGCCTCCCTCTGTGCTGGGTCTCCTGGACAGTCGGTCACCATC 60
Db 1 CAGTCTGCTCTGACTCAGCCTCCCTCTGTGCTGGGTCTCCTGGACAGTCGATCACCATT 60
Qy 61 TCCTGCACCTGAAACAGCGATGAGTGGTGGTTATTAACATATGCTCCTGGTACCAACAC 120
Db 61 TCCTGCACCTGAAACAGCGATGAGTGGTGGTTATTAACATATGCTCCTGGTACCAACAG 120
Qy 121 CACCCAGCAAGCCCAAACTCATGATTATGATGTGCTAAGCGGCTCAGGGTC 180
Db 121 CACCCAGCAAGCCCAAACTCATGATTATGAGGTCAAGTAAATCGGCCCTCAGGGGT 180
Qy 181 TCTGATCGCTTCTCTGCTCCAACTCTGCAACACGGCTCCCTGACCATCTCTGGGCTC 240

Db 181 CCTAATCGCTTCTCAGGCTCCAAAGCTCTGGCAACACAGCGCTCCCTGACCATCTCTGGGGTC 240
Qy 241 CAGCTGAGGACGAGGCTGATTATTACTGTTGTTTCATATACAACACAGTAGCAGCTTTGTTA 300
Db 241 CAGCTGAGGACGAGGCTGATTATTACTGAGCTCACTTACACGACAGTCACTGTGATC 300
Qy 301 TTCGAGAGGAGGACCGGTTGACCGTCTAGGT 333
Db 301 TTCGGCGGAGGACCAAGCTGACCGTCTAGGT 333

RESULT 6

US-08-958-201-11
; Sequence 11, Application US/08958201
; Patent No. 5977319
; GENERAL INFORMATION:
; APPLICANT: Pope, Anthony R
; APPLICANT: Pritchard, Kevin
; APPLICANT: Williams, Andrew J
; APPLICANT: Johnson, Kevin S
; TITLE OF INVENTION: Specific binding members for estradiol;
; TITLE OF INVENTION: materials and methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/958,201
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,897
; FILING DATE: 21-OCT-1996
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 333 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: D12 (light chain)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..333
US-08-958-201-11

Query Match 82.2%; Score 273.8; DB 2; Length 333;
Best Local Similarity 88.9%; Pred. No. 8.4e-77;
Matches 296; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
Qy 1 CAGTCTGCCCGGACTCAGCCTCCCTCTGTGTCGGGTCTCTGGACAGTCGGTCACCATC 60
Db 1 CAGTCTGTCTGACTCAGCCTGCCCTCTGTGTCGGGTCTCTGGACAGTCGATCACCATC 60
Qy 61 TCCTGCACTGGAACACGAGGATGACGTTGGTGGTTATAAATATGTCCTCTGGTACCAAC 120
Db 61 TCCTGCACTGGAACACGAGTGACGTTGGTGGTTATAAGTATGTCCTCTGGTACCAAC 120
Qy 121 CACCAGCAAGACCCCAACTCATGATTTATGATGTCGCTAGCGGGCTCAGGGGTC 180
Db 121 CACCAGCAAGACCCCAACTCATGATTTATGATGTCGCTAGCGGGCTCAGGGGTC 180
Qy 181 TCTGATCGCTTCTCTGGGTCCAAGTCTGGCAACACGGCTCCCTGACCATCTCTGGGGTC 240

Db 181 CCTAATCGCTTCTCAGGCTCCAAAGCTCTGGCAACACAGCGCTCCCTGACCATCTCTGGGGTC 240
Qy 241 CAGCTGAGGACGAGGCTGATTATTACTGTTGTTTCATATACAACACAGTAGCAGCTTTGTTA 300
Db 241 CAGCTTGAAGACGAGGCTGATTATTACTGAGCTCACTTACACGACAGTCACTGTGATC 300
Qy 301 TTCGAGAGGAGGACCGGTTGACCGTCTAGGT 333
Db 301 TTCGGCGGAGGACCAAGCTGACCGTCTAGGT 333

RESULT 7

US-10-039-785-54
; Sequence 54, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding TI014A04 scFv
US-10-039-785-54

Query Match 82.2%; Score 273.8; DB 4; Length 735;
Best Local Similarity 88.9%; Pred. No. 1.1e-76;
Matches 296; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
Qy 1 CAGTCTGCCCGGACTCAGCCTCCCTCTGTGTCGGGTCTCTGGACAGTCGGTCACCATC 60
Db 403 CAGTCTGTCTGACTCAGCACCCTCCGCTCCGGGTCTCTGGACAGTCAGTCAACATC 462
Qy 61 TCCTGCACTGGAACACGAGGATGACGTTGGTGGTTATAAATATGTCCTCTGGTACCAAC 120
Db 463 TCCTGCACTGGAACACCAACAGTGACGTTGGTGGTTATAAATATGTCCTCTGGTACCA 522
Qy 121 CACCAGCAAGACCCCAACTCATGATTTATGATGTCGCTAGCGGGCTCAGGGGTC 180
Db 523 CACCAGCAAGACCCCAACTCATGATTTATGAGGTCAATCAGCGGCCCTCAGGGGTC 582
Qy 181 TCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCTCCCTGACCATCTCTGGGGTC 240
Db 583 CCTGATGCTTCTCTGGCTCCAAGTCTGGCAACACGGCTCCCTGACCGTCTCTGGGGTC 642
Qy 241 CAGCTGAGGACGAGGCTGATTATTACTGTTGTTTCATATACAACACAGTAGCAGCTTTGTTA 300
Db 643 CAGCTGAGGATGAGGCTGATTATTACTGAGTTTCATATGTCAGTTCATATGACGAGCAACAATTGGGTG 702

QY 301 TTCCGAAGAGGACCCCGGTTGACCGTCTCTAGGT 333
| | | | |
Db 703 TTCCGGCGAGGACCAAGACTGACCGTCTCTAGGT 735
| | | | |

RESULT 8
US-09-049-672A-23
; Sequence 23, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; City: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0497 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 891 base pairs
; Type: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THYNOT10
; CLONE: 2872705
; US-09-049-672A-23

Query Match 82.2%; Score 273.8; DB 3; Length 891;
Best Local Similarity 88.9%; Pred. No. 1.2e-76;
Matches 296; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
QY 1 CAGTCTGCCGACTCAGCCCTCCCTGTGTCTGGGTCTCTGGACAGTGGTCAACATC 60
| | | | |
Db 91 CAGTCTGCCCTGACTCAGCCCTCCGCTGCTGGGTCTCTGGACAGTGGTCAACATC 150
| | | | |
QY 61 TCCTGCACTGAACACGAGGAGTGGTGGTTATTAACATGCTCTGCTGACCAACAC 120
| | | | |
Db 151 TCCTGCACTGAACACGAGGAGTGGTGGTTATTAACATGCTCTGCTGACCAACAG 210
| | | | |
QY 121 CACCCAGCAAAAGCCCAACTCATGATTTATGATGTCGCTAAGCGGGCTCAGGGGTC 180
| | | | |

Db 211 TCCCCAGGACGCCCCCAAACTCATGATTTATGAGTCAATATCGGCCCTCAGGGGTT 270
QY 181 TCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGCGCTCCCTGACCATCTCTGGGCTC 240
| | | | |
Db 271 TCTAATCGGTTCTCTGGCTCCAAAGTCTGGCAACACGCGCTCCCTGACCATCTCTGGGCTC 330
| | | | |
QY 241 CAGGCTGAGGACGAGGCTGATTATTAATGTTTTCATATACAAACCATGACATCTTTGTTA 300
| | | | |
Db 331 CAGGCTGAGGACGAGGCTGATTATTAATGTTTTCATATAGTAGGCAACAACTTGTGGTA 390
| | | | |
QY 301 TTCCGAAGAGGACCCCGGTTGACCGTCTCTAGGT 333
| | | | |
Db 391 TTCCGGCGAGGACCAAGCTGACCGTCTCTAGGT 423
| | | | |

RESULT 9
US-08-378-939-11
; Sequence 11, Application US/08378939
; Patent No. 5876961
; GENERAL INFORMATION:
; APPLICANT: CROWE, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 THIRTEENTH ST. N.W.
; CITY: WASHINGTON
; STATE: D. C.
; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,939
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: US 07/952640
; APPLICATION NUMBER:
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 902 base pairs
; Type: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 32..739
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 89..739
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 32..86
; US-08-378-939-11

Query Match 81.7%; Score 272.2; DB 2; Length 902;
Best Local Similarity 88.6%; Pred. No. 3.8e-76;
Matches 295; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCGACTCAGCCCTCCCTCTGTCTCGGTCTCTCTGGACAGTGGTCAACATC 60
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89 CAGTCTGCCCGACTCAGCCCTCCCTCTGTCTCGGTCTCTCTGGACAGTGGTCAACATC 148
Qy 61 TCCTGCACTGGAACACGAGGAGTGGTGGTTTATAAATATATGTCCTCTGGTACCAACAC 120
Db |||||
149 TCCTGCACTGGAACACGAGGAGTGGTGGAGTTATAAATCTTGTCTCTGGTACCAACAG 208
Qy 121 CACCCAGCAAGCCCAAACTCATGATTTATGATGTCGCTAAGCGGCGCTCAGGGGTC 180
Db |||||
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Qy 181 TCTGATCGCTTCTCTGGCTCAGGCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTC 240
Db |||||
269 TCTAATCGCTTCTCTGGCTCAGGCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTC 328
Qy 241 CAGGCTGAGGACGAGGCTGATTTACTTGTGTTTATATACCAACAGTAGCATTCTTTGTTA 300
Db |||||
329 CAGGCTGAGGACGAGGCTGATTTACTTGTGTTTATATGCTGCTCATATGAGGTAGTACATGTTGTT 388
Qy 301 TTCGGAAGAGGAGCCCGTTGACCGTCTTAGGT 333
Db |||||
389 TTCGCGGAGGAGCAAACTGACCGTCTTAGGT 421

RESULT 10

US-10-039-785-57
; Sequence 57, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785

; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 57
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding T1014A12 scFv
US-10-039-785-57

Query Match 80.3%; Score 267.4; DB 4; Length 735;
Best Local Similarity 87.7%; Pred. No. 1.1e-74;
Matches 292; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
Qy 1 CAGTCTGCCCGACTCAGCCCTCCCTCTGTCTCGGTCTCTCTGGACAGTGGTCAACATC 60
Db 403 CAGTCTGCCCGACTCAGCCCTCCCTCTGTCTCGGTCTCTCTGGACAGTGGTCAACATC 462

Qy 61 TCCTGCACTGGAACACGAGGAGTGGTGGTTTATAAATATATGTCCTCTGGTACCAACAC 120
Db |||||
463 TCCTGCACTGGAACACGAGGAGTGGTGGTTTATAAAGTATGTCCTCTGGTACCAACAA 522
Qy 121 CACCCAGCAAGCCCAAACTCATGATTTATGATGTCGCTAAGCGGCGCTCAGGGGTC 180
Db |||||
523 CACCCAGCAAGCCCAAACTCATGATTTATGATGTCGCTAAGCGGCGCTCAGGGGTT 582
Qy 181 TCTGATCGCTTCTCTGGCTCAGGCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTC 240
Db |||||
583 TCTGATCGCTTCTCTGGCTCAGGCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTC 642
Qy 241 CAGGCTGAGGACGAGGCTGATTTACTTGTGTTTATATACCAACAGTAGCATTCTTTGTTA 300
Db |||||
643 CAGGCTGAGGACGAGGCTGATTTACTTGTGTTTATATGCTGCTCATATGAGGTAGTACATGTTGTT 702
Qy 301 TTCGGAAGAGGAGCCCGTTGACCGTCTTAGGT 333
Db |||||
703 TTCGCGGAGGAGCAAACTGACCGTCTTAGGT 735

RESULT 11

US-10-039-785-60
; Sequence 60, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785

; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 60
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding T1014F08 scFv
US-10-039-785-60

Query Match 79.8%; Score 265.8; DB 4; Length 735;
Best Local Similarity 87.4%; Pred. No. 3.6e-74;
Matches 291; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
Qy 1 CAGTCTGCCCGACTCAGCCCTCCCTCTGTCTCGGTCTCTCTGGACAGTGGTCAACATC 60
Db 403 CAGTCTGCCCGACTCAGCCCTCCCTCTGTCTCGGTCTCTCTGGACAGTGGTCAACATC 462
Qy 61 TCCTGCACTGGAACACGAGGAGTGGTGGTTTATAAATATATGTCCTCTGGTACCAACAC 120
Db 463 TCCTGCACTGGAACACGAGGAGTGGTGGTTTATAAAGTATGTCCTCTGGTACCAACAG 522
Qy 121 CACCCAGCAAGCCCAAACTCATGATTTATGATGTCGCTAAGCGGCGCTCAGGGGTC 180

Db 523 CACCCAGGCAAGCCCAAACTCATGATTATGAGGTTCAGTATCGCGCGCTCAGGGGTC 582
Qy 181 TCTGATCGCTTCTGCTCCAACTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTC 240
Db 583 CCGGATCGCTTCTGCTCCAACTCTGGCAACAGCGCTCCCTGACCGTCTCTGGGCTC 642
Qy 241 CAGGCTGAGGATGAGGCTGATTATTAATCTGTTTATATACAAACAGTAGCATTCTTTGTTA 300
Db 643 CAGGCTGAGGATGAGGCTGATTATTAATCTGCGCTCATATGAGGAGCAACAATTGGGTG 702
Qy 301 TTCGGAAGAGGAGCCCGGTTGACCGTCTTAGGT 333
Db 703 TTCGCGGAGGAGCAAGCTGACCGTCTTAGGT 735

RESULT 12

US-10-039-785-58
; Sequence 58, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 58
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding T1014B01 scFv

US-10-039-785-58

Query Match 77.9%; Score 259.4; DB 4; Length 735;
Best Local Similarity 86.2%; Pred. No. 3.7e-72;
Matches 287; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
Qy 1 CAGTCTGCCCCGACTCAGCCTCCCTCTGTGTCGGGTCTCTCGACAGTCCGGTCAACATC 60
Db 403 CAGTCTGTCGTGACGAGCGCCCTCAGTGTCTGGTCTCTCGACAGTCACTCAGTCA 462
Qy 61 TCCTGCACTGGAACACAGCGATGACGTTGGTGTATTAATATGTTCTCTGATACCAAC 120
Db 463 TCCTGCACTGGAACACAGCGATGACGTTGGTGTATTAATATGTTCTCTGATCCAG 522
Qy 121 CACCCAGGCAAGCCCAAACTCATGATTATGATGTCGTAGCGGGCTCAGGGGTC 180
Db 523 CACCCAGGTAAGCCCAAACTCATTAATTTCTGAGGTCAAGTAAAGCGGCCCTCAGGG 582
Qy 181 TCTGATCGCTTCTGCTCCAACTCTGGAACACAGCGCTCCCTGACCATCTCTGGGCTC 240
Db 583 CACCCAGGTAAGCCCAAACTCATTAATTTCTGAGGTCAAGTAAAGCGGCCCTCAGGG 582
Qy 241 TCTGATCGCTTCTGCTCCAACTCTGGAACACAGCGCTCCCTGACCATCTCTGGGCTC 240

Db 583 CTTGATCGCTTCTGCTCCAACTCTGGAACACAGCGCTCCCTGACCGTCTCGGGGCTC 642
Qy 241 CAGGCTGAGGATGAGGCTGATTATTAATCTGTTTATATACAAACAGTAGCATTCTTTGTTA 300
Db 643 CAGGCTGAGGATGAGGCTGATTATTAATCTGCGCTCATATGAGGAGCAACAATTGGGTG 702
Qy 301 TTCGGAAGAGGAGCCCGGTTGACCGTCTTAGGT 333
Db 703 TTCGCGGAGGAGCAAGGTCAACCGTCTTAGGT 735

RESULT 13

US-10-039-785-61
; Sequence 61, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 61
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding T1014G04 scFv

US-10-039-785-61

Query Match 77.9%; Score 259.4; DB 4; Length 735;
Best Local Similarity 86.2%; Pred. No. 3.7e-72;
Matches 287; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCCGACTCAGCCTCCCTCTGTGTCGGGTCTCTCGACAGTCCGGTCAACATC 60
Db 403 CAGCCTGTGTCGTACTCAGCCCCCTCCGCGTCGCGGTGCGCTCGACAGTCACTCAGTCA 462
Qy 61 TCCTGCACTGGAACACAGCGATGACGTTGGTGTATTAATATGTTCTCTGATACCAAC 120
Db 463 TCCTGCACTGGAACACAGCGATGACGTTGGTGTATGATGATGTTCTCTGATCCAA 522
Qy 121 CACCCAGGCAAGCCCAAACTCATGATTATGATGTCGTAGCGGGCTCAGGGGTC 180
Db 523 CACCCAGGCAAGCCCAAACTCATGATTCTGAGGTCAATTAAGCGGCCCTCAGGGGTC 582
Qy 181 TCTGATCGCTTCTGCTCCAACTCTGGAACACAGCGCTCCCTGACCATCTCTGGGCTC 240
Db 583 CTTAATCGCTTCTCTGCTCCAACTCTGGAACACAGCGCTCCCTGACCGTCTCTGGGCTC 642
Qy 241 CAGGCTGAGGATGAGGCTGATTATTAATCTGTTTATATACAAACAGTAGCATTCTTTGTTA 300
Db 643 CAGGCTGAGGATGAGGCTGATTATTAATCTGAGCTCATATGAGGAGCAACAATTGGGTG 702

GenCore version 5.1.6
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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Listing first 45 summaries

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9: gb_pr.*

10: gb_ro.*

11: gb_ats.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_ats.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	271.6	74.2	435	9	AF416358	AP416358 Papio cyn
2	270	73.8	363	9	MMU57559	U57559 Macaca mula
3	270	73.8	441	9	AF416359	AF416359 Papio cyn
4	268.4	73.3	363	9	HSU279514	AJ279514 Homo sapi
5	268.4	73.3	363	9	HSU80179	U80179 Human immun
6	266.8	72.9	420	9	MMU57560	U57560 Macaca mula
7	266.8	72.9	1359	9	MACIGHVCDR	L13307 Macaca fasc
8	265.6	72.6	373	9	MMU57558	U57558 Macaca mula
9	263.4	72.0	366	9	HSU279520	AJ279520 Homo sapi
10	263	71.9	368	9	HSU80180	U80180 Human immun
11	262	71.6	420	9	MMU57565	U57565 Macaca mula
12	261.2	71.4	411	9	MMU57563	U57563 Macaca mula
13	260.4	71.1	363	9	HSU245032	AJ245032 Homo sapi
14	260.2	71.1	423	9	HSIGHXX28	X65910 H. sapiens m
15	259.2	70.8	414	9	MMU57568	U57568 Macaca mula
16	257.2	70.3	363	9	HSU279522	AJ279522 Homo sapi
17	257	70.2	426	9	AF062120	AF062120 Homo sapi
18	256.2	70.0	420	9	HUMIGHRH	M99607 Human (clon
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22	255.6	69.8	363	9	HSU244946	AJ244946 Homo sapi
23	255.6	69.8	363	9	HSU279549	AJ279549 Homo sapi
24	255.6	69.8	420	9	HSIGHXX25	X65907 H. sapiens m
25	255.4	69.8	366	9	HSU80141	U80141 Human immun
26	255	69.7	403	12	AF452899	AF452899 Synthetic
27	254.4	69.5	468	9	HUMIGHZF	L29122 Human immun
28	254.2	69.5	364	9	HSU80125	U80125 Human immun
29	254.2	69.5	466	9	MMU57582	U57582 Macaca mula
30	254.2	69.5	466	9	MMU57583	U57583 Macaca mula
31	254	69.4	375	9	HSU389176	AJ389176 Homo sapi
32	253.8	69.3	412	12	AF452934	AF452934 Synthetic
33	252.4	69.0	363	9	HSU556684	AJ556684 Homo sapi
34	252.2	68.9	366	9	HSU80176	U80176 Human immun
35	251.8	68.8	414	9	HST22X26	Z75399 H. sapiens m
36	251	68.6	457	9	MMU57586	U57586 Macaca mula
37	250	68.3	354	9	HSU245015	AJ245015 Homo sapi
38	249.6	68.2	414	9	HSIGHXX23	X65905 H. sapiens m
39	249	68.0	486	9	AF417843	AF417843 Homo sapi
40	248.4	67.9	354	9	HSU245026	AJ245026 Homo sapi
41	248	67.8	423	9	HST14X12	Z75364 H. sapiens m
42	248	67.8	435	9	MMU57566	U57566 Macaca mula
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ALIGNMENTS

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LOCUS
DEFINITION
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ACCSSION
AP416358
VERSION
AP416358.1
KEYWORDS
PAPIO ANUBIS (olive baboon)
SOURCE
ORGANISM
PAPIO ANUBIS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Cercopitheciidae; Papio.
REFERENCE
1 (bases 1 to 435)
Scinicariello, F., Jayashankar, L. and Attanasio, R.

AP416358 435 bp mRNA linear PRI 27-MAR-2002
Papio cynocephalus anubis clone VH4-4 immunoglobulin heavy chain
variable region mRNA, partial cds.


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AF416359.1 GI:19744279
Papio anubis (olive baboon)
Papio anubis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Papio.
REFERENCE
1 (bases 1 to 441)
Scinicariello, F., Jayashankar, L. and Attanasio, R.
Baboon immunoglobulin variable region heavy chains: identification
of genes homologous to members of the human IGHV1-IGHV7 subgroups
Immunogenetics 53 (10-11), 815-820 (2002)
MEDLINE
21850497
PUBMED
11862381
REFERENCE
2 (bases 1 to 441)
Scinicariello, F., Jayashankar, L. and Attanasio, R.
Direct Submission
TITLE
Submitted (04-SEP-2001) Department of Biology, Georgia State
University, PO BOX 4010, Atlanta, GA 30302, USA
JOURNAL
Location/Qualifiers
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/clone="VH4-7"
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Best Local Similarity 84.9%; Pred. No. 2.3e-67;
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HSA279514 363 bp mRNA linear PRI 01-JUN-2000
LOCUS
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region, partial, clone CD271ow-2.
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VERSION AJ279514.1 GI:6723525
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region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
Dono, M., Zupo, S., Leanza, N., Melioli, G., Fogli, M., Melagrana, A.,
Chiorazzi, N. and Ferrarini, M.
Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic
marginal zone equivalents
J. Immunol. 164 (11), 5596-5604 (2000)
MEDLINE
20281644
PUBMED
10820234
REFERENCE
2 (bases 1 to 363)
Dono, M.
Direct Submission
TITLE
Submitted (11-JAN-2000) Dono M., Istituto Nazionale per la Ricerca
sul Cancro, Immunologia Clinica, L.go Rosanna benzi 10- Genova,
ITALY
JOURNAL
Location/Qualifiers
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ORIGIN
Query Match 73.3%; Score 268.4; DB 9; Length 363;
Best Local Similarity 85.2%; Pred. No. 6.6e-67;
Matches 312; Conservative 0; Mismatches 51; Indels 3; Gaps 1;
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Qy 121 CCCCAGGAGGAGTGGAGTGGAGTGGATCTCTGTAGTGGTGGGGCCACCAAC 180
Db 121 CCCCAGGAGGAGTGGAGTGGAGTGGATCTCTATCATATTTTCAAGACAGTTC 177
Qy 181 TACAACCCCTCCCTCAAGAGTCGAGTCAATCATATTTTCAAGACAGTTC 240
Db 178 TACAACCCCTCCCTCAAGAGTCGAGTCAATCATATTTTCAAGACAGTTC 237
Qy 241 TCCCTGAACCTGAACCTGTGACCGCCGACACGCGCGTGTATTAATCTGTGCGAGAGAT 300
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Db      238 TCCCTGAAGCTGAGCTCTGTGACTGCCGCGACACGCGCGTGTATTACTGTGCCACGAT 297
Qy      301 TGGGCCCCAAATAGCTGGACACAGCTAGCTTCTGGGGCCAGGAGTCTCTGGTCAACGTC 360
Db      298 TCGTATTACGAATTTTGGAGTGGAAAGGAGTCTGGGGCCAGGGACACCTTGGTCAACGTC 357
Qy      361 TCCTCA 366
Db      358 TCCTCA 363

RESULT 5
LOCUS   HSU80179
DEFINITION Human immunoglobulin heavy chain variable region (V4-4b) gene, partial cds.
ACCESSION U80179
VERSION   U80179.1 GI:1791200
KEYWORDS Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
REFERENCE Glas,A.M., Nottenburg,C. and Milner,E.C.
AUTHORS   Glas,A.M., Nottenburg,C. and Milner,E.C.B.
TITLE     Direct Submission
JOURNAL   Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center, 1000 Seneca Street, Seattle, WA 98101, USA
MEDLINE   97182739
PUBMED    9030878
REFERENCE 2 (bases 1 to 363)
AUTHORS   Glas,A.M., Nottenburg,C. and Milner,E.C.B.
TITLE     Direct Submission
JOURNAL   Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center, 1000 Seneca Street, Seattle, WA 98101, USA
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gene      1. 363
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CDS       <1...>363
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BASE COUNT 76 a 108 c 108 g 71 t
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Matches 312; Conservative 0; Mismatches 51; Indels 3; Gaps 1;
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Qy      121 CCCCAGGGAAGGACTGGAGTGGATTGGACGTATCTCTGTAGTGTGGGGCCACCAAC 180
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Db      238 TCCCTGAAGCTGAGCTCTGTGACCGCGGACACGCGCTGTATTACTGTGCCAGAGGA 297
Qy      301 TGGGCCCAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGAGTCTCTGGTCAACGTC 360
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Qy      361 TCCTCA 366
Db      358 TCCTCA 363

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RESULT 6
LOCUS   MMU57560
DEFINITION Macaca mulatta Ig rearranged heavy chain variable region, anti-RBC antibody, mRNA, partial cds.
ACCESSION U57560
VERSION   U57560.1 GI:1575067
KEYWORDS Macaca mulatta (rhesus monkey)
SOURCE    Macaca mulatta
ORGANISM  Macaca mulatta
REFERENCE 1 (bases 1 to 420)
AUTHORS   Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Roubinet,F., Blancher,A. and Capra,J.D.
TITLE     Variable region gene segment utilization in rhesus monkey hybridomas producing human red blood cell-specific antibodies: predominance of the VH4 family but not VH4-21 (V4-34)
JOURNAL   Mol. Immunol. 34 (3), 237-253 (1997)
MEDLINE   97368199
PUBMED    9224966
REFERENCE 2 (bases 1 to 420)
AUTHORS   Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Blancher,A. and Capra,J.D.
TITLE     Direct Submission
JOURNAL   Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center, University of Texas Southwestern Medical Center, 6000 Harry Hines Blvd., Dallas, TX 75235-9140, USA
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Best Local Similarity 85.0%; Pred. No. 1.9e-66;
Matches 311; Conservative 0; Mismatches 52; Indels 3; Gaps 1;
Qy      1 CAGCTGCAGCTGCAGAGTCCGGGCCAGAGTGGTGAAGCCTTCGGAGACCTTCTCCTC 60

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JOURNAL
MEDLINE
PUBMED
REFERENCE
TITLE
AUTHORS
JOURNAL
J. Immunol. 164 (11), 5596-5604 (2000)
20281644
10820234
2 (bases 1 to 366)
Dono.M.
Direct Submission
Submitted (11-JAN-2000) Dono M., Istituto Nazionale per la Ricerca
sul Cancro, Immunologia Clinica, L.go Rosanna Benzi 10- Genova,
ITALY

FEATURES
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BASE COUNT
ORIGIN
72 a 109 c 114 g 78 t

Query Match 72.6%; Score 265.6; DB 9; Length 373;
Best Local Similarity 85.0%; Pred.No. 4.3e-66;
Matches 311; Conservative 0; Mismatches 49; Indels 6; Gaps 1;
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QY 361 TCCTCA 366
DB 368 TCCTCA 373

RESULT 9
HSA279520
LOCUS
DEFINITION
Homo sapiens mRNA for immunoglobulin mu heavy chain variable
region, partial, clone CD271low-8.
ACCESSION
VERSION
KEYWORDS
AJ279520.1
GI:6723537
IGM; IGM heavy chain; immunoglobulin mu heavy chain; variable
region.

SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
Dono, M., Zupo, S., Leanza, N., Melioli, G., Fogli, M., Melagrana, A.,
Chiorazzi, N. and Ferrarini, M.
TITLE
Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic
marginal zone equivalents

JOURNAL
MEDLINE
PUBMED
REFERENCE
TITLE
AUTHORS
JOURNAL
J. Immunol. 164 (11), 5596-5604 (2000)
20281644
10820234
2 (bases 1 to 366)
Dono.M.
Direct Submission
Submitted (11-JAN-2000) Dono M., Istituto Nazionale per la Ricerca
sul Cancro, Immunologia Clinica, L.go Rosanna Benzi 10- Genova,
ITALY

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Best Local Similarity 85.9%; Pred.No. 1.9e-65;
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QY 181 TACAACCCGTCCTCAAGAGTCGAGTCAATTTTCAAGACACGTCCTCAAGACAGTTC 240
DB 178 TACAACCCGTCCTCAAGAGTCGAGTCAATTTTCAAGACACGTCCTCAAGACAGTTC 237
QY 241 TCCCTGAACCTGAACTCTGTGACCGCCGCGACACGCGCTGTATTACTGTGCGCAGAGAT 300
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QY 358 GTCTCCTCA 366
DB 358 GTCTCCTCA 366

RESULT 10
HSU80180
LOCUS
DEFINITION
Human immunoglobulin heavy chain variable region (V4-4b) gene,

368 bp
DNA
linear
PRI 19-FEB-1997

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356	CCGTCCTCTCA	366
358	CCGTCCTCTCA	368
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Macaca mulatta Ig rearranged heavy chain variable region, anti-RBC antibody, mRNA, partial cds.		
U57565		
U57565.1	GI:1575077	
Macaca mulatta (rhesus monkey)		
Macaca mulatta		
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; Cercopitheciinae; Macaca.		
1 (bases 1 to 420)		
Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Roubinet,F., Blancher,A. and Capra,J.D.		
Variable region gene segment utilization in rhesus monkey hybridomas producing human red blood cell-specific antibodies: predominance of the VH4 family but not VH4-21 (V4-34)		
Mol. Immunol. 34 (3), 237-253 (1997)		
97368199		
9224966		
2 (bases 1 to 420)		
Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Blancher,A. and Capra,J.D.		
Direct Submission		
Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center, University of Texas Southwestern Medical Center, 6000 Harry Hines Blvd., Dallas, TX 75235-9140, USA		
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Best Local Similarity	84.2%;	Pred. No. 4.7e-65;
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61	ACCTGCGCTGTCTCTGGTGCTCTGTGTCAGCAGTAGTAACCTGGTGACCTGGATCCGCGAG	120
118	ACCTGCGCTGTCTCTGGTGCTCTCTTCAGC--AGTACTGGTGGGCTGGATCCGCGAG	174
121	CCCCAGGAGGAGGACTGGAGTGGATGGACGTATCTCTGGTAGTGGTGGGCCACCAAC	180
175	CCCCAGGAGGAGGCTGGAGTGGATGGAGTATCTATGGTAGTAGTGGGAGCACCAG	234
181	TACAACCCGTCCTCAAGAGTCGAGTCATCATTTTCAACAGACAGCTCCAAGAACCAAGTTC	240
235	TACAACCCCTCCCTCAAAAGTCGAGGCCACATTTTCAAGAGACAGCTCCAAGAACCAAGTTC	294

QY 241 TCCCTGAACCTGAACCTCTGTGACCGCCGCGACACGCGCGTGTATTACTGTGCCAGAGAT 300
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 QY 361 TCCTCA 366
 DB 415 TCCTCA 420

 RESULT 12
 LOCUS MMU57563 411 bp mRNA linear PRI 11-FEB-1998
 DEFINITION Macaca mulatta Ig rearranged heavy chain variable region, anti-RBC antibody, mRNA, partial cds.
 ACCESSION U57563
 VERSION U57563.1 GI:1575073
 KEYWORDS
 SOURCE Macaca mulatta (rhesus monkey)
 ORGANISM Macaca mulatta
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.
 REFERENCE 1 (bases 1 to 411)
 AUTHORS Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Roubinet, F., Blancher, A., and Capra, J.D.
 TITLE Variable region gene segment utilization in rhesus monkey hybridomas producing human red blood cell-specific antibodies: predominance of the VH4 family but not VH4-21 (V4-34)
 JOURNAL Mol. Immunol. 34 (3), 237-253 (1997)
 MEDLINE 97368199
 PUBMED 9224966
 REFERENCE 2 (bases 1 to 411)
 AUTHORS Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A., and Capra, J.D.
 TITLE Direct Submission
 JOURNAL Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center, University of Texas Southwestern Medical Center, 6000 Harry Hines Blvd., Dallas, TX 75235-9140, USA
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 Best Local Similarity 86.3%; Pred. No. 8.1e-65;
 Matches 316; Conservative 0; Mismatches 38; Indels 12; Gaps 2;

 QY 1 CAGCTGCAGCTGCAGAGTTCGGGCCAGGAGTGTGAAGCCCTTCGGAGACCCCTGTCCCTC 60
 DB 58 CAGGTGCAGCTGCAGAGTTCGGGCCAGGAGTGTGAAGCCCTTCGGAGACCCCTGTCCCTC 117
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 QY 361 TCCTCA 366
 Db 406 TCCTCA 411

 RESULT 13
 LOCUS HSA245032 363 bp mRNA linear PRI 01-JUN-2000
 DEFINITION Homo sapiens mRNA for immunoglobulin mu heavy chain variable region, partial, clone 1-F24.
 ACCESSION AJ245032
 VERSION AJ245032.1 GI:4995522
 KEYWORDS IGM; IGM heavy chain; immunoglobulin mu heavy chain; variable region.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1
 AUTHORS Dono, M., Zupo, S., Leanza, N., Melioli, G., Fogli, M., Melagrana, A., Chiorazzi, N., and Ferrarini, M.
 TITLE Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic marginal zone equivalents
 JOURNAL J. Immunol. 164 (11), 5596-5604 (2000)
 MEDLINE 20281644
 PUBMED 10820234
 REFERENCE 2 (bases 1 to 363)
 AUTHORS Dono, M.
 TITLE Direct Submission
 JOURNAL Submitted (24-MAY-1999) Dono M., Istituto Nazionale per la Ricerca sul Cancro, Immunologia Clinica, L.go Rosanna Benzi 10- Genova, ITALY
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Query Match 71.1%; Score 260.4; DB 9; Length 363;
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 Matches 307; Conservative 0; Mismatches 56; Indels 3; Gaps 1;

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 DB 178 TACAACCGTCCCTCAAGAGTCGAGTCATATCCGTAGACAGCTCCAAGAACGATTC 237

QY 241 TCCCTGAACCTGAACCTGTGACCGCGCACACGCGCGGTATTACTGTGCCAGAGAT 300
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 DB 298 GAGTATAGCAGCAGATTCACTGTTTGACCCCTGGGGCCAGGACCTGTGTCACCGTC 357

QY 361 TCCTCA 366
 DB 358 TCCTCA 363

RESULT 14
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 DEFINITION X65910 S59678
 ACCESSION X65910.1 GI:395108
 VERSION diversity region; Ig heavy chain; immunoglobulin; joining region;
 KEYWORDS variable region.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 AUTHORS Schiff, C.
 TITLE Direct Submission
 JOURNAL Submitted (08-APR-1992) C. Schiff, Centre D'Immunologie de
 Marseille, Case 906, 13288 Marseille, Cedex 9, FRANCE

REFERENCE 2 (bases 1 to 423)
 AUTHORS Millili, M., Le Deist, F., de Saint-Basile, G., Fischer, A.,
 Fougereau, M., and Schiff, C.
 TITLE Bone marrow cells in X-linked agammaglobulinemia express
 pre-B-specific genes (lambda-like and V pre-B) and present
 immunoglobulin V-D-J gene usage strongly biased to a fetal-like
 repertoire
 J. Clin. Invest. 91 (4), 1616-1629 (1993)

JOURNAL J9323287
 MEDLINE
 PUBMED 8473505

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 1. 57
 58. 353
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 Best Local Similarity 85.4%; Pred. No. 1.6e-64;
 Matches 315; Conservative 0; Mismatches 48; Indels 6; Gaps 2;

QY 1 CAGTGCAGCTGCAGGAGTCGGGCCAGGAGTGTGAAGCCTTCGGAGACCTGTCCCTC 60
 DB 58 CAGGTGCAGCTGCAGGAGTCGGGCCAGGAGTGTGAAGCCTTCGGAGACCTGTCCCTC 117

QY 61 ACCTGGCGTCTCTGTGGTCTCTCAGCAGTGTAACTGTCGACCTGATCCGCCAG 120
 DB 118 ACCTGGCGTCTCTGTGGTCTCTCAGCAGTGTAACTGTCGACCTGATCCGCCAG 177

QY 121 CCCCCAGGAAAGGAGTGGAGTGGAGTATCTCTGTAGTGGTGGGCCACCAAC 180
 DB 178 CCCCCAGGAAAGGAGTGGAGTGGAGTATCTATTATA---GTGGAGACCAAC 234

QY 181 TACAACCGTCCCTCAAGAGTCGAGTCATATTTTCAACAGACAGTCCTCAAGAACGATTC 240
 DB 235 TACAACCGTCCCTCAAGAGTCGAGTCATATTCAGTACAGTCCAAGAACGATTC 294

QY 241 TCCCTGAACCTGAACCTGTGACCGCGCACACGCGCGGTATTACTGTGCCAGAGAT 300
 DB 295 TCCCTGAAGCTGAGCTCTGTGACCGCGCACACGCGCGGTATTACTGTGCCAGAGAT 354

QY 301 TGGGCCCAATAGCTGG---AACAAAGCTAGGCTTCTGGGCCAGGAGTCTCTGTCACCC 357
 DB 355 TGGGATTTTGGAGTGGTATTCTTACTTGTACTTGGGCCAGGACCTGTGTCACC 414

QY 358 GTCTCCTCA 366
 DB 415 GTCTCCTCA 423

RESULT 15
 MMU57568
 LOCUS Macaca mulatta Ig rearranged heavy chain variable region, anti-RBC
 DEFINITION antibody, mRNA, partial cds.
 ACCESSION U57568
 VERSION U57568.1 GI:1575083
 KEYWORDS
 SOURCE Macaca mulatta (rhesus monkey)
 ORGANISM Macaca mulatta

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 Cercopitheidae; Macaca.
 AUTHORS Blumberg, P.M., Miller, A.B., Abraham, S.R., Cunningham, S., Roubinet, F.,
 and Capra, J.D.
 TITLE Variable region gene segment utilization in rhesus monkey
 hybridomas producing human red blood cell-specific antibodies:
 predominance of the VH4 family but not VH4-21 (V4-34)
 Mol. Immunol. 34 (3), 237-253 (1997)

JOURNAL J97368199
 MEDLINE
 PUBMED 9224966

REFERENCE 2 (bases 1 to 414)
 AUTHORS Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A.,
 and Capra, J.D.
 TITLE Direct Submission
 JOURNAL Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center,
 University of Texas Southwestern Medical Center, 6000 Harry Hines
 Blvd., Dallas, TX 75235-9140, USA

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Query Match      70.8%; Score 259.2; DB 9; Length 414;
Best Local Similarity 85.8%; Pred. No. 3.1e-64;
Matches 314; Conservative 0; Mismatches 43; Indels 9; Gaps 2;

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QY      58  CAGGTGCAGCTGCAGGAGTCGGGCCAGGACTGGTGAAGCCTTCGGAGACCCCTGTCCCTC 117
Db      58  |||||
QY      61  ACCTGCGCTGTCTCTGGTGGCTCTGTACAGTAGTAACTGGTGACCTGGATCGCCAG 120
Db      61  |||||
QY      118  ACCTGCGCTGTCTCTGGTTACTC---CATCAGCAGTAACCTGGAGCTGGATCGCCAG 174
Db      118  |||||
QY      121  CCCCAGGAGGAGGAGTGGAGTGGATTCGACGATATCTCTGGTAGTGGTGGGGCCACCAAC 180
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QY      175  CCCCAGGAGGAGGAGTGGAGTGGATTCGCTATATCTATGGTAGTGGGAGCGCCCTAC 234
Db      175  |||||
QY      181  TACAACCCGTCCTCAAGAGTCGAGTCATCTTCAAGACACGTCCTCAAGAACCCAGTTC 240
Db      181  |||||
QY      235  TACAACCCCTCCCTCAAGAGTCGAGTCACCATTTCAATAGACACGTCCTCAAGAACCCAGTTC 294
Db      235  |||||
QY      241  TCCCTGAACCTGAACCTCTGTACCGCCCGGACACGCGCGTGTATTACTGTGCCAGAGAT 300
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QY      295  TCCCTGAAGCTGAGCTCTGTGACCGCCGACAGACACGCGCGTCTATTACTGTGCCAGAGAT 354
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QY      355  -----CCCTACGGTCCACACATCTTTGACTACTGGGGCCAGGGAGTCTGGTCAACCGTC 408
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QY      361  TCCTCA 366
Db      361  |||||
QY      409  TCCTCA 414
Db      409  |||||
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Search completed: December 29, 2003, 19:01:25
Job time : 1517.15 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: December 29, 2003, 16:08:50 ; Search time 1593.73 Seconds
(without alignments)
5616.780 Million cell updates/sec

Title: US-09-019-441-2_COPY_58_423
Perfect score: 366
Sequence: 1 CAGCTGACGTGACGAGATC.....TCTGTGTCACCGTCTCCTCA 366

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: em_estba:*
2: em_estbm:*
3: em_estin:*
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5: em_estov:*
6: em_estpl:*
7: em_estro:*
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9: gb_estl:*
10: gb_est2:*
11: gb_hcc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	271.6	74.2	453	9 AW402337	AW402337 UI-HF-BK0
2	249.2	68.1	1036	13 BQ072430	BQ072430 AGENCOURT
3	247.4	67.6	524	13 BU429270	BU429270 UI-HF-BK0
4	246.4	67.3	680	14 CB551642	CB551642 MMSP0006

5	246	67.2	502	13	BX283435	BX283435
6	246	67.2	862	10	BG397580	BG397580 602438620
7	245.2	67.0	890	13	BX324929	BX324929 BX324929
8	244.2	66.7	921	13	BQ710000	BQ710000 AGENCOURT
9	243.6	66.6	867	10	BG685428	BG685428 602637281
10	242.6	66.3	925	13	BQ710876	BQ710876 AGENCOURT
11	241.6	66.0	532	2	HS070357	BX480350 Homo sapi
12	241	65.8	939	13	BQ708070	BQ708070 AGENCOURT
13	239.4	65.4	515	9	AW403935	AW403935 UI-HF-BK0
14	238.6	65.2	509	9	AW406349	AW406349 UI-HF-BK0
15	238.6	65.2	1058	13	BX337642	BX337642 BX337642
16	238.6	65.2	1201	13	BX365052	BX365052 BX365052
17	238.6	65.2	1201	13	BX396323	BX396323 BX396323
18	238.6	65.2	1201	13	BX399725	BX399725 BX399725
19	238.6	65.2	1201	13	BX439041	BX439041 BX439041
20	238.4	65.1	502	9	AW402706	AW402706 UI-HF-BK0
21	238.4	65.1	548	9	AW402602	AW402602 UI-HF-BK0
22	238	65.0	467	14	CB138507	CB138507 K-EST0191
23	238	65.0	527	14	CB147325	CB147325 K-EST0203
24	238	65.0	537	14	CB135937	CB135937 K-EST0188
25	238	65.0	552	14	CB135635	CB135635 K-EST0187
26	238	65.0	574	14	CB148794	CB148794 K-EST0205
27	238	65.0	588	14	CB146592	CB146592 K-EST0202
28	238	65.0	600	14	CB135761	CB135761 K-EST0188
29	238	65.0	603	14	CB121483	CB121483 K-EST0169
30	238	65.0	607	14	CB135254	CB135254 K-EST0187
31	237.8	65.0	1050	9	AL552672	AL552672 AL552672
32	236.2	64.5	1019	13	BQ072420	BQ072420 AGENCOURT
33	235.6	64.4	1201	13	BX377045	BX377045 BX377045
34	235.2	64.3	450	9	AW402094	AW402094 UI-HF-BK0
35	234.8	64.2	501	14	CB133184	CB133184 K-EST0183
36	234.6	64.1	447	9	AW402200	AW402200 UI-HF-BK0
37	234.6	64.1	904	13	BQ710488	BQ710488 AGENCOURT
38	234.6	64.1	1201	13	BX399940	BX399940 BX399940
39	234.4	64.0	955	13	BQ711653	BQ711653 AGENCOURT
40	233.6	63.8	647	14	CB553504	CB553504 MMSP0044
41	233.4	63.8	815	13	BX386888	BX386888 BX386888
42	233.2	63.7	798	12	BI771905	BI771905 603058919
43	233	63.7	495	9	AW403896	AW403896 UI-HF-BK0
44	233	63.7	850	10	BG686474	BG686474 602637417
45	233	63.7	915	13	BQ711871	BQ711871 AGENCOURT

ALIGNMENTS

RESULT 1

AW402337

LOCUS

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

UI-HF-BK0-aal-c-02-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
IMAGE:3053955 5', mRNA sequence.
453 bp mRNA linear EST 16-FEB-2000

AW402337
AW402337
AW402337.1 GI:6921023

EST.
Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 453)

NIH-MGC http://mgi.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgabs@email.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: M13 Forward.

FEATURES
source

Location/Qualifiers
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/lab_host="DH10B (LTI)"
/clone_lib="NIH MGC 36"
/note="Vector: pMT3-pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
88 a 145 c 129 g 91 t

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ORIGIN

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Best Local Similarity 85.8%; Pred. No. 4e-61;
Matches 314; Conservative 0; Mismatches 49; Indels 3; Gaps 1;
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Qy 121 CCCCAGGGAAGGAGCTGGAGTGGATTCAGAGTGTATCTCTGGTGTGGTGGGCCACCAAC 180
Db 158 CCCCAGGGAAGGAGCTGGAGTGGATTCAGAGTGTATCTATCATA---GTGGGAGCACCTAC 214
Qy 181 TACACCCGCTCCCTCAAGAGTCGAGTGCATCATTTTCAAGACACGCTCCAGAACCCAGTTC 240
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Qy 241 TCCCTGAACCTGAACCTGTGACCGCCGCGACACGCGCGTGTATTACTGTGCCAGAGAT 300
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Qy 301 TGGGCCCAATAGCTGGAAACACGCTAGGCTTCTGGGCCAGGAGTCTCTGGTCAAGCTC 360
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Qy 361 TCCTCA 366
Db 395 TCCTCA 400

RESULT 2
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LOCUS
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5', mRNA sequence.
ACCESSION BU072430
VERSION BU072430.1 GI:19901476
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1036)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1AM12810 row: h column: 21
High quality sequence stop: 626.

FEATURES
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Location/Qualifiers
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/clone_lib="NIH MGC 122"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site 1: NotI; Site 2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH MGC Library."
220 a 335 c 283 g 197 t 1 others

BASE COUNT
ORIGIN

Query Match 69.1%; Score 249.2; DB 13; Length 1036;
Best Local Similarity 83.9%; Pred. No. 4.4e-55;
Matches 307; Conservative 0; Mismatches 53; Indels 6; Gaps 2;
Qy 1 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 60
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Qy 121 CCCCAGGGAAGGAGCTGGAGTGGATTCAGAGTGTATCTCTGGTGTGGTGGGCCACCAAC 180
Db 193 CCCCAGGGAAGGAGCTGGAGTGGATTCAGAGTGTATCTATTTACA---GTGGGAGCACCAAC 249
Qy 181 TACACCCGCTCCCTCAAGAGTCGAGTGCATCATTTTCAAGACACGCTCCAGAACCCAGTTC 240
Db 250 TACACCCGCTCCCTCAAGAGTCGAGTGCATCATTTTCAAGACACGCTCCAGAACCCAGTTC 309
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Db 370 TGGAGCAGCAGCTGGTACCGGTGGTTCGACCCCTGGGGCCAGGGAACCTGTGTCACCGTC 429
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Db 430 TCCTCA 435

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UI-HF-BNO-aeq-c-02-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone
IMAGE:3065067 5', mRNA sequence.
ACCESSION BU429270
VERSION BU429270.1 GI:22767757
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 524)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished.
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 CDNA Library Preparation: Louis M. Staudt, M.D., Ph.D.
 CDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: M13 Forward.
 Location/Qualifiers
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 /notes="Vector: p77T3-Pac; Site 1: NotI; Site 2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (3.5-4.4kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

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Qy	61	ACCTGCGCTGCTCTGGTGGCTCTGTGACAGTAGTA---ACTGGTGACCTGGATCCGC	117	
Db	99	ACCTGCACTGCTCTGGTGGCTCTCATCAGCAGTAGTAGTACTTCTGGGGTGGATCCGC	158	
Qy	118	CAGCCCCCAGGGAAGGAGCTGGAGTGGATGGACGTATCTCTGGTAGTGGTGGGGCCACC	177	
Db	159	CAGCCCCCAGGGAAGGAGCTGGAGTGGATGGAGTATCTATATCTG---GAGCAC	215	
Qy	178	AACACACACCCCTCCCTCAGAGTCGAGTCATCTTTCACAGACACGTCACAGACCCAG	237	
Db	216	TACTACACCCCTCCCTCAGAGTCGAGTCATCTTTCACAGACACGTCACAGACCCAG	275	
Qy	238	TTCTCCCTGAACCTGAACCTGTGACCCCGGACACGGCGGTGATTACTGTGCCAGA	297	
Db	276	TTCTCCCTGAACCTGAGCTGTGTGACCCCGGACACGGCGGTGATTACTGTGCCAGA	335	
Qy	298	GATTGGGCCCAATAGCTG-----GAACACGCTAGGCTTTCTGGGGCCAGGAGTCCTG	351	
Db	336	CATTGGGCTTGGAGTGGGAGCAACACACCGGTGGGCCCTTGGGGCCAGGAAACCTG	395	
Qy	352	GTACCGCTCTCTCA	366	
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DEFINITION	MMSPO006 D02 MMSP Macaca mulatta cdna, mRNA sequence.			
ACCESSION	CB551642			
VERSION	CB551642.1	GI:31300837		
KEYWORDS	EST.			

Macaca mulatta (rhesus monkey)
 Macaca mulatta
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 Cercopitheidae; Macaca.
 1 (bases 1 to 680)
 Katze, M.G., Bungarner, R., Korth, M., Feldman, R., Amjadi, M. and
 Holzman, T.
 Expressed sequence tags from Rhesus macaque spleen
 Unpublished
 COMMENT Contact: Holzman T
 Katze Lab
 University of Washington
 Box 358070, Seattle, WA 98195-8070, USA
 Tel: 206 732 6156
 Fax: 206 732 6055
 Email: ted@locke.hs.washington.edu
 Similar to GenBank entry AF062240 Af062240 Homo sapiens clone
 23u-44 immunoglobulin heavy chain variable region (IGH) mRNA,
 partial cds. 5/2001
 Plate: MMSP0006 row: D column: 02.
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 /cell_type="monocytes"
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 Best Local Similarity 93.3%; Pred. No. 2e-54;
 Matches 280; Conservative 0; Mismatches 16; Indels 4; Gaps 2;
 Qy 1 CAGCTGCAGCTCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCTC 60
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 Qy 61 ACCTGCGCTGCTCTGGTGGCTCTGTGACAGTAGTAACCTGGTGACCTGGATCCGCCAG 120
 Db 114 ACCTGCGCTGCTCTGGTGGCTC---CATCAGCAGTAACCTGGATCCGCCAG 170
 Qy 121 CCCCCAG-GGAAGGAGCTGGAGTGGATTGACGTATCTCTGGTAGTGGTGGGCCACCA 179
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 IMAGE:4565020, mRNA sequence.
 ACCESSION BX283435
 VERSION BX283435.1
 KEYWORDS GI:28847889
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 502)
 Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,
 AUTHORS

Radelof, U., Schneider, D. and Korn, B.
 Human Unigeneset - RZPD3
 Unpublished
 Contact: Ina Rolfs
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
 RZPD: IMAGP958G051281.
 RZPDLIB; I.M.A.G.E. CDNA Clone Collection;
 Human Unigeneset - RZPD3 (RZPDLIB No.972)
<http://www.rzpd.de/cloneCards/cgi-bin/showLib.pl.cgi?response?libNo=972> Contact: Ina Rolfs
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Heubnerweg 6, D-14059 Berlin, Germany
 Tel: +49 30 32639 101
 Fax: +49 30 32639 111
 www.rzpd.de
 This clone is available royalty-free from RZPD;
 contact RZPD (clone@rzpd.de) for further information. Seq primer:
 PCMV-M13u, Primer sequence: CCGTGTAAACGACGGCCAGT.

FEATURES

source
 1..502
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGP958G051281 ; IMAGE:4565020"
 /tissue_type="primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 48"
 /note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGACGAG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH MGC Library."
 108 a 149 c 144 g 101 t

BASE COUNT

ORIGIN
 Query Match 67.2%; Score 246; DB 13; Length 502;
 Best Local Similarity 83.3%; Pred. No. 2.3e-54;
 Matches 305; Conservative 0; Mismatches 55; Indels 6; Gaps 2;
 QY 1 CAGCTGCAGCTGCAGAGTCGGGCCAGGAGTGTGAAGCCTTCGGAGACCCCTGTCCCTC 60
 Db |||||
 QY 61 ACCTCGCTGTCTCTGGTGGCTCTGCAGCAGTAGTAACTGGTGGACCTGGATCGCCAG 120
 Db |||||
 QY 140 ACCTCGCTGTCTCTGGTGGCTTCCATCAGCAGTAGTAACTGGTGGATGGGTCCGCCAG 199
 Db |||||
 QY 121 CCCCAGGAGGAGGACTGGAGTGGATTGGAAGTATCTCTGGTAGTGGTGGGGCCACCAAC 180
 Db |||||
 QY 200 CCCCAGGAGGAGGCTGGAGTGGATTGGGGAATCTATCATA---GTGGGAGACCAAC 256
 Db |||||
 QY 181 TACAACCCGCTCCCTCAAGAGTCGAGTCATCATTTTCAAGAAGACAGCTTCAAGAACAGGTTTC 240
 Db |||||
 QY 257 TACAACCCGCTCCCTCAAGAGTCGAGTCATCATATCAGTAGACAGTCCAAAGAACAGGTTTC 316
 Db |||||
 QY 241 TCCCTGAACCTGAACCTCTGTACCCCGGACACGGCCGTGTATTACTGTGGCAGAGAT 300
 Db |||||
 QY 317 TCCCTGAAGCTGAGCTCTGTGACCCCGGACACGGCCGTGTATTACTGTGGCAGAG---T 373
 Db |||||
 QY 301 TGGGCCCAATAGCTGGAAACAAACGCTAGGCTTCTGGGGCCAGGGAGTCTCTGGTCAACCGTC 360
 Db |||||
 QY 374 CTGGGAGACATCTACTACTACGGTATGACCGTCTCTGGGCCCAAGGACCAACCGTCAACCGTC 433
 Db |||||
 QY 361 TCCTCA 366
 Db |||||
 QY 434 TCCTCA 439

RESULT 6

BG397580
 LOCUS 602438620F1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4565020 5',
 DEFINITION mRNA sequence.
 ACCESSION BG397580
 VERSION BG397580.1 GI:13291028
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 1 (bases 1 to 862)
 REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgapbs-remail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 DNA distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LICM1281 row: g column: 05
 High quality sequence stop: 827.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 48"
 /note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGACGAG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH MGC Library."
 210 a 262 c 244 g 146 t

BASE COUNT

ORIGIN
 Query Match 67.2%; Score 246; DB 10; Length 862;
 Best Local Similarity 83.3%; Pred. No. 2.8e-54;
 Matches 305; Conservative 0; Mismatches 55; Indels 6; Gaps 2;
 QY 1 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGTGAAGCCTTCGGAGACCCCTGTCCCTC 60
 Db |||||
 QY 80 CAGTGCAGCTGCAGGAGTCGGGCCAGGAGTGTGAAGCCTTCGGGAGCCCTGTCCCTC 139
 Db |||||
 QY 61 ACCTCGCTGTCTCTGGTGGCTCTGTGACGAGTAGTAACTGGTGGACCTGGATCGCCAG 120
 Db |||||
 QY 140 ACCTCGCTGTCTCTGGTGGCTTCCATCAGCAGTAGTAACTGGTGGAGTGGGTCCGCCAG 199
 Db |||||
 QY 121 CCCCAGGAGGAGGACTGGAGTGGATTGGAAGTATCTCTGTAGTGGTGGGGCCACCAAC 180
 Db |||||
 QY 200 CCCCAGGAGGAGGCTGGAGTGGATTGGGGAATCTATCATA---GTGGGAGACCAAC 256
 Db |||||
 QY 181 TACAACCCGCTCCCTCAAGAGTCGAGTCATCATTTTCAAGAAGACAGTCCAAAGAACAGGTTTC 240
 Db |||||
 QY 257 TACAACCCGCTCCCTCAAGAGTCGAGTCATCATATCAGTAGACAGTCCAAAGAACAGGTTTC 316
 Db |||||
 QY 241 TCCCTGAACCTGAACCTCTGTGACCCCGGACACGGCCGTGTATTACTGTGGCAGAGAT 300
 Db |||||
 QY 317 TCCCTGAAGCTGAGCTCTGTGACCCCGGACACGGCCGTGTATTACTGTGGCAGAG---T 373
 Db |||||
 QY 301 TGGGCCCAATAGCTGGAAACAAACGCTAGGCTTCTGGGGCCAGGGAGTCTCTGGTCAACCGTC 360
 Db |||||

Db	355	TTCTCCCTGAGGCTGTACTGTGTACCGCCGGCACGCCCGCTGTATTACTGTGCGAGT	414
Qy	298	GATTG- <u>GGCCCCAATAAGCTGGAAACAACGC--TAGGGTTCTTGCGGCCAGGAGTCCTGGTC</u>	354
Db	415	GGTTGTAGTGGTGATAGCTGCTACCTCGCCTTTGACTACTCTGGGGCCAGGAACCTGGTC	474
Qy	355	ACCGTCTCCTCA	366
Db	475	ACCGTCTCCTCA	486

RESULT 8
BQ710000
LOCUS
DEFINITION BQ710000 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6302029 5'', mRNA sequence.

ACCESSION BQ710000
VERSION BQ710000.1 GI:21848899
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 921)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCW2518 row: n column: 14
High quality sequence start: 10
High quality sequence stop: 604.

FEATURES
Location/Qualifiers
1..921
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6302029"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_113"
 /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAACAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."

BASE COUNT 186 a 313 c 244 g 176 t 2 others
ORIGIN

Query Match 66.7%; Score 244.2; DB 13; Length 921;
Best Local Similarity 82.7%; Pred. No. 8.6e-54;
Matches 305; Conservative 0; Mismatches 58; Indels 6; Gaps 2;

Qy	1	CAGCTCAGCTGCAGAGTCGGGCCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC	60
Db	70	CAGCTGCAGCTGCAGAGTCGGGCCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTC	129
Qy	61	ACCTGGCGCTGTCTCTGGTGGCTCTGTGCAGCAGTAGTA---ACTGGTGGACCTGGATCCGC	117
Db	130	ACCTGCAGCTGTCTCTGGTGGCTCATCAGCAGTAGTAGTACTACTCTGGGCTGGATCCGC	189
Qy	118	CAGCCCCCAGGGAAGGGACTGGAGTGGATGGACGTATCTCTGGTACTGTGGTGGGCCACC	177
Db	190	CAGCCCCCAGGGAAGGGGTGGAGTGGATGGGAGTATCTATTTTACT---GGGACCCAC	246

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QY 178 AACTACAAACCGTCCCTCAGAGTCGAGTCATATTTTCAAGACACGTCCTCAAGAACCCAG 237
Db 247 TACTACAAACCGTCCCTCAGAGTCGAGTCATATTTTCAAGACACGTCCTCAAGAACCCAG 306

QY 238 TTCTCCCTGAACTGAACTCTGTGACCGCCGCGGACACGCGCGTGTATTACTGTGCCAGA 297
Db 307 TTCTCCCTGAACTGAGCTCTGTGACCGCCCTCAGACACGCGTGTATTACTGTGCCAGC 366

QY 298 GATTGGGCCCCAAATAGCTGGAACACGCTAGGCTTCTGGGGCCAGGGAGTCTGTGTCACC 357
Db 367 ACTAAGTACGGTGGTAACTTAACTGCTTTCAGCCCTCGGGCCAGGGAACCTGTGTCACC 426

QY 358 GTCTCCTCA 366
Db 427 GTCTCCTCA 435

RESULT 9
LOCUS BG685428 867 bp mRNA linear EST 01-MAY-2001
DEFINITION 602637281F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4764956 5',
mRNA sequence.
ACCESSION BG685428
VERSION BG685428.1 GI:13916825
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 867)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LNCM1623 row: a column: 21
High quality sequence stop: 637.
FEATURES
source
1..867
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4764956"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 48"
/note="Organ: B-cells; Vector: pOTB7; Site:1: XhoI;
Site:2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."
BASE COUNT 216 a 263 c 245 g 143 t
ORIGIN
Query Match 66.6%; Score 243.6; DB 10; Length 867;
Best Local Similarity 82.8%; Pred. No. 1.2e-53; Mismatches 59; Indels 4; Gaps 2;
Matches 303; Conservative 0;

QY 1 CAGCTGCAGCTGCAGAGTCGGGCCAGGAGTGGTGAAGCCCTTCGGAGACCTGTCCCTC 60
Db 80 CAGGTGCAGCTGCAGAGTCGGGCCAGGAGTGGTGAAGCCCTTCGGGACCTGTCCCTC 139

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QY 61 ACCTGGGCTCTCTCTGGTGGCTCTGTCTCAGCAGTAGTAACATGGTGGAGCTGGATCCGCCAG 120
Db 140 ACCTGGGCTCTCTCTGGTGGCTCCATCAGCAGTAGTAACATGGTGGAGTGGTGGTCCGCCAG 199

QY 121 CCCCCAGGGAAGGAGCTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAAC 180
Db 200 CCCCCAGGGAAGGAGCTGGAGTGGATTGGGGAATCTATCATAGTG--GGAGCACACAAC 257

QY 181 TACAACCCGTCCTCAGAGTCGAGTCATCATTTTCAAGACACGTCCTCAAGAACCAAGTTC 240
Db 258 TACAAGCCGTCCTCAGAGTCGAGTCATCATTTTCAAGAACCAAGTTC 317

QY 241 TCCTGAACCTGAACCTCTGTGACCGCCGCGGACACACGCGCTGTATTACTGTGCCAGAGAT 300
Db 318 TCCTGAAGCTGAGCTCTGTGACCGCCGCGGACACACGCGCTGTATTACTGTGCCAGATCT 377

QY 301 TGGGCCCAATAGCTGGAACACGCTAGGCTTCTGGGGCCAGGAGTCTGTGGTCCACGTC 360
Db 378 GGGAGACATCTACTACTA--CGGTATGGACGCTCTGGGGCCAGGAGTCCACGTC 435

QY 361 TCCTCA 366
Db 436 TCCTCA 441

RESULT 10
LOCUS BQ710876 925 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT 8485057 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301263
5', mRNA sequence.
ACCESSION BQ710876
VERSION BQ710876.1 GI:21849775
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 925)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LNCM2516 row: n column: 16
High quality sequence stop: 560.
FEATURES
source
1..925
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6301263"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 113"
/note="Organ: spleen; Vector: pOTB7; Site:1: XhoI; Site:2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
BASE COUNT 171 a 337 c 239 g 178 t
ORIGIN
Query Match 66.3%; Score 242.6; DB 13; Length 925;

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6301745"
/lab_host="NIH MGC 113"
/clone_lib="NIH MGC 113"
/notes="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."
BASE COUNT      206 a   308 c   246 g   179 t
ORIGIN
Query Match      65.8%; Score 241; DB 13; Length 939;
Best Local Similarity 82.1%; Pred. No. 6e-53;
Matches 303; Conservative 0; Mismatches 60; Indels 6; Gaps 2;
QY 1 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGTGAAGCCTTCGGAGACCTGTCCCTC 60
DB 80 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGTGAAGCCTTCGGAGACCTGTCCCTC 139
QY 61 ACCTGCGCTGTCTGTGGTCTGTCTCAGCAG---TAGTAACTGTGTGACCTGGATCCGC 117
DB 140 ACCTGCATCTGTCTGTGGTCTGTCTCAGCAGTAAATAAATACTCTGGGGCTGGATCCGC 199
QY 118 CAGCCCCAGGGAAGGAGCTGAGTGGATTTGGACGTATCTCTGTGTAGTGTGGGGCCACC 177
DB 200 CAGCCCCAGGGAAGGAGCTGAGTGGATTTGGAAATATCTATTATA---GTGGGAGCACC 256
QY 178 AACTACAAACCCGTCCCTCAAGAGTCGAGTCATCATTTCAAGACACATCCCAAGAACCG 237
DB 257 TACTACAAACCCGTCCCTCAAGAGTCGAGTCACCATATCCGTAGACACATCCCAAGAACCA 316
QY 238 TTCTCCCTGAACTGAATCTGTGACCCCGGACAGCGCGTGTATTCTGTGCCAGA 297
DB 317 TTCTCCCTGAACTGAATCTGTGACCCCGGACAGCGCGTGTATTCTGTGCCAGG 376
QY 298 GATTGGGCCAAATAGCTGGAAACACGCTAGGCTTTCTGGGGCCAGGAGTCTGTGTACC 357
DB 377 ACCGATTAACTGGGGCCAGAGAGTTTGTACTACTGGGGCCAGGAGTCTGTGTACC 436
QY 358 GTCTCCTCA 366
DB 437 GTCTCCTCA 445

RESULT 13
AW403935
LOCUS
DEFINITION
UI-HF-BK0-abn-g-08-0-UI.r1 NIH MGC_36 Homo sapiens cDNA clone
IMAGE:3056847 5', mRNA sequence.
ACCESSION
AW403935
VERSION
AW403935.1 GI:6922902
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 515)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6301745"
/lab_host="NIH MGC 113"
/clone_lib="NIH MGC 113"
/notes="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."
BASE COUNT      206 a   308 c   246 g   179 t
ORIGIN
Query Match      65.8%; Score 241; DB 13; Length 939;
Best Local Similarity 82.1%; Pred. No. 6e-53;
Matches 303; Conservative 0; Mismatches 60; Indels 6; Gaps 2;
QY 1 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGTGAAGCCTTCGGAGACCTGTCCCTC 60
DB 80 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGTGAAGCCTTCGGAGACCTGTCCCTC 139
QY 61 ACCTGCGCTGTCTGTGGTCTGTCTCAGCAG---TAGTAACTGTGTGACCTGGATCCGC 117
DB 140 ACCTGCATCTGTCTGTGGTCTGTCTCAGCAGTAAATAAATACTCTGGGGCTGGATCCGC 199
QY 118 CAGCCCCAGGGAAGGAGCTGAGTGGATTTGGACGTATCTCTGTGTAGTGTGGGGCCACC 177
DB 200 CAGCCCCAGGGAAGGAGCTGAGTGGATTTGGAAATATCTATTATA---GTGGGAGCACC 256
QY 178 AACTACAAACCCGTCCCTCAAGAGTCGAGTCATCATTTCAAGACACATCCCAAGAACCG 237
DB 257 TACTACAAACCCGTCCCTCAAGAGTCGAGTCACCATATCCGTAGACACATCCCAAGAACCA 316
QY 238 TTCTCCCTGAACTGAATCTGTGACCCCGGACAGCGCGTGTATTCTGTGCCAGA 297
DB 317 TTCTCCCTGAACTGAATCTGTGACCCCGGACAGCGCGTGTATTCTGTGCCAGG 376
QY 298 GATTGGGCCAAATAGCTGGAAACACGCTAGGCTTTCTGGGGCCAGGAGTCTGTGTACC 357
DB 377 ACCGATTAACTGGGGCCAGAGAGTTTGTACTACTGGGGCCAGGAGTCTGTGTACC 436
QY 358 GTCTCCTCA 366
DB 437 GTCTCCTCA 445

RESULT 14
AW406349
LOCUS
DEFINITION
UI-HF-BL0-aco-h-03-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3059933 5', mRNA sequence.
ACCESSION
AW406349
VERSION
AW406349.1 GI:6925406
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 509)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

```

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbr/image/image.html

Seq primer: M13 Forward.

FEATURES

source

1. 515
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3056847"
 /tissue_type="lymph"
 /cell_type="germinal center B cells"
 /cell_line="MGC85"
 /lab_host="DH10B (LTI)"
 /clone_lib="NIH MGC 36"
 /notes="Vector: pT7f3-Pac; Site 1: NotI; Site 2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 103 a 158 c 145 g 109 t

ORIGIN

Query Match 65.4%; Score 239.4; DB 9; Length 515;
 Best Local Similarity 90.2%; Pred. No. 1.3e-52;
 Matches 268; Conservative 0; Mismatches 26; Indels 3; Gaps 1;
 QY 1 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGTGAAGCCTTCGGAGACCTGTCCCTC 60
 DB 15 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGTGAAGCCTTCGGAGACCTGTCCCTC 74
 QY 61 ACCTGCCCTGTCTGTGTGCTCTGTCTCAGCAGTAGTAACCTGGTGGACCTGGATCCGCCAG 120
 DB 75 ACCTGCACTGTCTGTGTGCTCTCATCAGCAGTAGTAACCTGGTGGAGTGGTCCGCCAG 134
 QY 121 CCCCACGGAAGGAGCTGGAGTGGATTCCTCTGTGTAGTGTGGGGCCACCAC 180
 DB 135 CCCCACGGAAGGAGCTGGAGTGGATTCCTCTGTGTAGTGTGGGGCCACCAC 191
 QY 181 TACAGCCGCTCCCTCAGAGTCGAGTCATCATTTCAAGACACAGCTCCAGAACCACTTC 240
 DB 192 TACAACCCGCTCCCTCAGAGTCGAGTCATCATTTCAAGACAGTCCAGAACCACTTC 251
 QY 241 TCCCTGAACCTGAACCTCTGTGACCGCCGACACGCGCGTGTATTCTGTGCCAGA 297
 DB 252 TCCCTGAAGCTGAGCTCTGTGACCGCCGCGGACACGCGCGTGTATTCTGTGCCAGA 308

RESULT 14

LOCUS

DEFINITION
 UI-HF-BL0-aco-h-03-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
 IMAGE:3059933 5', mRNA sequence.

ACCESSION

VERSION

AW406349.1 GI:6925406

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 509)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab

cDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.lnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES

Location/Qualifiers

source

1..509
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3059933"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_lib="NIH MGC 37"

Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D.

BASE COUNT

94 a 171 c 146 g 98 t

ORIGIN

Query Match 65.2%; Score 238.6; DB 9; Length 509;
Best Local Similarity 84.0%; Pred. No. 2e-52;
Matches 310; Conservative 0; Mismatches 44; Indels 15; Gaps 3;

Qy 1 CAGCTGACGCTGCAGGAGTCCGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 60
Db 39 CAGCTGACGCTGCAGGAGTCCGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 98
Qy 61 ACCTGCGCTGTCTCTGGTGGCTCTGTCTCAGCAGTAGTA---ACTGGTGACCTGGATCCGC 117
Db 99 ACCTGCACTGTCTCTGGTGGCTCTCATCAGCAGTAGTAGTTACTACTGGGGCTGGATCCGC 158
Qy 118 CAGCCCCCAGGAGGAGCTGGAGTGGATTGGAGTATCTCTGTAGTGGTGGGGCCACC 177
Db 159 CAGCCCCCAGGAGGAGGCTGGAGTGGATTGGAGTATCTATTATA---GTGGGAGCACC 215
Qy 178 AACTACAAACCCGCTCCCTCAAGAGTCGAGTCATCATTTTCAAGACACACGTCCTCAAGACCCAG 237
Db 216 TACTACAAACCCGCTCCCTCAAGAGTCGAGTCATCATTTTCAAGACACACGTCCTCAAGACCCAG 275
Qy 238 TTCTCCCTGAAACCTGAACTGTGACCCGCCGACACGCGCGTGTATTACTGTGCCAGA 297
Db 276 TTCTCCCTGAAAGCTGAGCTGTGACCCGCCGACACGCGCGTGTATTACTGTGCCAGA 335
Qy 298 GATTGGGCCCAATAGCTGGAACACGCTAGCTTCTGGGGCCAGGAGTCTCTGTCCACC 357
Db 336 CCCTCTCTAC-----GGACCTGTGTCACCCCTGGGGCCAGGAAACCTGTGTACC 386
Qy 358 GTCTCCTCA 366
Db 387 GTCTCCTCA 395

RESULT 15

BX337642

LOCUS

BX337642 1058 bp mRNA linear EST 01-MAY-2003
DEFINITION BX337642 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1044YB21 5-PRIME, mRNA sequence.

ACCESSION

BX337642

VERSION

BX337642.1

KEYWORDS

EST

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1058)

Li W.B., Gruber C., Jessee J. and Polayes D.

Full-length cDNA libraries and normalization

Unpublished

JOURNAL

COMMENT

Contact: Genoscope
Genoscope - Centre National de Sequenage
BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7198.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0D1044CAL1Q1&cluster=7198.r. Contact :
Peng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0D1044CAL1Q1.

FEATURES

Location/Qualifiers

source

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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="CS0D1044YB21"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 214 a 327 c 283 g 216 t 18 others
ORIGIN

Query Match 65.2%; Score 238.6; DB 13; Length 1058;
Best Local Similarity 81.1%; Pred. No. 2.7e-52;
Matches 309; Conservative 0; Mismatches 54; Indels 18; Gaps 2;

Qy 1 CAGCTGACGCTGCAGGAGTCCGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 60
Db 150 CAGCTGACGCTGCAGGAGTCCGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 209
Qy 61 ACCTGCGCTGTCTCTGGTGGCTCTGTCTCAGCAGTAGTAACCTGGTGACCTGGATCCGCAG 120
Db 210 ACCTGCACTGTCTCTGGTGGCTCTCATCAGCAGTGGTGTACTACTGGGGCTGGATCCGCAG 269
Qy 121 CCCCAGGGAAGGAGCTGGAGTGGATTGGAGTATCTCTGTAGTGGTGGGGCCACCAC 180
Db 270 CCCCAGGGAAGGAGCTGGAGTGGATTGGAGTATCTATCATA---GTGGGAGCACCTAC 326
Qy 181 TACAAACCCGCTCCCTCAAGAGTCGAGTCATCATTTTCAAGACACACGTCCTCAAGAACAGTTTC 240
Db 327 TACAACCCGCTCCCTCAAGAGTCGAGTCATCATTTTCAAGACACGTCCTCAAGAACAGTTTC 386
Qy 241 TCCTGAACTGAACTCTGTGACCGCGGACACGCGCGTGTATTACTGTGCCAGAG-- 298
Db 387 TCCTGAACTGAGCTCTGTGACCGCGGACACGCGCGTGTATTACTGTGCCAGAGTT 446
Qy 299 -----ATTGGGCCCAATAGCTGGAAACACGCTAGGCTTTCTGGGGCCAGGGA 345
Db 447 CGGTATTACGATATTGTGACTCCCGGTTTAGCATCTCTGGTTTCGACCCCTGGGGCCAGGGA 506
Qy 346 GTCTGCTACCGTCTCTCTCA 366
Db 507 ACCTGCTACCGTCTCTCTCA 527

Search completed: December 29, 2003, 21:44:11
Job time : 1584.73 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 159.688 Seconds
(without alignments)
6187.013 Million cell updates/sec

Title: US-09-019-441-2_COPY_58_423

Perfect score: 366

Sequence: 1 CAGCTGACGCTGACGAGTCTCTCTCTCA 366

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq 19Jun03:*

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25: /SIDSI1/gcgdata/geneseq/geneseq-n-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	366	100.0	423	19	AAV333308 Anti-human CD23 6G
2	256.2	70.0	1431	18	AAT62513 Primatized anti-hu
3	256.2	70.0	1431	19	AAV35489 Macaque primatized
4	256.2	70.0	1431	24	AAS17247 DNA sequence of a
5	247.4	67.6	423	21	AAZ39331 Nucleotide sequenc
6	246	67.2	1404	18	AAT62868 Human gamma-4 heav
7	246	67.2	1404	18	AAT62869 Human gamma-4E hea
8	246	67.2	1404	18	AAT62870 Human gamma-4PE he

9	245	66.9	747	22	AAH76382	Nucleotide sequenc
10	244.4	66.8	423	14	AAQ35903	Anti-CD4 VH coding
11	244.4	66.8	423	18	AAT91564	Anti-CD4 cynomolgu
12	244.4	66.8	423	19	AAV31428	Anti-CD4 antibody
13	244.4	66.8	423	19	AAV05695	Monkey anti-CD4 he
14	244.4	66.8	423	25	ABX76616	DNA encoding cynom
15	244.2	66.7	619	22	AAS03048	Human diagnostic a
16	243.2	66.4	354	24	ABK24412	Heavy chain DNA fr
17	243	66.4	372	18	ABT54035	Human lung cancer
18	242.8	66.3	360	25	ABT57441	Human monoclonal a
19	242.8	66.3	363	24	ABA94218	ebvHgm MS19D10 h
20	242.8	66.3	420	21	AAT39335	Nucleotide sequenc
21	242.8	66.3	481	25	ABT31871	Anti-CD40 monoclon
22	242.6	66.3	614	20	AAV86218	EST clone O99. Ho
23	241.4	66.0	296	24	ABT62713	Germline anti-IGF-
24	241.4	66.0	420	18	AAT95167	Monkey anti-human
25	241.4	66.0	420	18	AAT62865	Monkey anti-CD4 he
26	241.4	66.0	420	19	AAV23760	Anti-CD4 antibody
27	241	65.8	294	20	AAZ25318	Multiple sclerosis
28	240	65.6	496	20	AAZ24416	Human bladder tumo
29	236.6	64.6	624	16	AAQ78966	Human immunoglobul
30	236.4	64.6	417	21	AAZ52907	Human LH11238 mono
31	236.2	64.5	840	22	AAD06194	PAM2 single chain
32	236.2	64.5	1634	21	AAZ50012	Human immune syste
33	235.4	64.3	358	24	ABS62723	Anti-IGF-IR antibo
34	235.4	64.3	1431	18	AAT62510	Primatized anti-hu
35	235.4	64.3	1431	19	AAV35485	Macaque primatized
36	235.4	64.3	1431	24	AAS17243	DNA sequence of a
37	234.6	64.1	366	14	AAQ33035	MAB 1-3-1 variable
38	234.4	64.0	351	21	AAZ49590	Human antibody clo
39	234.4	64.0	351	21	AAZ49608	DNA-1 related to h
40	234.2	64.0	1567	22	AAQ66522	Human immune syste
41	232.4	63.5	351	22	AAS03440	DNA encoding anti-
42	232.4	63.5	377	24	ABT73187	DNA encoding human
43	232.4	63.5	508	24	ABT73189	DNA encoding human
44	232.4	63.5	675	24	ABT73188	DNA encoding human
45	232.2	63.4	417	21	AAA13938	Human PTHrP monocl

ALIGNMENTS

RESULT 1

AAV333308

ID AAV333308 standard; DNA; 423 BP.

AC AAV333308;

XX 25-MAR-2003 (updated)

DT 18-NOV-1998 (first entry)

XX Anti-human CD23 6G5 monoclonal antibody heavy chain variable region DNA.

DE Anti-human CD23 6G5 monoclonal antibody; heavy chain variable region; human CD23; IGE; FcεRII/CD23; gamma-1 constant region;

XX human CD23; IGE; FcεRII/CD23; gamma-1 constant region;

KW gamma-3 constant region; allergy; inflammation; autoimmune disease;

KW allergic rhinitis; conjunctivitis; autoimmune haemolytic anaemia; ss.

XX Macaca fascicularis

OS Macaca fascicularis

XX Key Location/Qualifiers

PH 1..423

FT /*tag= a

FT /*product= "anti-human CD23 6G5 heavy chain variable region"

FT /*note= "CDS does not contain a stop codon"

FT sig_peptide 1..57

FT /*tag= b

FT mat_peptide 58..423

FT /*tag= c

FT misc_feature 148..165

FT /*tag= d

FT /*note= "encodes CDR 1 region"

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FT misc_feature 208..258
FT /*tag=e
FT /note= "encodes CDR 2 region"
XX
XX WO9837099-A1.
XX
XX 27-AUG-1998.
XX
XX 17-FEB-1998; 98WO-US02253.
XX
XX 20-FEB-1997; 97US-0803085.
XX
XX 05-FEB-1998; 98US-0019441.
XX
XX (IDEC-) IDEC PHARM CORP.
XX (SEKG) SEIKAGAKU CORP.
XX
XX Kloezer WS, Nakamura T, Reff ME;
XX
XX WPI; 1998-467495/40.
XX P-PSDB; AAW70378.
XX
XX New anti-human CD23 monoclonal antibody - used for inhibiting IgE
XX expression to treat or prevent allergic, inflammatory and
XX auto:immune conditions
XX
XX Example 1; Pages 104-106; 146pp; English.
XX
XX The present sequence represents a DNA sequence encoding the heavy
XX chain variable region of primate monoclonal antibody anti-human CD23 6G5.
XX The invention provides primate monoclonal antibodies which specifically
XX bind human CD23, the low affinity receptor for IgE (FcεRI/CD23), and
XX and comprise either of a human gamma-1 or human gamma-3 constant region
XX that binds to human Fc gamma receptors and inhibits IgE expression.
XX The monoclonal antibodies of the invention are claimed to be useful
XX for inhibiting induced IgE production for treating or preventing
XX allergic, inflammatory and autoimmune conditions e.g. allergic rhinitis
XX conjunctivitis, autoimmune haemolytic anaemia, etc.
XX (Updated on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 423 BP; 83 A; 128 C; 122 G; 90 T; 0 other;
XX
XX Query Match 100.0%; Score 366; DB 19; Length 423;
XX Best Local Similarity 100.0%; Pred. No. 2.2e-91;
XX Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CAGCTGCAGCTGCAGAGTCCGGCCAGAGTGGTGAAGCCCTTCGGAGACCCCTGTCCCTC 60
XX 58 CAGCTGCAGCTGCAGAGTCCGGCCAGAGTGGTGAAGCCCTTCGGAGACCCCTGTCCCTC 117
XX
XX 61 ACCTGCGCTGTCTCTGTGGTCTCTGTACAGAGTAGTAACTGGTGACCTGGATCGGCAG 120
XX 118 ACCTGCGCTGTCTCTGTGGTCTCTGTACAGAGTAGTAACTGGTGACCTGGATCGGCAG 177
XX
XX 121 CCCCAGGAAGGAGTGGAGTGGAGTCTCTGTAGTGGTGGGGCCACCAAC 180
XX 178 CCCCAGGAAGGAGTGGAGTGGAGTCTCTGTAGTGGTGGGGCCACCAAC 237
XX
XX 181 TACAACCCGCTCCCTCAAGAGTCGAGTCATCATTTTCAAGACACGCTCCAAAGACCAAGTTC 240
XX 238 TACAACCCGCTCCCTCAAGAGTCGAGTCATCATTTTCAAGACACGCTCCAAAGACCAAGTTC 297
XX
XX 241 TCCCTGAACCTGAATCTGTGACCGCCGAGACACGCGCGGTGTATTCTGTGCCAGAGAT 300
XX 298 TCCCTGAACCTGAATCTGTGACCGCCGAGACACGCGCGGTGTATTCTGTGCCAGAGAT 357
XX
XX 301 TGGGCCCCAAATAGCTGGACACGCTAGGCTTCCTGGGGCCAGGGAGTCTCTGTCAACGCTC 360
XX 358 TGGGCCCCAAATAGCTGGACACGCTAGGCTTCCTGGGGCCAGGGAGTCTCTGTCAACGCTC 417
XX
XX 361 TCCTCA 366
XX
XX 418 TCCTCA 423
```

```
RESULT 2
AAT62513
ID AAT62513 standard; DNA; 1431 BP.
XX
XX AAT62513;
XX
XX 25-MAY-1997 (first entry)
XX
XX Primatised anti-human B7.1 antigen antibody 16C10 heavy chain DNA.
XX
XX Monoclonal antibody; cynomolgus monkey; macaque; 16C10;
XX primatised antibody; B7 antigen; CD28; immunosuppressive;
XX autoimmune disease; idiopathic thrombocytopaenia purpura;
XX systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
XX type 1 diabetes mellitus; graft versus host disease;
XX hetero-hybridoma; transfectoma; ss.
XX
XX Chimeric Macaca cynomolgus;
XX Chimeric Homo sapiens.
XX
XX WO9640878-A1.
XX
XX 19-DEC-1996.
XX
XX 06-JUN-1996; 96WO-US10053.
XX
XX 07-JUN-1995; 95US-0487550.
XX (IDEC-) IDEC PHARM CORP.
XX
XX Anderson DR, Brams P, Hanna N, Shestowsky WS;
XX WPI; 1997-108638/10.
XX P-PSDB; AAW01822.
XX
XX Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
XX useful for treating autoimmune disease or graft-versus-host disease
XX
XX Claim 11; Fig 10B; 81pp; English.
XX
XX 2 DNA sequences (AAT62512 and AAT62513) respectively code for
XX primatised forms (AAW01821 and AAW01822) of the light and heavy chains
XX of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody
XX 16C10. Cloned 16C10 light and heavy variable genes are inserted
XX into an expression vector (pref. NEOSPLA) which contains human light
XX and heavy chain constant region genes to allow prodn. of primatised
XX antibody in e.g. CHO cells. Primatised 7C10 and 7B6 anti-B7.1
XX antibodies have also been produced (see also AAW01817-20). The
XX primatised antibodies inhibit the B7:CD28 pathway, making them
XX useful immunosuppressants for the treatment of autoimmune disorders
XX and graft-versus-host disease.
XX
XX Sequence 1431 BP; 319 A; 462 C; 385 G; 265 T; 0 other;
```

```
Query Match 70.0%; Score 256.2; DB 18; Length 1431;
Best Local Similarity 82.2%; Pred. No. 6.1e-61;
Matches 313; Conservative 0; Mismatches 53; Indels 15; Gaps 1;
XX
XX 1 CAGCTGCAGCTGCAGAGTCCGGCCAGAGTGGTGAAGCCCTTCGGAGACCCCTGTCCCTC 60
XX 58 CAGCTGCAGCTGCAGAGTCCGGCCAGAGTGGTGAAGCCCTTCGGAGACCCCTGTCCCTC 117
XX
XX 61 ACCTGCGCTGTCTCTGTGGTCTCTGTACAGAGTAGTAACTGGTGGACCTGGATCGGCAG 120
XX 118 ACCTGCGCTGTCTCTGTGGTCTCTGTACAGAGTAGTAACTGGTGGACCTGGATCGGCAG 177
XX
XX 121 CCCCAGGAAGGAGTGGAGTGGAGTCTCTGTAGTGGTGGGGCCACCAAC 180
XX 178 CCCCAGGAAGGAGTGGAGTGGAGTCTCTGTAGTGGTGGGGCCACCAAC 237
XX
XX 181 TACAACCCGCTCCCTCAAGAGTCCAGTCTCATTTTCAAGACACGCTCCAAAGACCAAGTTC 240
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Db 238 TACAACCCCTCCCTCAAGAGTCAAGTCAACCATTTCAACAGACAGCTCAAGAACCCAGTTC 297
 Qy 241 TCCTGAACTGAACCTGTGACCGCGGACACCGCGCTGTATTACTGTGCCAGAGAT 300
 Db 298 TCCTGAACTGAACCTGTGACCGCGGACACCGCGCTGTATTACTGTGTGAGAGAT 357
 Qy 301 TGGGCCCAATAGCTGGAAACA-----CGTAGGCTTCTGGGGCCAGGGA 345
 Db 358 CGTCTTTTTCAGTTGTGGATGTTTACAACTGTTTCGATGTCTGGGCGCCGGGA 417
 Qy 346 GTCTGTGTACCGTCTCTCA 366
 Db 418 GTCTGTGTACCGTCTCTCA 438
 RESULT 3
 AAV35489
 ID AAV35489 standard; DNA; 1431 BP.
 AC AAV35489;
 XX 29-SEP-1998 (first entry)
 DT Macaque primatized 16C10 heavy chain DNA.
 DE
 XX Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80;
 KW CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
 KW T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
 KW immunogen; anti-idiotypic reagent; interleukin-2; IgG; immunoglobulin G;
 KW T cell proliferation; ss.
 XX Macaca fascicularis.
 OS
 XX Key Location/Qualifiers
 FT 1..1431
 CDS /*tag= a
 FT /product= 16C10 heavy chain
 PN WO9819706-A1.
 XX
 XX 14-MAY-1998.
 XX 29-OCT-1997; 97WO-US19906.
 XX 08-NOV-1996; 96US-0746361.
 XX (IDEC-) IDEC PHARM CORP.
 XX Anderson DR, Brams P, Hanna N;
 XX WPI; 1998-286601/25.
 DR P-PSDB; AAW63765.
 XX New monoclonal antibodies specific for B7.1 or B7.2 antigens and
 PT inhibiting binding to CD28 - useful as specific immunosuppressants
 PT for treating diseases that involve interactions between T and B
 PT cells, e.g. graft rejection or tumours
 XX
 XX Example 7; Fig 5b; 87pp; English.
 XX
 XX This sequence encodes a primatized form of the antibody 16C10 heavy chain
 CC from macaque. This sequence is used in a method which studies new
 CC monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to
 CC B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
 CC Mab's are specific immunosuppressants for treatment of diseases involving
 CC T cell/B cell interactions, particularly autoimmune disease, specifically
 CC idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type
 CC I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
 CC inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
 CC host diseases, B cell lymphoma, infections (including by human immune
 CC deficiency virus) or inflammatory disease and tumours. Optionally the
 CC Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can
 CC also be used as imaging agents and as vaccines or immunogens to develop

CC anti-idiotypic reagents. Mab's are optionally combined with other proteins
 CC or small molecule immunosuppressants. Blocking B7/CD28 interactions
 CC induces long-term, antigen-specific immunosuppression, i.e. it inhibits
 CC production of interleukin-2 (IL-2), T cell proliferation and
 CC antigen-specific immunoglobulin G (IgG) responses.
 XX
 SQ Sequence 1431 BP; 319 A; 462 C; 385 G; 265 T; 0 other;
 Query Match 70.0%; Score 256.2; DB 19; Length 1431;
 Best Local Similarity 82.2%; Pred. No. 6.1e-61;
 Matches 313; Conservative 0; Mismatches 53; Indels 15; Gaps 1;
 Qy 1 CAGCTGCAGCTGCAGGAGTCGGGCCCGAGGAGTGTGAAGCCTTCGGAGACCCCTGTCCCTC 60
 Db 58 CAGTGCAGCTGCAGGAGTCGGGCCCGAGGAGTGTGAAGCCTTCGGAGACCCCTGTCCCTC 117
 Qy 61 ACCTGGCTGTCTCTGGTGGCTCTGTTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAG 120
 Db 118 ACCTGGCTGTCTCTGGTGGCTCCATCAGCGGTGGTTATGGCTGGGGCTGGATCCGCCAG 177
 Qy 121 CCCCAGGGAAGGAGCTGGAGTGGATTGGACGTATCTCTGGTAGTGTGGGGCCACCAAC 180
 Db 178 CCCCAGGGAAGGAGCTGGAGTGGATTGGAGTTTCTATAGTAGTAGTGGGAACACCTAC 237
 Qy 181 TACAACCCCTCCCTCAAGAGTCGAGTCATCATTTTCAAGACACGTCCTCAAGAACCCAGTTC 240
 Db 238 TACAACCCCTCCCTCAAGAGTCGAGTCGAGTCATCATTTTCAAGACACGTCCTCAAGAACCCAGTTC 297
 Qy 241 TCCTGAACTGAACCTGTGTGACCGCGGACACCGCGCTGTATTACTGTGCCAGAGAT 300
 Db 298 TCCTGAACTGAACCTGTGTGACCGCGGACACCGCGCTGTATTACTGTGTGAGAGAT 357
 Qy 301 TGGGCCCAATAGCTGGAAACA-----CGTAGGCTTCTGGGGCCAGGGA 345
 Db 358 CGTCTTTTTCAGTTGTGGATGTTTACAACTGTTTCGATGTCTGGGCGCCGGGA 417
 Qy 346 GTCTGTGTACCGTCTCTCA 366
 Db 418 GTCTGTGTACCGTCTCTCA 438
 RESULT 4
 AAS17247
 ID AAS17247 standard; DNA; 1431 BP.
 XX AAS17247;
 XX 12-MAR-2002 (first entry)
 DT DNA sequence of a primatized form of the heavy chain of 16C10 antibody.
 DE
 XX Human; macaque monkey; light chain; primatized antibody; 16C10 antibody;
 KW neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
 KW B7.1 antigen; CD80; B7.2 antigen; CD86; B cell cancer; metastasis;
 KW tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
 KW graft-vs-host disease; immunosuppression; organ rejection;
 KW interleukin-2; IL-2; mutant; ds.
 XX
 OS Chimeric - Homo sapiens.
 OS Chimeric - Macaca sp.
 OS Synthetic.
 XX Key Location/Qualifiers
 FT 1..1431
 CDS /*tag= a
 FT /product= "Heavy chain of 16C10 antibody"
 XX WO200189567-A1.
 XX 29-NOV-2001.
 XX 22-MAY-2001; 2001WO-US16364.
 XX

PR 22-MAY-2000; 2000US-0576424.
 XX (IDEC-) IDEC PHARM CORP.
 XX Anderson DR, Hanna N, Brams P;
 XX WPI; 2002-089895/12.
 DR P-PSDB; AAU11646.
 XX Use of monoclonal antibody which specifically binds to B7.1 antigen
 PT CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
 PT treating cancer, graft-vs-host disease and autoimmune disease such as
 PT allergy
 XX
 XX Example 8; Fig 5b; 89pp; English.
 XX
 CC The present invention relates to a new use of a monoclonal antibody
 CC which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
 CC (CD86) for inducing the apoptosis of B7+ cells. The invention is
 CC useful for treating diseases such as B cell cancer, lymphoma, a
 CC cancer where B cells promote the growth and/or metastasis of tumours,
 CC B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
 CC idiopathic thrombocytopenia purpura, systemic lupus, erythematosus,
 CC type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
 CC anaemia, inflammatory bile disease, allergy, multiple sclerosis
 CC or graft-vs-host disease. The antibody is useful for immunosuppression
 CC in a human or animal and for treating or preventing resistance to or
 CC rejection of transplanted organ or tissue for treating proliferative
 CC and hyperproliferative diseases, for treating reversible obstructive
 CC airways disease, intestinal inflammations and allergies e.g. Crohn's
 CC disease and ulcerative colitis, food-related allergies e.g. migraine,
 CC rhinitis and eczema, and other types of allergies. The present nucleic
 CC acid sequence encodes the heavy chain of 16C10, a primatised antibody
 CC used in the invention to induce apoptosis and inhibit production of
 CC interleukin-2 (IL-2).
 XX
 XX Sequence 1431 BP; 319 A; 462 C; 385 G; 265 T; 0 other;

Query Match 70.0%; Score 256.2; DB 24; Length 1431;
 Best Local Similarity 82.2%; Pred. No. 6.1e-61;
 Matches 313; Conservative 0; Mismatches 53; Indels 15; Gaps 1;
 QY 1 CAGTGCAGTGCAGGAGTGGGCGCCAGGAGTGGTGAAGCCTTCGGAGACCTTCCTCCTC 60
 DB 58 CAGTGCAGTGCAGGAGTGGGCGCCAGGAGTGGTGAAGCCTTCGGAGACCTTCCTCCTC 117
 QY 61 ACCTGCGCTGTCTCTGGTGGCTCTGTGACAGTAGTAACTGGTGGACCTGGATCCGCCAG 120
 DB 118 ACCTGCGCTGTCTCTGGTGGCTTCATCAGCGTGGTATGTGCTGGGCTGGATCCGCCAG 177
 QY 121 CCCCAGGGAAGGAGTGGAGTGGATGGACGTAATCTCTGTGTAGTGGTGGGCGCCACCAAC 180
 DB 178 CCCCAGGGAAGGAGTGGAGTGGATGGAGTGGATTTCTATAGTAGTGGGAAACACCTAC 237
 QY 181 TACAACCGTCCCTCAAGAGTGGAGTGCATATTTTCAACAGACAGCTCCAAAGACAGTTC 240
 DB 238 TACAACCGTCCCTCAAGAGTCAAGTACCATTTCACACAGACAGCTCCAAAGACAGTTC 297
 QY 241 TCCCTGAACCTGAACCTGTGACCGCGGACACGCGCGGTATTAATCTGTGCGCAGAGAT 300
 DB 298 TCCCTGAACCTGAACCTGTATACCGCGCGGACACGCGCGGTATTAATCTGTGCGCAGAGAT 357
 QY 301 TGGGCGCCAAATAGCTGGAAACAA-----CGTAGGCTTCCTGGGCGCAGGGA 345
 DB 358 CGTCTTTTTCAGTTGTTGGAATGGTTTAAACAACTGGTTCGATGTCTGGGCGCCGGA 417
 QY 346 GTCTGTGTCAAGCTCTCTCA 366
 DB 418 GTCTGTGTCAAGCTCTCTCA 438

RESULT 5
 AAZ39331

ID AAZ39331 standard; DNA; 423 BP.
 XX
 AC AAZ39331;
 XX
 DT 15-FEB-2000 (first entry)
 XX
 DE Nucleotide sequence of Cynomolgous VH cDNA clone 2-5.
 XX
 KW Complementarity determining region; antibody; primate; immunogenicity;
 KW Old World ape; Old World monkey; antigen-binding affinity; ss.
 XX
 OS Macaca cynomolgus.
 XX
 PN W09955369-A1.
 XX
 PD 04-NOV-1999.
 XX
 XX 28-APR-1999; 99WO-US09131.
 PF
 XX 28-APR-1998; 98US-0083367.
 PR
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA
 XX Taylor AH;
 PI
 XX WPI; 2000-023265/02.
 DR P-PSDB; AAY56663, AAY56728.
 DR
 XX Antibodies containing donor complementarity determining regions and
 PT non-human primate acceptor frameworks, having reduced immunogenicity in
 PT humans -
 PT
 XX Example 3; Page 79; 123pp; English.
 PS
 XX The invention provides an antibody (Ab) comprising donor CDRs
 CC (complementarity determining regions) derived from a non-human antigen-
 CC specific donor antibody, and an acceptor framework from a non-human
 CC primate. The Abs are prepared by grafting CDRs from a non-human antigen-
 CC specific donor antibody onto homologous Old World ape or monkey acceptor
 CC frameworks. The Abs have reduced immunogenicity and are better tolerated
 CC in humans (because of the close similarity between the human and primate
 CC proteins), but retain the full antigen-binding affinity of the donor
 CC antibody.
 CC
 XX Sequence 423 BP; 76 A; 125 C; 122 G; 100 T; 0 other;

Query Match 67.6%; Score 247.4; DB 21; Length 423;
 Best Local Similarity 83.2%; Pred. No. 1.2e-58;
 Matches 307; Conservative 0; Mismatches 56; Indels 6; Gaps 2;
 QY 1 CAGCTGCAGCTGCAGGAGTGGGCGCCAGGAGTGGTGAAGCCTTCGGAGACCTTCCTCCTC 60
 DB 58 CAGCTGCAGTTCGAGGAGTGGGCGCCAGGAGTGGTGAAGCCTTCGGAGACCTTCCTCCTC 117
 QY 61 ACCTGCGCTCTCTCTGGTGGCTCTGTGACAGTAGTAACTGGTGGACCTGCATCCGCCAG 120
 DB 118 ACCTGCACTGTCTCTGGTGGCTC---CTTCAGTACTTACTTGGAAATTGATCCGCCAG 174
 QY 121 CCCCAGGGAAGGAGTGGAGTGGATGGACGTAATCTCTGTGTAGTGGTGGGCGCCACCAAC 180
 DB 175 CCCCAGGGAAGGAGTGGAGTGGATGGATATATCGTGTGTGGTGGTGGCGCCCAAC 234
 QY 181 TACAACCGTCCCTCAAGAGTGCAGTGCATCATTTTCAACAGACAGCTCCAAAGACAGTTC 240
 DB 235 TACAATTCCTCCCTCAAGAGTGCATCACCCTGTCTACTAGACGCGTCCAAAGAACAGTTC 294
 QY 241 TCCCTGAACCTGAACCTGTGACCGCGCGGACACGCGCGGTATTAATCTGTGCGCAGAGAT 300
 DB 295 TCCCTGAACCTGAGCTCTGTGACCGCGCGGACACGCGCGGTACTACTGTGCGCAGAGAT 354
 QY 301 TGGGCGCCAAATAGCTGGAA---CAACGCTAGGCTTCCTGGGCGCCAGGAGTCTCTGTCACC 357
 DB 355 CGGGCTACGGTGCACCAATGATGCTTTTGAATTCCTGGGCGCCAGGCTCAGGGTCAACC 414

```

QY 358 GTCTCTCA 366
DB 415 GTCTCTCA 423

RESULT 6
AAT62868
ID AAT62868 standard; DNA; 1404 BP.
XX
AC AAT62868;
XX
DT 18-OCT-1997 (first entry)
XX
DE Human gamma-4 heavy chain DNA.
XX
KW CD4; monoclonal antibody; chimaeric antibody; recombinant antibody;
KW cynomolgus monkey; autoimmune disease; rheumatoid arthritis;
KW leukaemia; lymphoma; graft-versus-host disease; asthma;
KW transplant rejection; HIV; therapy; CE9 gamma 4; ss.
XX
OS Homo sapiens.
XX
XX WO9709351-A1.
XX
XX 13-MAR-1997.
XX
XX 05-SEP-1996; 96WO-US14324.
XX
XX 06-SEP-1995; 95US-0523894.
XX
XX (IDEC-) IDEC PHARM CORP.
XX
XX Hanna N, Newman RA, Reff ME;
XX
XX WPI; 1997-201913/18.
XX
XX P-PSDB; AAW14925.
XX
XX Chimeric antibody comprising monkey variable domains and human
XX constant domains - affects CD4-mediated immune functions, esp.
XX useful for treatment of autoimmune disease, e.g. rheumatoid
XX arthritis
XX
XX Disclosure; Page 82-84; 155pp; English.
XX
XX DNA sequences (AAT62868-70) respectively code for the heavy chain
XX regions of human gamma-4 (AAW14925), gamma-4E carrying the L236E
XX mutation (AAW14926) and gamma-4PE (AAW14927) carrying L236E and S229P
XX mutations. They can be used to provide novel monoclonal and
XX chimeric antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9
XX gamma-4PE, in which the human IgG4 Fc binding domain framework is
XX combined with the antigen binding domains (see also AAW14922-23) of
XX macaque anti-human CD4 monoclonal antibody E9.1. These antibodies
XX show high affinity to human CD4, have little or no immunogenicity
XX in humans and show reduced or absence of effector function. They
XX can be used to treat autoimmune diseases such as rheumatoid
XX arthritis.
XX
XX Sequence 1404 BP; 312 A; 448 C; 377 G; 267 T; 0 other;

Query Match 67.2%; Score 246; DB 18; Length 1404;
Best Local Similarity 81.4%; Pred. No. 4e-58;
Matches 298; Conservative 0; Mismatches 65; Indels 3; Gaps 1;

QY 1 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCCTTCGGAGACCTGTCCCTC 60
DB 58 CAGGTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCCTTCGGAGACCTGTCCCTC 117
QY 61 ACCTGCGCTGTCTGTGTGGTCTGTGTAGCAGTAGTAACTGGTGAACCTGATCGGCAG 120
DB 118 ACCTGCGAGTGTCTGTGTGGTCTGTGTAGCAGTAGTAACTGGTGTGATCGGCAG 177
QY 121 CCCCAGGAGGAGGAGTGGAGTGGATGGACGTATCTCTGTGTGGTGGGCCACCAAC 180

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SQ Sequence 1404 BP; 313 A; 446 C; 379 G; 266 T; 0 other;
Query Match 67.2%; Score 246; DB 18; Length 1404;
Best Local Similarity 81.4%; Pred. No. 4e-58;
Matches 298; Conservative 0; Mismatches 65; Indels 3; Gaps 1;
QY 1 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC 60
DB 58 CAGGTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC 117
QY 61 ACCTGCGCTGCTCTCTGGTGGTCTGTCTCAGCAGTAGTAACCTGGTGGACCTGGATCCGCAG 120
DB 118 ACCTGCGAGTGTCTCTGGTGGTCTTCATCAGCGGTGACTATTATTTGTTCTGGATCCGCAG 177
QY 121 CCCCAGGGAAGGAGTGGAGTGGATGGATTGGACGTATCTCTGGTGGACCTGGATCCGCAG 180
DB 178 TCCCAGGGAAGGAGTGGAGTGGATGGATGGATGGATGGATGGATGGATGGATGGATGGAT 237
QY 181 TACAACCCGTCCTCAAGAGTCGAGTCATCATTTTCAAGACACGCTCCAGAACCCAGTTC 240
DB 238 TACAATCCCTCCCTCAACAAATCGAGTCTCCATTTTCAATAGACAGCTCCAGAACCTCTTC 297
QY 241 TCCCTGAACTGAACTCTGTGACCGCCGCGGACACGCGCGTGTATTACTGTGCCAGAGAT 300
DB 298 TCCCTGAACTGAGGTCTGTGACCGCCGCGGACACGCGCGTGTATTACTGTGCCAGTAA 357
QY 301 TGGGCCCCAATAGCTGGAAACAACGCTAGGCTTCTGGGGCCAGGAGTCTTGGTCAACGTC 360
DB 358 ---ATATTGAAATATCTTCACTGGTTATTATATCTGGGGCCAGGAGTCTTGGTCAACGTC 414
QY 361 TCCTCA 366
DB 415 TCCTCA 420

RESULT 8
AAH762870
ID AAH762870 standard; DNA; 1404 BP.
XX
AC AAH762870;
XX
XX 18-OCT-1997 (first entry)
XX
XX Human gamma-4PE heavy chain DNA.
XX
XX CD4; monoclonal antibody; chimeric antibody; recombinant antibody;
KW cynomolgus monkey; autoimmune disease; rheumatoid arthritis;
KW leukaemia; lymphoma; graft-versus-host disease; asthma;
KW transplant rejection; HIV; therapy; CE9 gamma-4PE; ss.
XX
OS Homo sapiens.
XX
XX WO9709351-A1.
XX
XX 13-MAR-1997.
XX
XX 05-SEP-1996; 96WO-US14324.
XX
XX 06-SEP-1995; 95US-0523894.
XX
XX (IDEC-) IDEC PHARM CORP.
XX
XX Hanna N, Newman RA, Reff ME;
XX
XX WPI; 1997-201913/18.
XX
XX P-PSDB; AAH14927.
XX
XX Chimeric antibody comprising monkey variable domains and human
PT constant domains - affects CD4-mediated immune functions, esp.
PT useful for treatment of autoimmune disease, e.g. rheumatoid
PT arthritis
XX
XX Disclosure; Page 91-93; 155pp; English.
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```
XX DNA sequences (AAH2868-70) respectively code for the heavy chain
CC regions of human gamma-4 (AAH14925), gamma-4E carrying the L236E
CC mutation (AAH14926) and gamma-4PE (AAH14927) carrying L236E and S229P
CC mutations. They can be used to provide novel monoclonal and
CC chimeric antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9
CC gamma-4PE, in which the human IgG4 Fc binding domain framework is
CC combined with the antigen binding domains (see also AAH14922-23) of
CC macaque anti-human CD4 monoclonal antibody E9.1. These antibodies
CC show high affinity to human CD4, have little or no immunogenicity
CC in humans and show reduced or absence of effector function. The
CC gamma-4E and -4PE mutations confer activity enhanced stability and
CC eliminate depleting activity. The antibodies can be used to treat
CC autoimmune diseases such as rheumatoid arthritis.
SQ Sequence 1404 BP; 313 A; 447 C; 379 G; 265 T; 0 other;
Query Match 67.2%; Score 246; DB 18; Length 1404;
Best Local Similarity 81.4%; Pred. No. 4e-58;
Matches 298; Conservative 0; Mismatches 65; Indels 3; Gaps 1;
QY 1 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC 60
DB 58 CAGGTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC 117
QY 61 ACCTGCGCTGCTCTCTGGTGGTCTGTCTCAGCAGTAGTAACCTGGTGGACCTGGATCCGCAG 120
DB 118 ACCTGCGAGTGTCTCTGGTGGTCTTCATCAGCGGTGACTATTATTTGTTCTGGATCCGCAG 177
QY 121 CCCCAGGGAAGGAGTGGAGTGGATGGATTGGACGTATCTCTGGTGGACCTGGATCCGCAG 180
DB 178 TCCCAGGGAAGGAGTGGAGTGGATGGATGGATGGATGGATGGATGGATGGATGGATGGAT 237
QY 181 TACAACCCGTCCTCAAGAGTCGAGTCATCATTTTCAAGACACGCTCCAGAACCCAGTTC 240
DB 238 TACAATCCCTCCCTCAACAAATCGAGTCTCCATTTTCAATAGACAGCTCCAGAACCTCTTC 297
QY 241 TCCCTGAACTGAACTCTGTGACCGCCGCGGACACGCGCGTGTATTACTGTGCCAGAGAT 300
DB 298 TCCCTGAACTGAGGTCTGTGACCGCCGCGGACACGCGCGTGTATTACTGTGCCAGTAA 357
QY 301 TGGGCCCCAATAGCTGGAAACAACGCTAGGCTTCTGGGGCCAGGAGTCTTGGTCAACGTC 360
DB 358 ---ATATTGAAATATCTTCACTGGTTATTATATCTGGGGCCAGGAGTCTTGGTCAACGTC 414
QY 361 TCCTCA 366
DB 415 TCCTCA 420

RESULT 9
AAH76382
ID AAH76382 standard; DNA; 747 BP.
XX
XX AAH76382;
XX
XX 30-NOV-2001 (first entry)
XX
XX Nucleotide sequence of antibody directed against K293 superantigen.
XX
XX Antibody; tumor; epithelial; colorectal; pancreatic; breast; lung;
KW carcinoma; K293; immunostimulant; cytostatic; antisense therapy; vaccine;
KW antagonist; ds.
XX
XX Macaca fascicularis.
XX
XX OS
XX
XX Key Location/Qualifiers
XX CDS 1..747
XX /tag= a
XX misc_feature 1..330
XX /tag= b
XX /note= "light chain variable region coding sequence"
XX misc_feature 331..747
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FT FT /*tag= c
XX FT /note= "heavy chain variable region coding sequence"
XX PN WO200162286-A1.
XX PD 30-AUG-2001.
XX PF 23-FEB-2001; 2001WO-SE00395.
XX PR 24-FEB-2000; 2000SE-0000597.
XX PA (ACT1-) ACTIVE BIOTECH AB.
XX PI Brodin TN, Karlstroem PJ, Nilsson BHK, Ohlsson LG, Tordsson MJ;
XX PN WPI; 2001-565403/63.
XX DR P-PSDB; AAB85908.
XX XX
XX XX A binding structure, such as an antibody, binding to tumor cells,
XX PT especially epithelial tumor cells such as colorectal, pancreatic,
XX PT breast or lung carcinoma cells, useful in the therapy, diagnosis and
XX PT prognosis of human malignant disease -
XX XX
XX PS Disclosure; Page 70-71; 73pp; English.
XX XX
XX CC The invention provides a binding structure, such as an antibody, binding
XX CC to tumor cells, especially epithelial tumor cells such as colorectal,
XX CC pancreatic, breast or lung carcinoma cells. The binding structures,
XX CC target structures to the binding structures or the substances, i.e.
XX CC antisense oligonucleotides and ribozymes, are useful in the therapy and
XX CC in vitro histopathological diagnosis and prognosis of human malignant
XX CC disease. The present sequence represents the nucleotide sequence of
XX CC antibody directed against K293 superantigen.
XX XX
XX SQ Sequence 747 BP; 149 A; 216 C; 211 G; 171 T; 0 other;

Query Match 66.9%; Score 245; DB 22; Length 747;
Best Local Similarity 83.3%; Pred. No. 6.4e-58;
Matches 304; Conservative 0; Mismatches 55; Indels 6; Gaps 2;

QY 2 AGCTGCAGCTCAGGAGTCGGGCCAGAGTGGTGAAGCCTTCGGAGACCTGTGCTCTCA 61
DB 389 AGGTGCAGCTCAGGAGTCGGGCCAGAGTGGTGAAGCCTTCGGAGACCTGTGCTCTCA 448
QY 62 CTTGGCTGTCTCTGGTCTCTCTCAGCAGTACTGCTGACCTGGATCCGCCAGC 121
DB 449 CTTGGCTGTCTCTGGTCTCTCTCAGCAGTACTGCTGACCTGGATCCGCCAGT 508
QY 122 CCCAGGGAAGGAGTGGAGTGGATTTGACGTATCTCTGGTGGTGGGCCACCAACT 181
DB 509 CCCAGGGAAGGAGTGGATGGATTTGAGACATCTCTTATA---GTGGGAATCCAGGT 565
QY 182 ACAACCCGTCCCTCAAGAGTCAGATCATATTTCACAGACACGTCCCAAGAACAGTTCT 241
DB 566 ACAACCCGTCCCTCAAGAGTCAGATCCACATTTCAAGAGACACGTCCCAAGAACAGTTCT 625
QY 242 CCCTGAACCTCAACTCTGTGACCCCGCGGACACGGCCGTATTAATGTCGACAGATT 301
DB 626 CCCTGAAGCTGACCTCTGTGACCCCGCGGACACGGCCGTATTAATGTCGACAGATT 684
QY 302 GGGCCCAATAGCTGGAACACGCTAGGCTTTCTGGGGCCAGGAGTCTGTGTCACCGTCT 361
DB 685 --GATAGAGGCTGGCAGCAATACTTCGACTTCTGGGGCCAGGAGTCTGTGTCACCGTCT 742
QY 362 CCTCA 366
DB 743 CCTCA 747

RESULT 10
AAQ35903
ID AAQ35903 standard; DNA; 423 BP.
XX

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AC AAQ35903;
XX XX
XX DT 25-MAR-2003 (updated)
XX DT 08-JUN-1993 (first entry)
XX XX
XX DE Anti-CD4 VH coding sequence.
XX XX
XX KW PCR; amplify; clone; heavy; light; chain; variable; region; lambda;
XX KW immortalised B-cell; vector; TCAB 6; human; IgG1; constant; antigen;
XX KW recombinant; antibody; chimpanzee; Ig; Ag; old world monkey; eczema;
XX KW immunoglobulin; therapeutic; rheumatoid arthritis; ss.
XX OS Simian sp.
XX XX
XX PN WO9302108-A1.
XX XX
XX PD 04-FEB-1993.
XX XX
XX PF 24-JUL-1992; 92WO-US06194.
XX XX
XX PR 25-JUL-1991; 91US-0735064.
XX PR 23-MAR-1992; 92US-0856281.
XX XX
XX PA (IDEC-) IDEC PHARM CORP.
XX XX
XX PI Hanna N, Newman RA, Raab RW;
XX XX
XX DR WPI; 1993-058729/07.
XX DR P-PSDB; AAR31948.
XX XX
XX PT Recombinant antibodies including Old World monkey portion and
XX PT human portion - used for treatment of auto-immune diseases,
XX PT infectious diseases, AIDS, tumours, diabetes, proliferative
XX PT diseases, intestinal inflammations and allergies, etc.
XX XX
XX PS Disclosure; Page 53-54; 92pp; English.
XX XX
XX CC The sequences given in AAQ35903-04 encode the Simian anti CD4 VH and
XX CC V-lambda sequences respectively. These sequences were derived using
XX CC the primer sequences given in AAQ35901-02. The amplification products
XX CC were sequentially cloned into the vector TCAB 6, which contains human
XX CC IgG1 and human lambda constant regions. The amplified sequences could
XX CC be used in the production of a recombinant antibody, comprising a
XX CC human, chimpanzee or old world monkey immunoglobulin (Ig) constant
XX CC region and an antigen (Ag) binding portion of an old world monkey Ig
XX CC variable region, where the old world monkeys may be the same or
XX CC different. The recombinant antibody may be used as a therapeutic
XX CC agent for the treatment of rheumatoid arthritis, eczema and
XX CC immunological disorders.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX XX
XX SQ Sequence 423 BP; 85 A; 122 C; 113 G; 103 T; 0 other;

Query Match 66.8%; Score 244.4; DB 14; Length 423;
Best Local Similarity 81.1%; Pred. No. 8.2e-58;
Matches 297; Conservative 0; Mismatches 66; Indels 3; Gaps 1;

QY 1 CAGCTGCAGTTCGAGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTGCTCTC 60
DB 61 CAGTGCAGTTCGAGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTGCTCTC 120
QY 61 ACCTGCGCTCTCTCTGCTGCTCTGTCCAGCAGTAGTAACCTGGTGGACCTCGATCCGCCAG 120
DB 121 ACCTGAGTGTCTCTGCTGCTCTCCATCAGCGGTGACTATTATTGTTCTGATCCGCCAG 180
QY 121 CCCCCAGGGAAGGAGTGGAGTGGATTTGAGCGTATCTCTGGTAGTGGGGCCACCAAC 180
DB 181 TCCCCAGGGAAGGAGTGGAGTGGATTCGCTACATCTATGCGAGTGGTGGGACCAAT 240
QY 181 TACAACCCGTCCCTCAAGAGTCAGTCAATTCATTCACAGACACGTCCCAAGAACCAATTC 240
DB 241 TACAATCCCTCCCTCAACAAATCGAGTCTCCATTTCAATAGACACGTCCCAAGAACCTCTTC 300

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QY 241 TCCCTGAACCTGAACCTGTGACCGCGCGGACACGCGCGTGTATTACTGTGCGAGAGAT 300
 Db 301 TCCCTGAACCTGAACCTGTGACCGCGCGGACACGCGCGTGTATTACTGTGCGAGTAAT 360
 QY 301 TGGGCCCCAATAGCTGGGAACACGCTAGGCTTCTGGGGCCAGGAGTCTGCTGTCACCGTC 360
 Db 361 ---ATATTGAATATCTTCACTGGTTATTATTAATCTGGGGCCAGGAGTCTGCTGTCACCGTC 417
 QY 361 TCCTCA 366
 Db 418 TCCTCA 423
 RESULT 11
 AAT91564
 ID AAT91564 standard; DNA; 423 BP.
 AC AAT91564;
 XX
 XX 25-MAR-2003 (updated)
 DT 16-JAN-1998 (first entry)
 XX
 XX Anti-CD4 cynomolgus monkey immunoglobulin heavy chain variable region.
 DE
 XX Anti-CD4 antibody; cynomolgus monkey; immunoglobulin; Ig;
 KW chimpanzee; chimeric antibody; human therapy; Old World monkey;
 KW antigen binding region; tumour; ss.
 XX
 OS Macaca fascicularis.
 XX
 XX Key Location/Qualifiers
 FH 4..420
 FT /*tag= a
 FT /product= Anti-CD4 VH region
 FT /note= "No stop codon given"
 XX
 PN US5658570-A.
 XX
 PD 19-AUG-1997.
 XX
 XX 25-JAN-1995; 95US-0379072.
 XX
 PR 10-JUL-1992; 92US-0912292.
 PR 25-JUL-1991; 91US-0735064.
 PR 23-MAR-1992; 92US-0856281.
 PR 25-JAN-1995; 95US-0379072.
 XX
 PA (IDEC-) IDEC PHARM CORP.
 XX
 PI Hanna N, Newman RA, Raab RW;
 XX
 DR WPI; 1997-424183/39.
 DR P-PSDB; AAW32477.
 XX
 PT Chimeric antibodies for human therapy - comprising human or
 PT chimpanzee immunoglobulin constant region and an Old World monkey
 PT antigen-binding region
 XX
 PS Claim 33; Fig 13; 46pp; English.
 XX
 CC A new chimeric antibody (Ab) has been developed comprising a human or
 CC chimpanzee immunoglobulin (Ig) constant region and an Old World monkey
 CC antigen (Ag)-binding region. The present sequence encodes an anti-CD4
 CC cynomolgus monkey Ig heavy chain variable region. An anti-CD4 antibody
 CC (Ab) comprising the light- and heavy-chain variable regions encoded by
 CC the present sequence and that of AAT91565 is also new. The Abs are
 CC useful for human therapy, especially of tumours. Old world monkeys are
 CC sufficiently different from humans to allow Abs against human Ags, even
 CC relatively conserved Ags such as CD4 and CD54, to be raised in these
 CC monkeys, and are sufficiently similar to humans to avoid host anti-Ab
 CC immune responses when the Abs are introduced into humans.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX

SQ Sequence 423 BP; 85 A; 122 C; 113 G; 103 T; 0 other;
 Query Match 66.8%; Score 244.4; DB 18; Length 423;
 Best Local Similarity 81.1%; Pred. No. 8.2e-58;
 Matches 297; Conservative 0; Mismatches 66; Indels 3; Gaps 1;
 QY 1 CAGCTGCAGCTGCAGAGTCCGGCCCGAGGAGTGGTGAAGCTTTCGGAGACCTGTCCCTC 60
 Db 61 CAGGTGCAGCTGCAGGAGGCGGCGCCAGGACTGGTGAAGCTTTCGGAGACCTGTCCCTC 120
 QY 61 ACCTGGCTGTCTCTGGTGGCTCTGTCCAGCAGTAGTAACCTGGTGGACCTGGATCCGCCAG 120
 Db 121 ACCTGCAGTGTCTCTGGTGGCTCCATCAGCGGTGACTATTATTGGTTCTGGATCCGCCAG 180
 QY 121 CCCCCAGGGAAGGAGCTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAAC 180
 Db 181 TCCCCAGGGAAGGAGCTGGAGTGGATCGGTACATCTATGGCAGTGGTGGGGCCACCAAT 240
 QY 181 TACAACCCGTCCTCAAGAGTCCAGTCAATCATTTTCAACAAGACGTCCTCAAGAACAATTTC 240
 Db 241 TACAATCCCTCCCTCAACATCGAGTCTCCATTTCAATAGACACGTCCTCAAGAACAATTTC 300
 QY 241 TCCTGAACTGAACTCTGTGACCGCGCGGACACGCGCGTGTATTACTGTGCGAGAGAT 300
 Db 301 TCCTGAACTGAGGTCTGTGACCGCGCGGACACGCGCGTCTATTACTGTGCGAGTAAT 360
 QY 301 TGGGCCCCAATAGCTGGGAACACGCTAGGCTTCTGGGGCCAGGAGTCTGCTGTCACCGTC 360
 Db 361 ---ATATTGAATATCTTCACTGGTTATTATTAATCTGGGGCCAGGAGTCTGCTGTCACCGTC 417
 QY 361 TCCTCA 366
 Db 418 TCCTCA 423
 RESULT 12
 AAV31428
 ID AAV31428 standard; DNA; 423 BP.
 XX
 AC AAV31428;
 XX
 DT 10-AUG-1998 (first entry)
 XX
 DE Anti-CD4 antibody variable heavy (VH) region encoding DNA.
 XX
 KW Anti-CD4 antibody; antigen-binding; treatment; chimeric; human;
 KW monkey; rheumatoid arthritis; psoriatic arthritis; ss.
 XX
 OS Chimeric - Macaca cynomolgus.
 OS Chimeric - Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 4..423
 FT /*tag= a
 FT /transl_except= (pos:415..417, aa:Ser)
 FT /product= "Variable heavy chain antigen binding
 FT region"
 XX
 PN US5756096-A.
 XX
 PD 26-MAY-1998.
 XX
 XX 07-JUN-1995; 95US-0476237.
 XX
 PR 07-JUN-1995; 95US-0476237.
 PR 25-JUL-1991; 91US-0735064.
 PR 23-MAR-1992; 92US-0856281.
 PR 10-JUL-1992; 92US-0912292.
 PR 25-JAN-1995; 95US-0379072.
 XX
 PA (IDEC-) IDEC PHARM CORP.
 XX
 PI Hanna N, Newman RA, Raab RW;

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XX WPI; 1998-321461/28.
DR P-PSDB; AAW57446.
XX
XX Treatment of rheumatoid and psoriatic arthritis - comprises
PT administration of chimeric human-monkey anti-CD4 antibody
XX
XX Claim 2; Columns 35-36; 47pp; English.
XX
XX This DNA encodes the heavy chain variable region (VH) of the cynomolgus
CC monkey anti-CD4 antibody. The antibody comprises antigen-binding
CC sequences from an Old World monkey antibody and human constant domain
CC sequences. The antibody specifically binds to CD4 and can be used in the
CC treatment of rheumatoid or psoriatic arthritis.
XX
XX Sequence 423 BP; 85 A; 122 C; 113 G; 103 T; 0 other;
SQ
Query Match 66.8%; Score 244.4; DB 19; Length 423;
Best Local Similarity 81.1%; Pred. No. 8.2e-58;
Matches 297; Conservative 0; Mismatches 66; Indels 3; Gaps 1;
QY 1 CAGTGCAGTCGACGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCTC 60
DB 61 CAGTGCAGTCGACGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCTC 120
QY 61 ACCTGCGCTGTCTCTGTGGTCTCTCAGCAGTAGTAACCTGGTGACCTGGATCGGCAG 120
DB 121 ACCTGCACTGTCTGTGGTGGTCCATCAGCGGTGACTATTATGGTTCGGATCGGCAG 180
QY 121 CCCCAGGAAGGACGTGGAGTGGATGGATGGATGGATGGATGGATGGATGGATGGAT 240
DB 181 TACAAACCGTCCCTCAAGAGTCGAGTGCATCATTTTCAAGACACGCTCCAAACACGATTC 240
QY 241 TACAAACCGTCCCTCAAGAGTCGAGTGCATCATTTTCAAGACACGCTCCAAACACGATTC 300
DB 301 TCCCTGAACCTGAACTCTGTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 360
QY 301 TGGGCCCAATAGCTGGAAACACGCTAGGCTTCTGGGGCCAGGGAGTCTTGTCACCGTC 360
DB 361 ---ATATTGAATATCTTCACTGGTATTATTAATGAGGAGTCTTGTCACCGTC 417

RESULT 13
AAV05695
ID AAV05695 standard; DNA; 423 BP.
XX
XX AAV05695;
AC
DT 05-MAY-1998 (first entry)
XX
XX Monkey anti-CD4 heavy chain variable region coding sequence.
DE
XX
XX Primer; PCR; amplification; leader sequence; human; monkey; baboon;
KW macaque; immunoglobulin; heavy chain variable region; chimpanzee; hybrid;
KW lymphoma; AIDS; autoimmune disease; inflammatory disease; transplant;
KW tumour; antibody; ss.
XX
XX Macaca cynomolgus.
OS
XX
XX Key Location/Qualifiers
FH 4..420
CDS
FT
FT /product= "Ig heavy chain variable region"
FT /note= "no stop codon given at the 3' end of sequence"
FT sig_peptide 4..60

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FT mat_peptide /*tag= b
FT 61..420
FT /*tag= c
XX
XX US5693780-A.
XX
XX 02-DEC-1997.
XX
XX 07-JUN-1995; 95US-0481869.
XX
XX 10-JUL-1992; 92US-0912292.
XX 25-JUL-1991; 91US-0735064.
XX 23-MAR-1992; 92US-0856281.
XX 25-JAN-1995; 95US-0379072.
XX 07-JUN-1995; 95US-0481869.
XX
XX (IDEC-) IDEC PHARM CORP.
XX
XX Hanna N, Newman RA, Raab RW;
PT
XX WPI; 1998-031820/03.
DR P-PSDB; AAW43430.
XX
XX Nucleic acid encoding hybrid antibody - comprising monkey
PT antigen-binding region and human or chimp constant region
XX
XX Example 3; Fig 13; 46pp; English.
XX
XX This sequence represents the coding sequence for the heavy chain
CC variable region from an anti-human CD4 immunoglobulin raised in
CC cynomolgus monkeys. The sequence was PCR amplified and used in the
CC construction of a recombinant antibody comprising: (i) an Old World
CC monkey Ig antigen-binding region; and (ii) a human or chimpanzee Ig
CC constant region. The hybrid antibodies can be used as passive or
CC active therapeutic agents against human diseases, e.g. B-cell lymphoma,
CC AIDS, autoimmune and inflammatory diseases, transplant rejection or
CC tumours, or for producing therapeutic and diagnostic conjugates.
CC Although evolutionary distant monkeys are used to raise antibodies
CC against human antigens, they are sufficiently similar that they produce
CC antibodies similar to human antibodies, such that when the monkey
CC antibodies are introduced into humans, no host anti-antibody response
CC is stimulated.
XX
XX Sequence 423 BP; 85 A; 122 C; 113 G; 103 T; 0 other;
SQ
Query Match 66.8%; Score 244.4; DB 19; Length 423;
Best Local Similarity 81.1%; Pred. No. 8.2e-58;
Matches 297; Conservative 0; Mismatches 66; Indels 3; Gaps 1;
QY 1 CAGTGCAGTCGACGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCTC 60
DB 61 CAGTGCAGTCGACGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCTC 120
QY 61 ACCTGCGCTGTCTCTGTGGTCTCTGTCAGCAGTAGTAACCTGGTGACCTGGATCGGCAG 120
DB 121 ACCTGCACTGTCTGTGGTGGTCCATCAGCGGTGACTATTATGGTTCGGATCGGCAG 180
QY 121 CCCCAGGAAGGACGTGGAGTGGATGGATGGATGGATGGATGGATGGATGGATGGAT 180
DB 181 TACAAACCGTCCCTCAAGAGTCGAGTGCATCATTTTCAAGACACGCTCCAAACACGATTC 240
QY 241 TACAAACCGTCCCTCAAGAGTCGAGTGCATCATTTTCAAGACACGCTCCAAACACGATTC 300
DB 301 TCCCTGAACCTGAACTCTGTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 360
QY 301 TGGGCCCAATAGCTGGAAACACGCTAGGCTTCTGGGGCCAGGGAGTCTTGTCACCGTC 360
DB 361 ---ATATTGAATATCTTCACTGGTATTATTAATGAGGAGTCTTGTCACCGTC 417

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QY 361 TCCTCA 366
 Db 418 TCCTCA 423

RESULT 14
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 XX
 AC ABX76616;
 CC
 DT 03-APR-2003 (first entry)
 XX
 DE DNA encoding cynomolgus monkey immunoglobulin heavy chain.
 XX
 KW Old world monkey; monkey; tumour; cancer; ds;
 KW immunoglobulin constant region; immunoglobulin variable region;
 KW autoimmune response; rheumatoid arthritis; eczema; lymphoma;
 KW immunomodulatory disease; leukaemia; Hashimoto's thyroiditis;
 KW autoimmune carditis; Addison's disease; type I-diabetes mellitus;
 KW multiple sclerosis; male infertility; autoimmune hemolytic anaemia;
 KW inflammatory bowel disease; Sjogren's syndrome; psoriasis;
 KW systemic lupus erythematosus.
 XX
 OS Macaca cynomolgus.
 XX
 XX US2002150580-A1.
 PN
 XX 17-OCT-2002.
 XX
 XX 08-MAY-2001; 2001US-0850165.
 XX
 PR 10-JUL-1992; 92US-0912292.
 PR 07-JUN-1995; 95US-0476237.
 PR 21-MAY-1998; 98US-0082472.
 PR 25-JUL-1991; 91US-0735064.
 PR 23-MAR-1992; 92US-0856281.
 PR 17-APR-1995; 95US-0397072.
 XX
 XX (IDEC-) IDEC PHARM CORP.
 PA
 XX Newman RA, Hanna N, Raab RW;
 PI
 XX WPI; 2003-182483/18.
 DR
 DR P-PSDB; ABUS6789.
 XX
 PT New recombinant chimeric antibodies comprising human, chimpanzee and
 PT Old world monkey portions, useful for treating e.g. cancer, eczema,
 PT leukemia, lymphoma, Hashimoto's thyroiditis, multiple sclerosis or male
 PT infertility -
 XX
 PS Disclosure; Page 19-20; 101pp; English.
 XX
 CC The invention describes a recombinant antibody comprising a human,
 CC chimpanzee or a first Old World monkey immunoglobulin constant region,
 CC and an antigen-binding portion of a second Old World monkey
 CC immunoglobulin variable region. The first and second Old World monkey
 CC can be the same or different. The recombinant antibody is useful for
 CC treating a human having the antigen described above, e.g. for treating
 CC cancer in a human having a tumour antigen, or for treating a human
 CC suffering from an autoimmune response (where the antigen is involved in
 CC an autoimmune response in the human). In particular, the recombinant
 CC antibody is useful for treating rheumatoid arthritis, eczema, or an
 CC immunomodulatory disease. The recombinant antibody is also useful for
 CC treating tumours, leukaemia, lymphoma, Hashimoto's thyroiditis,
 CC autoimmune carditis, Addison's disease, type I-diabetes mellitus,
 CC multiple sclerosis, male infertility, autoimmune hemolytic anaemia,
 CC inflammatory bowel disease, Sjogren's syndrome, psoriasis, or systemic
 CC lupus erythematosus. This is the amino acid sequence of a monkey
 CC immunoglobulin heavy variable chain polypeptide for creation of the
 CC recombinant antibody.
 XX
 XX Sequence 423 BP; 85 A; 122 C; 113 G; 103 T; 0 other;

Query Match 66.8%; Score 244.4; DB 25; Length 423;
 Best Local Similarity 81.1%; Pred. No. 8.2e-58;
 Matches 297; Conservative 0; Mismatches 66; Indels 3; Gaps 1;

QY 1 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 60
 Db 61 CAGGTGCAGCTGCAGGAGGCGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 120
 QY 61 ACCTGCGCTGTCTGTGTGCTCTGTGCAGAGTAGTAACCTGGTGGACCTGGATCCGCCAG 120
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 QY 121 CCCCAGGAGGAGGAGTGGAGTGGATTGGAGTATCTCTGTAGTGTGGGGCCACCAAC 180
 Db 181 TCCCCAGGAGGAGGAGTGGAGTGGATCGGTACATCTATGGCAGTGTGGGGGCCACCAAT 240
 QY 181 TACAACCCGCTCCCTCAAGAGTTCAGATCATCATTTTCAACAAGACAGTCCTCAAGAACCAGTTC 240
 Db 241 TACATCCCTCCCTCAACATCGAGTCTCCATTTCAATAGACAGTCCTCAAGAACCCTCTTC 300
 QY 241 TCCCTGAACCTGAACTCTGTGACCGCGCGGACACGCGCGTGTATTACTGTGCCAGAGAT 300
 Db 301 TCCCTGAACCTGAGGTCTGTGACCGCGCGGACACGCGCGTGTATTACTGTGCCAGTAAT 360
 QY 301 TGGGCCCCAATAGCTGGAAACAACGCTAGGCTTCTGGGGCCAGGGAGTCTGGTCAACGTC 360
 Db 361 ---ATATTGAATATCTTCACTGTGTTATTATCTGGGGCCAGGGAGTCTGGTCAACGTC 417
 QY 361 TCCTCA 366
 Db 418 TCCTCA 423

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 ID AAS03048 standard; cDNA; 619 BP.
 XX
 AC AAS03048;
 XX
 DT 29-AUG-2001 (first entry)
 XX
 DE Human diagnostic and therapeutic (dithp) cDNA sequence #37.
 XX
 KW Human diagnostic and therapeutic molecule; dithp; gene therapy;
 KW thalassemia; cardiovascular disorder; cell proliferative disorder;
 KW cancer; neurodegenerative disorder; autoimmune disorder;
 KW infectious disorder; inflammatory disorder; developmental disorder;
 KW Incyte ID number 4442487dec; antigen recognition molecule; aa.
 XX
 OS Homo sapiens.
 XX
 PN WO200121836-A2.
 XX
 PD 29-MAR-2001.
 XX
 PF 19-SEP-2000; 2000WO-US25643.
 XX
 XX 23-SEP-1999; 99US-0155760.
 PR 24-SEP-1999; 99US-0155939.
 PR 24-SEP-1999; 99US-0156294.
 PR 28-SEP-1999; 99US-0156585.
 PR 28-SEP-1999; 99US-0156624.
 PR 28-SEP-1999; 99US-0156625.
 PR 24-NOV-1999; 99US-0167410.
 PR 24-NOV-1999; 99US-0167453.
 PR 24-NOV-1999; 99US-0167517.
 PR 24-NOV-1999; 99US-0167520.
 PR 24-NOV-1999; 99US-0167542.
 PR 29-NOV-1999; 99US-0167943.
 PR 29-NOV-1999; 99US-0167945.
 PR 30-NOV-1999; 99US-0168197.
 PR 30-NOV-1999; 99US-0168265.

Search completed: December 29, 2003, 16:25:37
Job time : 161.688 secs

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PR 30-NOV-1999; 99US-0168429.
PR 30-NOV-1999; 99US-0168432.
PR 01-DEC-1999; 99US-0168468.
PR 01-DEC-1999; 99US-0168599.
XX (INCY-) INCYTE GENOMICS INC.
XX PA
XX PI Hodgson DM, Lincoln SE, Russo FD, Spiro PA, Banville SC;
XX PI Bratcher SR, Dufour GE, Cohen HJ, Rosen BH, Shah P, Chalup MS;
XX PI Hillman JL, Jones AL, Yu JY, Greenawalt LB, Panzer SR;
XX PI Roseberry AM, Wright RU, Chen W, Liu TF, Yap FE, Stockdreher TK;
XX PI Ameshey S, Fong WT;
XX DR WPI; 2001-281607/29.
XX PT Novel diagnostic and therapeutic polynucleotides, used in disease
XX PT diagnosis and for gene therapy of conditions such as cancer and
XX PT thalassemia -
XX PS
XX PS Claim 1; Page 273; 299pp; English.
XX CC The present sequence for human diagnostic and therapeutic (dithp) cDNA
XX CC sequence #37 is 1 of 71 (AAS03012-AAS03082) novel sequences described
XX CC in the invention. The present sequence (incyte ID No: 4442487dec)
XX CC encodes an antigen recognition molecule. The dithp polynucleotides
XX CC may be used to diagnose a condition disease or disorder associated with
XX CC human molecules. They can be used to identify the presence of similar
XX CC nucleic acids. Dithp polynucleotides may be used to generate hybridisation
XX CC probes for use in chromosomal mapping. Polypeptides (dithp) encoded by
XX CC dithp are used to screen for molecules which bind to them and modulate
XX CC their activity. Dithp polynucleotides can be used for gene therapy of
XX CC disorders such as severe combined immunodeficiency syndrome (SCID),
XX CC cystic fibrosis, thalassemia, haemophilia resulting from Factor VIII
XX CC or IX deficiencies, cardiovascular disorders e.g familial
XX CC hypercholesterolaemia (FH), cell proliferative disorders e.g. cancers,
XX CC neurodegenerative disorders, autoimmune/inflammatory disorders,
XX CC infectious disorders and developmental disorders. The antibodies can be
XX CC used to analyse protein expression levels.
XX SQ Sequence 619 BP; 121 A; 192 C; 176 G; 130 T; 0 other;

Query Match 66.7%; Score 244.2; DB 22; Length 619;
Best Local Similarity 82.7%; Pred. No. 1e-57;
Matches 305; Conservative 0; Mismatches 58; Indels 6; Gaps 2;

QY 1 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGTGAAGCCTTCGGAGACCTGTCCCTC 60
DB 93 CAGGTGCAGCTGCAGGAGTCGGGCCAGGAGTGTGAAGCCTTCGGAGACCTGTCCCTC 152
QY 61 ACCTCGCGTCTCTGTGGCTCTCTCAGCAGTAGTAACTGGTGACCTGGATCGCCAG 120
DB 153 ACCTCGCGTCTCTGTGGTACTTCCATCAGCAGTGGTTACTCTGGGGCTGGATCGGCAG 212
QY 121 CCCCCAGGAGGGAGCTGGAGTGGAGTGAAGCTATCTCTGGTAGTGGTGGGCCACCAAC 180
DB 213 CCCCCAGGAGGGAGCTGGAGTGGAGTGGAGTATCTATCATA---GTGGGAGCACCTAC 269
QY 181 TACAACCCGTCCTCAAGAGTCGAGTCATCAATTCACAAGACACGTCACAAGAACGAGTTC 240
DB 270 TACAACCCGTCCTCAAGAGTCGAGTCATCAATTCACAAGACACGTCACAAGAGCCAGTTG 329
QY 241 TCCCTGAACCTGAACCTCTGTACCGCCGGGACACGGCCGCTGTATTACTGTGCCA--GA 297
DB 330 TCCCTGAACCTGAACCTCTGTACCGCCGGGACACGGCCGCTGTATTACTGTGCCA--GA 357
QY 298 GATTGGGCCCAATAGCTGGAACACAGCTAGGCTTCTGGGGCCAGGAGTCTGTGTACCC 357
DB 390 TACTATGATGAAGTAGTGGCCATATCTTGACTACTGGGGCCAGGAGACCTGTGTACCC 449
QY 358 GTCTCCTCA 366
DB 450 GCCTCCTCA 458
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GenCore version 5.1.6
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Title: US-09-019-441-2_COPY_58_423

Perfect score: 366

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2244575 seqs, 1713117285 residues

Total number of hits satisfying chosen parameters: 4489150

Minimum DB seq length: 0

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Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	256.2	70.0	1431	13	US-10-124-807-11
5	256.2	70.0	1431	13	US-10-291-532-11
6	256.2	70.0	1431	14	US-10-124-905-11
7	256.2	70.0	1431	14	US-10-073-138-6
8	247.4	67.6	423	9	US-09-905-243-40
9	246	67.2	1404	15	US-10-211-357-7
10	246	67.2	1404	15	US-10-211-357-9
11	246	67.2	1404	15	US-10-211-357-11
12	245	66.9	747	13	US-10-182-132-1
13	244.4	66.8	423	10	US-09-850-165-15
14	242.8	66.3	420	9	US-09-905-243-44
15	241.4	66.0	420	15	US-10-211-357-1

16	238.8	65.2	669	11	US-09-972-656-65	Sequence 65, Appl
17	236.4	64.6	417	13	US-10-300-675-1	Sequence 1, Appl
18	235.4	64.3	1431	10	US-09-948-429B-3	Sequence 3, Appl
19	235.4	64.3	1431	13	US-10-124-807-3	Sequence 3, Appl
20	235.4	64.3	1431	13	US-10-291-532-3	Sequence 3, Appl
21	235.4	64.3	1431	14	US-10-124-905-3	Sequence 3, Appl
22	234.4	64.0	1431	14	US-10-073-138-2	Sequence 2, Appl
23	231.6	63.3	414	12	US-10-309-764-110	Sequence 110, App
24	230.2	62.9	3128	13	US-10-027-632-114467	Sequence 114467,
25	230.2	62.9	3128	14	US-10-309-764-106	Sequence 106, App
26	230	62.8	414	12	US-10-067-800-59	Sequence 59, Appl
27	228.2	62.3	363	15	US-10-309-764-114	Sequence 114, App
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29	226.8	62.0	432	13	US-10-389-221-9	Sequence 1183, Ap
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31	225.6	61.6	785	13	US-10-360-828-59	Sequence 32297, A
32	225.2	61.5	362	9	US-09-864-761-28297	Sequence 28401, A
33	223.8	61.1	319	9	US-09-972-656-79	Sequence 79, Appl
34	223.8	61.1	663	11	US-10-330-613-27	Sequence 27, Appl
35	222.6	60.8	358	13	US-10-330-530-27	Sequence 27, Appl
36	222.6	60.8	358	13	US-10-330-530-27	Sequence 11, Appl
37	221.8	60.6	364	13	US-10-330-613-11	Sequence 39, Appl
38	221.8	60.6	364	13	US-10-330-613-39	Sequence 11, Appl
39	221.8	60.6	364	13	US-10-330-530-11	Sequence 39, Appl
40	221.8	60.6	364	13	US-10-330-530-39	Sequence 23, Appl
41	220.4	60.2	384	12	US-10-173-551-23	Sequence 15, Appl
42	220.2	60.2	352	13	US-10-330-613-15	Sequence 15, Appl
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44	219	59.8	378	15	US-10-067-800-67	Sequence 4, Appl
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ALIGNMENTS

RESULT 1

US-09-019-441-2

Sequence 2, Application US/09019441

Publication No. US20030086921A1

GENERAL INFORMATION:

APPLICANT: REFF, Mitchell E.

KLOETZER, William S.

NAKAMURA, Takehiko

TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL

ANTIBODIES AND USE THEREOF AS THERAPEUTICS

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/019,441

FILING DATE: 05-Feb-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/803,085

FILING DATE: 20-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-502

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..423
NAME/KEY: mat peptide
LOCATION: 58..423
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-019-441-2

Query Match 100.0%; Score 366; DB 11; Length 423;
Best Local Similarity 100.0%; Pred. No. 4.5e-104;
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTCTGCCTC 60
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Qy 181 TACAACCCGTCCTCAAGAGTCAGTGCATCATTTTCAAGAAGACAGTCCAGAACAGTTC 240
Db 238 TACAACCCGTCCTCAAGAGTCAGTGCATCATTTTCAAGAAGACAGTCCAGAACAGTTC 297

Qy 241 TCCCTGAACCTGAACTCTGTACCGCCGACAGCGCGGTATTACTGTGCGCAGAGAT 300
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Qy 301 TGGGCCCAAAATAGCTGGAACACGCTAGGCTTCTGGGCCAGGAGTCTCTGTCACCGTC 360
Db 358 TGGGCCCAAAATAGCTGGAACACGCTAGGCTTCTGGGCCAGGAGTCTCTGTCACCGTC 417

Qy 361 TCCTCA 366
Db 418 TCCTCA 423

RESULT 2
US-10-103-686-2
; Sequence 2, Application US/10103686
; Publication No. US20030059424A1
; GENERAL INFORMATION:
; APPLICANT: REFF, Mitchell E.
; KLOETZER, William S.
; NAKAMURA, Takaniko
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE THEREOF AS THERAPEUTICS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10103,686

FILING DATE: 25-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/803,085
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-353
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..423
NAME/KEY: mat peptide
LOCATION: 58..423
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-103-686-2

Query Match 100.0%; Score 366; DB 15; Length 423;
Best Local Similarity 100.0%; Pred. No. 4.5e-104;
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTCTGCCTC 60
Db 58 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTCTGCCTC 117

Qy 61 ACCTGCGCTGCTCTGGTGGCTCTGTACAGCAGTAGTAACCTGTGAGACTGATCGCCAG 120
Db 118 ACCTGCGCTGCTCTGGTGGCTCTGTACAGCAGTAGTAACCTGTGAGACTGATCGCCAG 177

Qy 121 CCCCAGGGAAGGAGCTGAGTGGATTGGACGTATCTCTGTAGTGGTGGGCCACCAAC 180
Db 178 CCCCAGGGAAGGAGCTGAGTGGATTGGACGTATCTCTGTAGTGGTGGGCCACCAAC 237

Qy 181 TACAACCCGTCCTCAAGAGTCAGTGCATCATTTTCAAGAAGACAGTCCAGAACAGTTC 240
Db 238 TACAACCCGTCCTCAAGAGTCAGTGCATCATTTTCAAGAAGACAGTCCAGAACAGTTC 297

Qy 241 TCCCTGAACCTGAACTCTGTACCGCCGACAGCGCGGTATTACTGTGCGCAGAGAT 300
Db 298 TCCCTGAACCTGAACTCTGTACCGCCGACAGCGCGGTATTACTGTGCGCAGAGAT 357

Qy 301 TGGGCCCAAAATAGCTGGAACACGCTAGGCTTCTGGGCCAGGAGTCTCTGTCACCGTC 360
Db 358 TGGGCCCAAAATAGCTGGAACACGCTAGGCTTCTGGGCCAGGAGTCTCTGTCACCGTC 417

Qy 361 TCCTCA 366
Db 418 TCCTCA 423

RESULT 3
US-09-948-429B-11
; Sequence 11, Application US/09948429B
; Patent No. US20020177689A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF."
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
LENGTH: 1431 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:

NAME/KEY: CDS
LOCATION: 1..1431
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1..1431

US-09-948-429B-11

Query Match 70.0%; Score 256.2; DB 10; Length 1431;
Best Local Similarity 82.2%; Pred. No. 9.2e-70;
Matches 313; Conservative 0; Mismatches 53; Indels 15; Gaps 1;

Qy	1	CAGCTGCAGTGCAGGAGTGGGCGCCAGGAGTGGTGAAGCTTCGGAGACCTGTCCCTC	60
Db	58	CAGGTGCAGCTGCAGGAGTGGGCGCCAGGAGTGGTGAAGCTTCGGAGACCTGTCCCTC	117
Qy	61	ACCTGCGCTGTCTGTGGTCTGTGCAGCAGTAGTAACCTGGTGGACCTGGCCAG	120
Db	118	ACCTGCGCTGTCTGTGGTCTGTGCAGCAGTAGTAACCTGGTGGACCTGGCCAG	177
Qy	121	CCCCCAGGAGGAGTGGGCGCCAGGAGTGGTGAAGCTTCGGAGACCTGTCCCTC	180
Db	178	CCCCCAGGAGGAGTGGGCGCCAGGAGTGGTGAAGCTTCGGAGACCTGTCCCTC	237
Qy	181	TACAACCCCTCCCTCAAGAGTGCAGTCAATTTTCAAGAAGACAGTCCAAAGAACCAAGTTC	240
Db	238	TACAACCCCTCCCTCAAGAGTGCAGTCAATTTTCAAGAAGACAGTCCAAAGAACCAAGTTC	297
Qy	241	TCCTGTGAACCTGAACTGTGACCGCCGCGACACGGCCGCTGATTACTGTGCCAGAGAT	300
Db	298	TCCTGTGAACCTGAACTGTGACCGCCGCGACACGGCCGCTGATTACTGTGTGAGAGAT	357
Qy	301	TGGGCCCCAAATAGCTTGAACAAA-----CGCTAGGCTTCTGGGGCCAGGGA	345
Db	358	CGTCTTTTTCAGTGTGTTGGAAATGGTTTAAACAACCTGGTTTCGATGTCTGGGGCCCGGGA	417
Qy	346	GTCTGTGTCAACCGTCTCTCTCA	366
Db	418	GTCTGTGTCAACCGTCTCTCTCA	438

RESULT 4

US-10-124-807-11
Sequence 11, Application US/10124807
Publication No. US20030166207A1
GENERAL INFORMATION:

APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESSANTS"

NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,807
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
LENGTH: 1431 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:

NAME/KEY: CDS
LOCATION: 1..1431
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1..1431

US-10-124-807-11

Query Match 70.0%; Score 256.2; DB 13; Length 1431;
Best Local Similarity 82.2%; Pred. No. 9.2e-70;
Matches 313; Conservative 0; Mismatches 53; Indels 15; Gaps 1;

Qy	1	CAGCTGCAGTGCAGGAGTGGGCGCCAGGAGTGGTGAAGCTTCGGAGACCTGTCCCTC	60
Db	58	CAGGTGCAGCTGCAGGAGTGGGCGCCAGGAGTGGTGAAGCTTCGGAGACCTGTCCCTC	117
Qy	61	ACCTGCGCTGTCTGTGGTCTGTGCAGCAGTAGTAACCTGGTGGACCTGGCCAG	120
Db	118	ACCTGCGCTGTCTGTGGTCTGTGCAGCAGTAGTAACCTGGTGGACCTGGCCAG	177
Qy	121	CCCCCAGGAGGAGTGGGCGCCAGGAGTGGTGAAGCTTCGGAGACCTGTCCCTC	180
Db	178	CCCCCAGGAGGAGTGGGCGCCAGGAGTGGTGAAGCTTCGGAGACCTGTCCCTC	237
Qy	181	TACAACCCCTCCCTCAAGAGTGCAGTCAATTTTCAAGAAGACAGTCCAAAGAACCAAGTTC	240

Db 238 TACAAACCCCTCCCTCAGAGTCAAGTACCAATTTCAACAGACACGTCACAGAACCAAGTTC 297
Qy 241 TCCTGAACTGAACTCTGTGACCGCGGACACGCGCGTGTATTACTGTGCGCAGAGAT 300
Db 298 TCCCTGAAGCTGAACTCTATGACCGCGGACACGCGCGTGTATTACTGTGTGAGAGAT 357
Qy 301 TGGGCCCCAATAGCTGGAACAA-----CGCTAGGCTTCTGGGCGCCAGGA 345
Db 358 CGTCTTTTTCAGTTGTGGAAATGGTTTACAACAACCTGGTTTCGATGTCTGGGCGCCGGA 417
Qy 346 GTCTGTGTCACCGTCTCTCTCA 366
Db 418 GTCTGTGTCACCGTCTCTCTCA 438
RESULT 5
US-10-291-532-11
; Sequence 11, Application US/10291532
; Publication No. US20030180290A1
; GENERAL INFORMATION:
; APPLICANT: HANNA, NABIL
; APPLICANT: HANNA, KANDASAMY
; TITLE OF INVENTION: ANTI-CD80 ANTIBODY HAVING ADCC ACTIVITY FOR ADCC
; TITLE OF INVENTION: MEDIATED KILLING OF B CELL LYMPHOMA CELLS ALONE OR IN
; TITLE OF INVENTION: COMBINATION WITH OTHER THERAPIES
; FILE REFERENCE: 037003/291872
; CURRENT APPLICATION NUMBER: US/10/291,532
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 60/331,187
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 09/758,173
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/383,916
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: 08/487,950
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 11
; LENGTH: 1431
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: primatized nucleotide sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1428)
US-10-291-532-11
Query Match 70.0%; Score 256.2; DB 13; Length 1431;
Best Local Similarity 82.2%; Pred. No. 9.2e-70;
Matches 313; Conservative 0; Mismatches 53; Indels 15; Gaps 1;
Qy 1 CAGCTGACGTGCAGGAGTCGGGCGCCAGAGTGGTGAAGCCTTCGGAGACCCCTGTCCCTC 60
Db 58 CAGGTGACGTGCAGGAGTCGGGCGCCAGAGTGGTGAAGCCTTCGGAGACCCCTGTCCCTC 117
Qy 61 ACCTGCGCTGCTCTGTGGTGGTCTGTCTGACGAGTGTAACTGCTGGTGAACCTGATCGCCAG 120
Db 118 ACCTGCGCTGCTCTGTGGTGGTCTGTCTGACGAGTGTAACTGCTGGTGAACCTGATCGCCAG 177
Qy 121 CCCCAGGGAAGGGAAGTGGATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT 180
Db 178 CCCCAGGGAAGGGAAGTGGATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT 237
Qy 181 TACAACCCGTCCTCAAGAGTCGAGTCATCATTTTCAAGACACGTCACAAACCAAGTTC 240
Db 238 TACAACCCCTCCCTCAAGAGTCGAGTCATCATTTTCAAGACACGTCACAAACCAAGTTC 297
Qy 241 TCCCTGAACTTGAACCTCTGTGACCGCGGACACGCGCGTGTATTACTGTGCGCAGAGAT 300

Db 298 TCCTGAACTGAACTCTATGACCGCGGACACGCGCGTGTATTACTGTGAGAGAT 357
Qy 301 TGGGCCCCAATAGCTGGAACAA-----CGCTAGGCTTCTGGGCGCCAGGA 345
Db 358 CGTCTTTTTCAGTTGTGGAAATGGTTTACAACAACCTGGTTTCGATGTCTGGGCGCCGGA 417
Qy 346 GTCTGTGTCACCGTCTCTCTCA 366
Db 418 GTCTGTGTCACCGTCTCTCTCA 438
RESULT 6
US-10-124-905-11
; Sequence 11, Application US/10124905
; Publication No. US20020166136A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,905
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1431 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1431
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..1431
US-10-124-905-11
Query Match 70.0%; Score 256.2; DB 14; Length 1431;
Best Local Similarity 82.2%; Pred. No. 9.2e-70;
Matches 313; Conservative 0; Mismatches 53; Indels 15; Gaps 1;
Qy 1 CAGCTGACGTGCAGGAGTCGGGCGCCAGAGTGGTGAAGCCTTCGGAGACCCCTGTCCCTC 60
Db 58 CAGGTGACGTGCAGGAGTCGGGCGCCAGAGTGGTGAAGCCTTCGGAGACCCCTGTCCCTC 117

NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: heavy chain gamma 4 with the E mutation
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1404
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1..1404
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-211-357-9

Query Match 67.2%; Score 246; DB 15; Length 1404;
Best Local Similarity 81.4%; Pred. No. 1.4e-66;
Matches 298; Conservative 0; Mismatches 65; Indels 3; Gaps 1;

Qy 1 CAGTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 60
Db |||||
Qy 58 CAGGTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 117
Db |||||
Qy 61 ACCTGCGCTGTCTCTGGTGGCTCTGTGACAGTAGTAATCTGGTGAACCTGGATCGGCAG 120
Db |||||
Qy 118 ACCTGCGCTGTCTCTGGTGGCTCTGTGACAGTAGTAATCTGGTGAACCTGGATCGGCAG 177
Db |||||
Qy 121 CCCCAGGGAAGGAGCTGGAGTGGATGAGTCTCTGTGAGTGGTGGGGCCACCAAC 180
Db |||||
Qy 178 TCCCAGGGAAGGAGCTGGAGTGGATGAGTCTCTGTGAGTGGTGGGGCCACCAAT 237
Db |||||
Qy 181 TACAACCCGTCCTCAAGAGTCGAGTCAATCTTCAAGACACGCTCCAGAACCTCTTC 240
Db |||||
Qy 238 TACAATCCCTCCCTCAACAATCGAGTCTCCATTCAATAGACAGCTCCAGAACCTCTTC 297
Db |||||
Qy 241 TCCCTGAACCTGAACCTCTGTGACCGCGGACACAGCCCGTGTATTACTGTGCGAGAT 300
Db |||||
Qy 298 TCCCTGAACCTGAACCTCTGTGACCGCGGACACAGCCCGTGTATTACTGTGCGAGAT 357
Db |||||
Qy 301 TGGGCCCAAAATAGCTGGAAACAACGCTAGGCTTCTGGGGCCAGGAGTCTGTGTCACCGTC 360
Db |||||
Qy 358 ---ATATTGAATAATCTTCACTGGTGTATTATCTGGGGCCAGGAGTCTGTGTCACCGTC 414
Db |||||

RESULT 11
US-10-211-357-11
Sequence 11, Application US/10211357
Publication No. US2003007275A1
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
Newman, Roland A.
Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street

CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/211.357
FILING DATE: 05-Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/612.914A
FILING DATE: 10-Jul-2000
APPLICATION NUMBER: US 08/523,894
FILING DATE: 06-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: heavy chain gamma 4 with the P and E mutation
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1404
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1..1404
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-211-357-11

Query Match 67.2%; Score 246; DB 15; Length 1404;
Best Local Similarity 81.4%; Pred. No. 1.4e-66;
Matches 298; Conservative 0; Mismatches 65; Indels 3; Gaps 1;

Qy 1 CAGTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 60
Db |||||
Qy 58 CAGGTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 117
Db |||||
Qy 61 ACCTGCGCTGTCTCTGGTGGCTCTGTGACAGTAGTAATCTGGTGAACCTGGATCGGCAG 120
Db |||||
Qy 118 ACCTGCGCTGTCTCTGGTGGCTCTGTGACAGTAGTAATCTGGTGAACCTGGATCGGCAG 177
Db |||||
Qy 121 CCCCAGGGAAGGAGCTGGAGTGGATGAGTCTCTGTGAGTGGTGGGGCCACCAAC 180
Db |||||
Qy 178 TCCCAGGGAAGGAGCTGGAGTGGATGAGTCTCTGTGAGTGGTGGGGCCACCAAT 237
Db |||||
Qy 181 TACAACCCGTCCTCAAGAGTCGAGTCAATCTTCAAGACACGCTCCAGAACCTCTTC 240
Db |||||
Qy 238 TACAATCCCTCCCTCAACAATCGAGTCTCCATTCAATAGACAGCTCCAGAACCTCTTC 297
Db |||||
Qy 241 TCCCTGAACCTGAACCTCTGTGACCGCGGACACAGCCCGTGTATTACTGTGCGAGAT 300
Db |||||
Qy 298 TCCCTGAACCTGAACCTCTGTGACCGCGGACACAGCCCGTGTATTACTGTGCGAGAT 357
Db |||||
Qy 301 TGGGCCCAAAATAGCTGGAAACAACGCTAGGCTTCTGGGGCCAGGAGTCTGTGTCACCGTC 360
Db |||||
Qy 358 ---ATATTGAATAATCTTCACTGGTGTATTATCTGGGGCCAGGAGTCTGTGTCACCGTC 414
Db |||||

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Qy 361 TCCTCA 366
Db 415 TCCTCA 420

RESULT 12
US-10-182-132-1
; Sequence 1, Application US/10182132
; Publication No. US20030176661A1
; GENERAL INFORMATION:
; APPLICANT: Brodin, Thomas N.
; APPLICANT: Karlstrom, Pia J.
; APPLICANT: Nilsson, Bo. H.K.
; APPLICANT: Ohlsson, Lennart G.
; APPLICANT: Tordsson, M. Jesper
; TITLE OF INVENTION: No. US20030176661A1el Antibody with Specificity for Colon Cancer
; FILE REFERENCE: 003300-984
; CURRENT APPLICATION NUMBER: US/10/182,132
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: PCT/SE01/00395
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: SE 0000597-5
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 747
; TYPE: DNA
; ORGANISM: Macaca fascicularis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(747)
; OTHER INFORMATION: K293 variable region (scFv); PRT (aa)-sequence V1
; OTHER INFORMATION: (1-110), mod Huston (111-129), Vh (130-249)
US-10-182-132-1

Query Match 66.9%; Score 245; DB 13; Length 747;
Best Local Similarity 83.3%; Pred. No. 2.5e-66;
Matches 304; Conservative 0; Mismatches 55; Indels 6; Gaps 2;

Qy 2 AGCTCAGCTGCAGGAGTCGGGCCCGAGGAGTGGTGAAGCCCTTCGGAGACCCCTGTCCCTCA 61
Db 389 AGGTGCAGCTGCAGGAGTCGGGCCCGAGGAGTGGTGAAGCCCTTCGGAGACCCCTGTCCCTCA 448
Qy 62 CTTGGCTGTCTCTGGTGGCTCTGTTCAGCAGTAGTAAGTGTGGACCTGGATCCGCCAGC 121
Db 449 CTTGGCTGTCTCTGGTGGCTCTGTTCAGCAGTAGTAAGTGTGGACCTGGATCCGCCAGT 508
Qy 122 CCCAGGGAAGGAGTGGAGTGGATGGACGTATCTCTGGTAGTGGTGGGCCCACT 181
Db 509 CCCAGGGAAGGAGTGGAGTGGATGGAGACATCTCTTATA---GTGGGAACCTCCAGGT 565
Qy 182 ACAACCCGTCTCCTCAAGAGTCAGTCACTATTTCACAAGACACGTCCTCAAGAACCAAGTTCT 241
Db 566 ACAACCCGTCTCCTCAAGAGTCAGTCACTATTTCACAAGACACGTCCTCAAGAACCAAGTTCT 625
Qy 242 CCCTGAACCTGAACCTCTGTGACCGCCGCGACACGCGCGTGTATTTACTGTGCCAGAGATT 301
Db 626 CCCTGAACCTGAACCTCTGTGACCGCCGCGACACGCGCGTGTATTTACTGTGCCAGACAT- 684
Qy 302 GGGCCCAATAGCTGGACCAACGCTAGGCTTCTGGGGCCAGGAGTCTGTGTCACCGTCT 361
Db 685 --GATAGAGGCTGGCAGCAACTTTCGACTTCTGGGGCCAGGAGTCTGTGTCACCGTCT 742
Qy 362 CCTCA 366
Db 743 CCTCA 747
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RESULT 13
US-09-850-165-15
; Sequence 15, Application US/09850165

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; Patent No. US20020150580A1
; GENERAL INFORMATION:
; APPLICANT: NEWMAN, ROLAND A.
; APPLICANT: HANNA, NABIL
; APPLICANT: RAAB, RONALD W.
; TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY
; FILE REFERENCE: 037003-0280614
; CURRENT APPLICATION NUMBER: US/09/850,165
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: 09/082,472
; PRIOR FILING DATE: 1998-05-21
; PRIOR APPLICATION NUMBER: 08/476,237
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/397,072
; PRIOR FILING DATE: 1995-04-17
; PRIOR APPLICATION NUMBER: 07/912,292
; PRIOR FILING DATE: 1992-07-10
; PRIOR APPLICATION NUMBER: 07/856,281
; PRIOR FILING DATE: 1992-03-23
; PRIOR APPLICATION NUMBER: 07/735,064
; PRIOR FILING DATE: 1991-07-25
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 423
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: anti-CD4 VH nucleic acid
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(420)
; OTHER INFORMATION:
US-09-850-165-15
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Query Match 66.8%; Score 244.4; DB 10; Length 423;
Best Local Similarity 81.1%; Pred. No. 3.5e-66;
Matches 297; Conservative 0; Mismatches 66; Indels 3; Gaps 1;

Qy 1 CAGTGCAGCTGCAGGAGTCGGGCCCGAGGAGTGGTGAAGCCCTTCGGAGACCCCTGTCCCTC 60
Db 61 CAGTGCAGCTGCAGGAGTCGGGCCCGAGGAGTGGTGAAGCCCTTCGGAGACCCCTGTCCCTC 120
Qy 61 ACCTGCGCTCTCTGGTGGCTCTGTCCAGCAGTAGTAACCTGGTGACCTGGATCCGCGCAG 120
Db 121 ACCTGCGAGTGTCTCTGGTGGCTCCATCAGCGGTGACTATTATTGGTTCTGGATCCGCGCAG 180
Qy 121 CCCCCAGGGAAGGAGTGGAGTGGATGGAGCTATCTCTGGTAGTGGTGGGGCCACCAAC 180
Db 181 TCCCCAGGGAAGGAGTGGAGTGGATGGATCGGCTACATCTATGGCAGTGGTGGGGCCACCAAT 240
Qy 181 TACAACCCGTCTCCTCAAGAGTCAGATCATCATTTTCAACAAGACAGCTCCAGAACCAGTTC 240
Db 241 TACAATCCCTCCCTCAACAATTCGAGTCTCCATTTTCAATAGACACGTCCTCAAGAACCCTTTC 300
Qy 241 TCCTGTAACCTGTAACCTGTGACCGCCGCGACACGCGCGTGTATTACTGTGCCAGAGAT 300
Db 301 TCCTGTAACCTGAGGTCTGTGACCGCCGCGACACGCGCGTGTATTACTGTGCCAGTAA 360
Qy 301 TGGSCCCAAATAGCTGGAAACAACGCTAGGCTTCTGGGGCCAGGAGTCTGTGGTCAACCGTC 360
Db 361 ---ATATTGAATATCTTCACTGGTTATTATATCTGGGGCCAGGAGTCTGTGGTCAACCGTC 417
Qy 361 TCCTCA 366
Db 418 TCCTCA 423
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RESULT 14
US-09-905-243-44
; Sequence 44, Application US/09905243
; Patent No. US20020062009A1
; GENERAL INFORMATION:

APPLICANT: Taylor, Alexander H
TITLE OF INVENTION: Monoclonal Antibodies with Reduced
FILE REFERENCE: P50770
CURRENT APPLICATION NUMBER: US/09/905,243
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/300,970
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 97
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 44
LENGTH: 420
TYPE: DNA
ORGANISM: Macaca cynomolgus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(420)
US-09-905-243-44

Query Match 66.3%; Score 242.8; DB 9; Length 420;
Best Local Similarity 80.9%; Pred. No. 1.le-65;
Matches 296; Conservative 0; Mismatches 67; Indels 3; Gaps 1;

Qy 1 CAGCTGAGCTGCAGGAGTCGGGCCAGGAGTGTGAAGCTTCGGAGACCTGTCCCTC 60
Db |||||
Qy 58 CAGGTTCAACTACAGGAGTCGGGCCAGGAGCTGATGAAGCCTTCGGAGACCTGTCCCTC 117
Db |||||
Qy 61 ACCTGCGCTGTCTGTGGTCTGTGACGAGTAGTAACCTGGTGACCTGATCCGCCAG 120
Db |||||
Qy 118 ACCTGCGCTGTCTGTGGTCTGTGACGAGTAGTAACCTGGTGACCTGATCCGCCAG 177
Db |||||
Qy 121 CCCCAGGAGGAGTGGAGTGGAGTATCTGTGTAGTGTGGGCCACCAAC 180
Db |||||
Qy 178 TCCCGGGAGGGCTGGATGATGATGGAGTTTCTACTACTACTGGAATACCTTC 237
Db |||||
Qy 181 TACAACCCGCTCCCTCAAGAGTCGAGTCATCATTTTCAAGAAGACGTCCTCAAGAACAGTTC 240
Db |||||
Qy 238 TCCAACCCCTCCCTCAAGAGTCGAGTCACCATTTTCAGCGGACAGCTCCAAGAACAGTTC 297
Db |||||
Qy 241 TCCCTGAACCTGAACCTGTGACCGCGGACAGCGCGGTATTACTGTGCGAGAGAT 300
Db |||||
Qy 298 TCCCTGAACCTGAACCTGTGACCGCGGACAGCGCGGTATTACTGTGCGAGAGAT 357
Db |||||
Qy 301 TGGSCCAATAGCTGGAACAACTAGGCTTCTGGGGCCAGGAGTCCTGGTCACCGTC 360
Db |||||
Qy 358 ---CTCTAGCAGCGCTATAATTTTACTACTGCGGCCAGGAGTCTGGTCACCGTC 414
Db |||||
Qy 361 TCCTCA 366
Db |||||
Qy 415 TCCTCA 420

RESULT 15
US-10-211-357-1
Sequence 1, Application US/10211357
Publication No. US2003007725A1
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
Newman, Roland A.
Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/211,357
FILING DATE: 05-Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/612,914A
FILING DATE: 10-Jul-2000
APPLICATION NUMBER: US 08/523,894
FILING DATE: 06-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Monkey
POSITION IN GENOME:
CHROMOSOME/SEGMENT: light variable domain of CE9.1
FEATURE:
NAME/KEY: CDS
LOCATION: 4..420
NAME/KEY: mat_peptide
LOCATION: 61..420
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-211-357-1

Query Match 66.0%; Score 241.4; DB 15; Length 420;
Best Local Similarity 81.0%; Pred. No. 3e-65;
Matches 294; Conservative 0; Mismatches 66; Indels 3; Gaps 1;

Qy 1 CAGCTCAGCTGCAGGAGTCGGGCCAGGAGTGTGAAGCTTCGGAGACCTGTCCCTC 60
Db |||||
Qy 61 CAGTGCAGCTGCAGGAGGCGGCCAGGAGTGTGAAGCTTCGGAGACCTGTCCCTC 120
Db |||||
Qy 61 ACCTGCGCTGTCTGTGGTCTGTGACGAGTAGTAACCTGGTGACCTGATCCGCCAG 120
Db |||||
Qy 121 ACCTGAGTGTCTGTGGTCTCCATCAGCGGTGACTATTATTGGTTCTGGATCCGCCAG 180
Db |||||
Qy 121 CCCCAGGAGGAGTGGAGTGGAGTATCTGTGTAGTGTGGGCCACCAAC 180
Db |||||
Qy 181 TCCCGAGGAGGAGTGGAGTGGAGTATCTGTGTAGTGTGGGCCACCAAC 240
Db |||||
Qy 181 TACAACCCGCTCCCTCAAGAGTCGAGTCATCATTTTCAAGAAGACGTCCTCAAGAACAGTTC 240
Db |||||
Qy 241 TACAATCCCTCCCTCAACAATCGAGTCTCCATTTTCAATAGACACGTCCTCAAGAACCTCTTC 300
Db |||||
Qy 241 TCCTGAACCTGAACCTGTGACCGCGGAGACACCGCGGTGTATTACTGTGCGAGAT 300
Db |||||
Qy 301 TCCTGAACCTGAAGTCTGTGACCGCGGAGACACCGCGGTGTATTACTGTGCGAGAT 360
Db |||||
Qy 301 TGGGCCCAATAGCTGGAACAACTAGGCTTCTGGGGCCAGGAGTCTGGTCACCGTC 360
Db |||||
Qy 361 ---ATATTGAATATCTTCACTGGTTATTATCTGGGGCCAGGAGTCTGGTCACCGTC 417
Db |||||
Qy 361 TCC 363
Db |||||
Qy 418 TCC 420

Search completed: December 30, 2003, 03:42:10
Job time : 529.775 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 40.2876 Seconds
(without alignments)
4009.823 Million cell updates/sec

Title: US-09-019-441-2_COPY_58_423

Perfect score: 366

Sequence: 1 CAGCTGCAGTGCAGGAGTC.....TCTGTGTCACCGTCTCTCA 366

Scoring table: IDENTITY NUC

Gapop 10.0., Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA.*

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2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*

3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*

4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*

5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq.*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	366	100.0	423	3	US-08-803-085-2
2	256.2	70.0	1431	3	US-08-487-550-11
3	256.2	70.0	1431	4	US-09-526-098-11
4	246	67.2	1404	3	US-08-523-894-7
5	246	67.2	1404	3	US-08-523-894-9
6	246	67.2	1404	3	US-08-523-894-11
7	244.4	66.8	423	1	US-08-379-072A-19
8	244.4	66.8	423	1	US-08-481-869-19
9	244.4	66.8	423	1	US-08-476-237-15
10	241.4	66.0	420	1	US-08-478-039-107
11	241.4	66.0	420	1	US-08-476-349A-107
12	241.4	66.0	420	1	US-08-523-894-1
13	237.8	65.0	366	1	US-08-360-125-9
14	237.8	65.0	366	2	US-08-450-578-9
15	237.8	65.0	366	2	US-09-017-628-9
16	237.8	65.0	366	2	US-09-014-880-9
17	237.8	65.0	366	4	US-08-450-363-9
18	236.6	64.6	624	3	US-08-545-809A-28
19	236.2	64.5	840	3	US-09-260-527-4
20	235.4	64.3	1431	3	US-08-487-550-3
21	235.4	64.3	1431	4	US-09-526-098-3
22	234.2	64.0	1567	3	US-09-049-672A-17
23	230.2	62.9	800	3	US-08-545-809A-55
24	226.8	62.0	1212	3	US-08-545-809A-61
25	225.4	61.6	650	3	US-08-545-809A-4
26	225.2	61.5	800	3	US-08-545-809A-39
27	223.8	61.1	622	3	US-08-545-809A-59

Sequence 46, Appl
Sequence 50, Appl
Sequence 1, Appl
Sequence 20, Appl
Sequence 13, Appl
Sequence 31, Appl
Sequence 49, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 23, Appl
Sequence 357, App
Sequence 205, App
Sequence 34, Appl
Sequence 3, Appl
Sequence 355, App

ALIGNMENTS

RESULT 1

US-08-803-085-2

; Sequence 2, Application US/08803085

; Patent No. 6011138

; GENERAL INFORMATION:

; APPLICANT: REFF, Mitchell E.

; APPLICANT: KLOETZER, William S.

; APPLICANT: NAKAMURA, Takehiko

; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL

; TITLE OF INVENTION: ANTIBODIES AND USE THEREOF AS THERAPEUTICS

; NUMBER OF SEQUENCES: 35

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/803,085

; FILING DATE: 20-FEB-1997

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Teskin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/DOCKET NUMBER: 012712-353

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 423 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..423

; FEATURE:

; NAME/KEY: mat_peptide

; LOCATION: 58..423

; US-08-803-085-2

Query Match 100.0%; Score 366; DB 3; Length 423;

Best Local Similarity 100.0%; Pred. No. 3.5e-101;
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCTGCAGCTGCAGGAGTCGGGCCAGAGTGTGAAGCCTTCGGAGACCTGTCCCTC 60
Db |||||
Qy 58 CAGCTGCAGCTGCAGGAGTCGGGCCAGAGTGTGAAGCCTTCGGAGACCTGTCCCTC 117
Db |||||

Qy 61 ACCTGCGCTGTCTGTGGTGTCTGTACAGCTAGTAACTGTGGACCTGGATCCGCCAG 120
Db |||||

Qy 118 ACCTGCGCTGTCTGTGGTGTCTGTACAGCTAGTAACTGTGGACCTGGATCCGCCAG 177
Db |||||

Qy 121 CCCCAGGAGGAGTGTGGAGTGTGAGCTATCTCTGTAGTGTGGGGCCACCAAC 180
Db |||||

Qy 178 CCCCAGGAGGAGTGTGGAGTGTGAGCTATCTCTGTAGTGTGGGGCCACCAAC 237
Db |||||

Qy 181 TACAACCGTCCCTCAGAGTGTGATCATATTTCAAGACACGTCCAAGAACCAAGTTC 240
Db |||||

Qy 238 TACAACCGTCCCTCAGAGTGTGATCATATTTCAAGACACGTCCAAGAACCAAGTTC 297
Db |||||

Qy 241 TCCCTGAACCTGAACCTGTGACCGCCGCGACACGCGCGTGTATTACTGTGCCAGAT 300
Db |||||

Qy 298 TCCCTGAACCTGAACCTGTGACCGCCGCGACACGCGCGTGTATTACTGTGCCAGAT 357
Db |||||

Qy 301 TGGGCCCAATAGCTGGAAACACGCTAGGCTTCTGGGGCCAGGGAGTCTCTGGTCAACCGTC 360
Db |||||

Qy 358 TGGGCCCAATAGCTGGAAACACGCTAGGCTTCTGGGGCCAGGGAGTCTCTGGTCAACCGTC 417
Db |||||

Qy 361 TCCTCA 366
Db |||||

Qy 418 TCCTCA 423
Db |||||

RESULT 2
US-08-487-550-11
; Sequence 11, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1431 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1431
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..1431
US-08-487-550-11

Query Match 70.0%; Score 256.2; DB 3; Length 1431;
Best Local Similarity 82.2%; Pred. No. 6.7e-68;
Matches 313; Conservative 0; Mismatches 53; Indels 15; Gaps 1;

Qy 1 CAGCTGCAGCTGCAGGAGTCGGGCCAGAGTGTGAAGCCTTCGGAGACCTGTCCCTC 60
Db |||||

Qy 58 CAGCTGCAGCTGCAGGAGTCGGGCCAGAGTGTGAAGCCTTCGGAGACCTGTCCCTC 117
Db |||||

Qy 61 ACCTGCGCTGTCTGTGGTGTCTGTACAGCTAGTAACTGTGGAGACCTGGATCCGCCAG 120
Db |||||

Qy 118 ACCTGCGCTGTCTGTGGTGTCTGTACAGCTAGTAACTGTGGAGACCTGGATCCGCCAG 177
Db |||||

Qy 121 CCCCAGGAGGAGTGTGGAGTGTGAGCTATCTCTGTAGTGTGGGGCCACCAAC 180
Db |||||

Qy 178 CCCCAGGAGGAGTGTGGAGTGTGAGCTATCTCTGTAGTGTGGGGCCACCTAC 237
Db |||||

Qy 181 TACAACCGTCCCTCAGAGTGTGATCATATTTCAAGACACGTCCAAGAACCAAGTTC 240
Db |||||

Qy 238 TACAACCGTCCCTCAGAGTGTGATCATATTTCAAGACACGTCCAAGAACCAAGTTC 297
Db |||||

Qy 241 TCCCTGAACCTGAACCTGTGACCGCCGCGACACGCGCGTGTATTACTGTGCCAGAT 300
Db |||||

Qy 298 TCCCTGAACCTGAACCTGTGACCGCCGCGACACGCGCGTGTATTACTGTGCCAGAT 357
Db |||||

Qy 301 TGGGCCCAATAGCTGGAAACAA-----CGTAGGCTTCTGGGGCCAGGGA 345
Db |||||

Qy 358 CGTCTTTTTCAGTGTGTGAAGTGTTCACAACTGGTTCGATGTCTGGGGCCCGGGA 417
Db |||||

Qy 346 GTCTGTGTACCGTCTCTCTCA 366
Db |||||

Qy 418 GTCTGTGTACCGTCTCTCTCA 438
Db |||||

RESULT 3
US-09-526-098-11
; Sequence 11, Application US/09526098
; Patent No. 6492134
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/526,098
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995

RESULT 4

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 base pairs
TYPE: nucleic acid
STRADEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-481-869-19

Query Match 66.8%; Score 244.4; DB 1; Length 423;
Best Local Similarity 81.1%; Pred. No. 1.6e-64;
Matches 297; Conservative 0; Mismatches 66; Indels 3; Gaps 1;
QY 1 CAGCTGCAGCTGCAGGAGTCGGGCGCCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCCTC 60
DB 61 CAGGTGCAGCTGCAGGAGTCGGGCGCCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCCTC 120
QY 61 ACCTGCGCTGTCTCTGTGGTCTGTGTCAGCAGTAGTAACCTGGTGACCTGGATCCGCCAG 120
DB 121 ACCTGCGCTGTCTCTGTGGTCTGTGTCAGCAGTAGTAACCTGGTGACCTGGATCCGCCAG 180
QY 121 CCCCAGGAGGAGTGGAGTGGATGGAGCTATCTCTGTAGTGGTGGGGCCACCAAC 180
DB 181 TCCCAGGAGGAGTGGAGTGGATGGAGCTATCTGTATGGCAGTGGTGGGGCCACCAAC 240
QY 181 TACAACCCGCTCCCTCAAGAGTCGAGTGCATCATTTTCAACAAGACAGCTCCAAAGAACCACTTC 240
DB 241 TACAATCCCTCCCTCAACAATCGAGTCTCCATTTCAATAGACAGCTCCAAAGAACCTTC 300
QY 241 TCCCTGAACCTGAACCTGTGACCGCCGCGACACGCGGTGTATTAATCTGTGCGAGAT 300
DB 301 TCCCTGAACCTGAACCTGTGACCGCCGCGACACGCGGTGTATTAATCTGTGCGAGTAAT 360
QY 301 TGGGCCCCAAATAGCTGGAAACAGCTAGGCTTCTGGGGCCAGGAGTCTGTGTCACCGTC 360
DB 361 ---ATATTGAATAATCTTCACTGGTTATTATCTGGGGCCAGGAGTCTGTGTCACCGTC 417
QY 361 TCCTCA 366
DB 418 TCCTCA 423

RESULT 9
US-08-476-237-15
Sequence 15, Application US/08476237
Patent No. 5756096
GENERAL INFORMATION:
APPLICANT: NEWMAN, Roland A.
APPLICANT: HANNA, Nabil
APPLICANT: RAAB, Ronald W.
TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY.
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,237
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281

FILING DATE: 23-MAR-1992
PRIOR APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 base pairs
TYPE: nucleic acid
STRADEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-476-237-15

Query Match 66.8%; Score 244.4; DB 1; Length 423;
Best Local Similarity 81.1%; Pred. No. 1.6e-64;
Matches 297; Conservative 0; Mismatches 66; Indels 3; Gaps 1;
QY 1 CAGCTGCAGCTGCAGGAGTCGGGCGCCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCCTC 60
DB 61 CAGGTGCAGCTGCAGGAGTCGGGCGCCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCCTC 120
QY 61 ACCTGCGCTGTCTCTGTGGTCTGTGTCAGCAGTAGTAACCTGGTGACCTGGATCCGCCAG 120
DB 121 ACCTGCGCTGTCTCTGTGGTCTGTGTCAGCAGTAGTAACCTGGTGACCTGGATCCGCCAG 180
QY 121 CCCCAGGAGGAGTGGAGTGGATGGAGCTATCTCTGTAGTGGTGGGGCCACCAAC 180
DB 181 TCCCAGGAGGAGTGGAGTGGATGGAGCTATCTGTATGGCAGTGGTGGGGCCACCAAC 240
QY 181 TACAACCCGCTCCCTCAAGAGTCGAGTGCATCATTTTCAACAAGACAGCTCCAAAGAACCACTTC 240
DB 241 TACAATCCCTCCCTCAACAATCGAGTCTCCATTTCAATAGACAGCTCCAAAGAACCTTC 300
QY 241 TCCCTGAACCTGAACCTGTGACCGCCGCGACACGCGGTGTATTAATCTGTGCGAGAT 300
DB 301 TCCCTGAACCTGAACCTGTGACCGCCGCGACACGCGGTGTATTAATCTGTGCGAGTAAT 360
QY 301 TGGGCCCCAAATAGCTGGAAACAGCTAGGCTTCTGGGGCCAGGAGTCTGTGTCACCGTC 360
DB 361 ---ATATTGAATAATCTTCACTGGTTATTATCTGGGGCCAGGAGTCTGTGTCACCGTC 417
QY 361 TCCTCA 366
DB 418 TCCTCA 423

RESULT 10
US-08-478-039-107
Sequence 107, Application US/08478039
Patent No. 5681722
GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: HANNA, Nabil
APPLICANT: RAAB, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,039

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072

FILING DATE: 25-JAN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292

FILING DATE: 10-JUL-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281

FILING DATE: 23-MAR-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064

FILING DATE: 25-JUL-1991

ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-160

TELEPHONE: 703-836-6620

TELEFAX: 703-836-6620

INFORMATION FOR SEQ ID NO: 107:

SEQUENCE CHARACTERISTICS:

LENGTH: 420 base pairs

TYPE: nucleic acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: peptide

ORGANISM: Monkey

POSITION IN GENOME:

CHROMOSOME/SEGMENT: Anti-CD4 VH

FEATURE:

NAME/KEY: CDS

LOCATION: 4..420

NAME/KEY: mat_peptide

LOCATION: 61..420

US-08-478-039-107

Query Match 66.0%; Score 241.4; DB 1; Length 420;

Best Local Similarity 81.0%; Pred. No. 1.3e-63;
Matches 294; Conservative 0; Mismatches 66; Indels 3; Gaps 1;

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QY 1 CAGCTGCAGCTGCAGGAGTCCGGCCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCTC 60
DB 61 CAGGTGCAGCTGCAGGAGGCGGCGCCAGGACTGGTGAAGCCTTCGGAGACCCCTGTCCTC 120
QY 61 ACCTGCAGCTGCTCTGGTGCTCTGTTCAGCAGTAGTAACCTGGTGACCTGGATCCGCCAG 120
DB 121 ACCTGCAGCTGCTCTGGTGCTCTCCATCAGCGGTGACTATTATTGGTTCTGATCCGCCAG 180
QY 121 CCCCAGGAGGAGGAGTGGAGTGGATGGAGTATCTCTGGTAGTGGTGGGCCACCAAC 180
DB 181 TCCCAGGAGGAGGAGTGGAGTGGATCGGCTACATCTATGTCAGTGGTGGGGGACCAAT 240
QY 181 TACAACCCGTCCTCAAGAGTGCAGTCAATTTCAAGACACGTCCTCAAGAACAGTTC 240
DB 241 TACATCCCTCCCTCAACATTCGAGTCTCCATTTCAATAGACAGTCCAGAACCTCTTC 300
QY 241 TCCCTGAACCTGAACCTCTGTGACCGCGCGGACACGCGCGGTGTTACTGTGCGCAGAGAT 300
DB 301 TCCCTGAACCTGAAGTCTGTGACCGCGCGGACACGCGCGGTGTTACTGTGCGCAGTAAT 360
QY 301 TGGGCCCCAATAGCTGGAAACACCTAGGCTTCTGGGGCCAGGAGTCTGGTCAACCGTC 360
DB 361 ---ATATTGAATATCTTCACTGTTTATTATCTGTTGGGCGGAGGAGTCTGTTGTCACCGTC 417
QY 361 TCC 363
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Db 418 TCC 420

RESULT 11

US-08-476-349A-107

Sequence 107, Application US/08476349A

Patent No. 5750105

GENERAL INFORMATION:

APPLICANT: Newman, Roland A.

APPLICANT: Hanna, Nabil W.

TITLE OF INVENTION: Recombinant Antibodies for Human Therapy

NUMBER OF SEQUENCES: 114

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince St.

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/476,349A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/379,072

FILING DATE: 25-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/912,292

FILING DATE: 10-JUL-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/856,281

FILING DATE: 23-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/735,064

FILING DATE: 25-JUL-1991

ATTORNEY/AGENT INFORMATION:

NAME: Teskin Esq., Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-161

TELEPHONE: 703-836-6620

TELEFAX: 703-836-6620

INFORMATION FOR SEQ ID NO: 107:

SEQUENCE CHARACTERISTICS:

LENGTH: 420 base pairs

TYPE: nucleic acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: peptide

ORGANISM: Monkey

POSITION IN GENOME:

CHROMOSOME/SEGMENT: Anti-CD4 VH

FEATURE:

NAME/KEY: CDS

LOCATION: 4..420

NAME/KEY: mat_peptide

LOCATION: 61..420

US-08-476-349A-107

Query Match 66.0%; Score 241.4; DB 1; Length 420;

Best Local Similarity 81.0%; Pred. No. 1.3e-63;
Matches 294; Conservative 0; Mismatches 66; Indels 3; Gaps 1;

QY 1 CAGCTGCAGCTGCAGGAGTCCGGCCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCTC 60

Db 61 CAGTGCAGCTGCAGGAGGCGGCCAGGACTGGTGAAGCCTTCGGAGACCTGTCCCTC 120
Qy 61 ACCTGCGCTGTCTGTGGTGGCTGTGTGAGAGTAGTAACTGGTGAGCTGTGATCCGCCAG 120
Db 121 ACCTGCAGTGTCTGTGGTGGCTGTGTGAGAGTAGTAACTGGTGAGCTGTGATCCGCCAG 180
Qy 121 CCCCAGGAGGAGGAGCTGGAGTGGATGGAGTATCTGTGTAGTGGTGGGCGCACCAAC 180
Db 181 TCCCAGGAGGAGGAGCTGGAGTGGATGGAGTATCTGTGTAGTGGTGGGCGCACCAAT 240
Qy 181 TACAACCCGCTCCCTCAAGAGTGGAGTGCATCATTTTCAAGACACGTCCTCAAGAACCTGTC 240
Db 241 TACAATCCCTCCCTCAACATCGAGTCTCCATTTCAATAGACACGTCCTCAAGAACCTGTC 300
Qy 241 TCCCTGAACCTGAACCTGTGTGACCGCGCGGACACGCGCGGTGTATTAATCTGTGCGAGAT 300
Db 301 TCCCTGAACCTGAAGTCTGTGACCGCGCGGACACGCGCGGTGTATTAATCTGTGCGAGTAAT 360
Qy 301 TGGGCCCCAATAGCTGGNACACGCTAGGCTTCTGGGGCCAGGAGTCTGTGTCACCGTC 360
Db 361 ---ATATTGAATAATCTTCACTGCTGTATTATTAATCTGGGGCCAGGAGTCTGTGTCACCGTC 417
Qy 361 TCC 363
Db 418 TCC 420

RESULT 12
US-08-523-894-1
; Sequence 1, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; TITLE OF INVENTION: Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/523,894
; FILING DATE: 06-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: light variable domain of CB9.1

FEATURE:
; NAME/KEY: CDS
; LOCATION: 4..420
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 61..420
US-08-523-894-1
Query Match 66.0%; Score 241.4; DB 3; Length 420;
Best Local Similarity 81.0%; Pred. No. 1.3e-63;
Matches 294; Conservative 0; Mismatches 66; Indels 3; Gaps 1;
Qy 1 CAGTGCAGCTGCAGGAGTCCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 60
Db 61 CAGTGCAGCTGCAGGAGGCGGCCAGGACTGGTGAAGCCTTCGGAGACCTGTCCCTC 120
Qy 61 ACCTGCGCTGTCTGTGGTGGCTGTGTGAGAGTAGTAACTGGTGAGCTGTGATCCGCCAG 120
Db 121 ACCTGCAGTGTCTGTGGTGGCTGTGTGAGAGTAGTAACTGGTGAGCTGTGATCCGCCAG 180
Qy 121 CCCCAGGAGGAGGAGCTGGAGTGGATGGAGTATCTGTGTAGTGGTGGGCGCACCAAC 180
Db 181 TCCCAGGAGGAGGAGCTGGAGTGGATGGAGTATCTGTGTAGTGGTGGGCGCACCAAT 240
Qy 181 TACAACCCGCTCCCTCAAGAGTGGAGTGCATCATTTTCAAGACACGTCCTCAAGAACCTGTC 240
Db 241 TACAATCCCTCCCTCAACATCGAGTCTCCATTTCAATAGACACGTCCTCAAGAACCTGTC 300
Qy 241 TCCCTGAACCTGAACCTGTGTGACCGCGCGGACACGCGCGGTGTATTAATCTGTGCGAGAT 300
Db 301 TCCCTGAACCTGAAGTCTGTGACCGCGCGGACACGCGCGGTGTATTAATCTGTGCGAGTAAT 360
Qy 301 TGGGCCCCAATAGCTGGNACACGCTAGGCTTCTGGGGCCAGGAGTCTGTGTCACCGTC 360
Db 361 ---ATATTGAATAATCTTCACTGCTGTATTATTAATCTGGGGCCAGGAGTCTGTGTCACCGTC 417
Qy 361 TCC 363
Db 418 TCC 420

RESULT 13
US-08-360-125-9
; Sequence 9, Application US/08360125
; Patent No. 5767246
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5767246ihiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,125
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534

FILING DATE: June 29, 1992
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
LENGTH: 366 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:

STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:

CELL TYPE: Hybridoma producing human antibody 1-3-1

CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:

LIBRARY:
CLONE:

POSITION IN GENOME:
CHROMOSOME/SEGMENT:

MAP POSITION:
UNITS:

FEATURE:
NAME/KEY:

LOCATION:
IDENTIFICATION METHOD:

OTHER INFORMATION:
PUBLICATION INFORMATION:

AUTHORS:
TITLE:

JOURNAL:
VOLUME:

ISSUE:
PAGES:

DATE:
DOCUMENT NUMBER:

FILING DATE:
PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-9

Query Match 65.0%; Score 237.8; DB 1; Length 366;

Best Local Similarity 81.6%; Pred. NO. 1.5e-62;

Matches 301; Conservative 0; Mismatches 62; Indels 6; Gaps 2;

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Db	1		
Qy	61	ACCTGCGCTGCTCTGGTGGCTCTGTGACAGTAGTA---ACTGGTGACCTGGATCCGC	117
Db	61		
Qy	118	CAGCCCCCAGGAAAGGAGCTGAGTGGATTGGACGATATCTCTGGTAGTGGGGGCCACC	177
Db	121		

Qy	178	AACTACAACCCGTCCTCCTCAAGAGTCGAGTCATCATTTCAACAAGACAGTCCTCAAGAACAG	237
Db	178		
Qy	238	TTCTCCCTGAACCTGAACTCTGTGACCGCGCGGACACGCGCTGTATTACTGTGCCAGA	297
Db	238		
Qy	298	GATTGGGCCCAAAATAGCTGGAACAAACGCTAGGCTTCTGGGGCCAGGAGTCTCTGCTCACC	357
Db	298		
Qy	358	GTCTCCTCA 366	
Db	358		

RESULT 14

US-08-450-578-9

; Sequence 9, Application US/08450578

; Patent No. 5837845

; GENERAL INFORMATION:

; APPLICANT: Saiko HOSOKAWA

; APPLICANT: Yoshiaki TAGAWA

; APPLICANT: Yoko HIRAKAWA

; APPLICANT: No. 5837845ihiko ITO

; APPLICANT: Kazuhiro NAGAIKE

; TITLE OF INVENTION: Human Monoclonal Antibody

; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer

; TITLE OF INVENTION: Cell Membrane

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Wenderoth, Lind & Ponack

; STREET: 805 Fifteenth Street, N.W., #700

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: Wordperfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/450,578

; FILING DATE: May 25, 1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/360,125

; FILING DATE: December 20, 1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/905,534

; FILING DATE: June 29, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Warren M. Cheek, Jr.

; REGISTRATION NUMBER: 33,367

; REFERENCE/DOCKET NUMBER:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-371-8850

; TELEFAX:

; TELEX:

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 366 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL:

; ANTI-SENSE:

; FRAGMENT TYPE:

; ORIGINAL SOURCE:

; ORGANISM:

STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE: Hybridoma producing human antibody 1-3-1
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:

US-08-450-578-9

Query Match 65.0%; Score 237.8; DB 2; Length 366;
Best Local Similarity 81.6%; Pred. No. 1.5e-62;
Matches 301; Conservative 0; Mismatches 62; Indels 6; Gaps 2;
Qy 1 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 60
Db 1 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 60
Qy 61 ACCTGCGCTGTCTGTGGTGGTCTCTCAGCAGTAGTA---ACTGGTGGACCTGGATCCGC 117
Db 61 ACCTGCACTGTCTGTGGTGGTCTCCATCAGCAGTAGTAGTACTACTGGGGCTGGATCCGC 120
Qy 118 CAGCCCCCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTGGTGGGGCCACC 177
Db 121 CAGCCCCCAGGGAAGGGGCTGGAGTGGATTGGAGTATCTATTATA---GTGGGAGCACC 177
Qy 178 AACTACAAACCGTCCCTCAAGAGTCGAGTCATCATTTTCAAGACACGTCCTCAAGAACCCAG 237
Db 178 TACTACAAACCGTCCCTCAAGAGTCGAGTCATCATTTTCAAGACACGTCCTCAAGAACCCAG 237
Qy 238 TTCTCCCTGAACCTGAACCTGTGTGACCGCGGACACGCGCGGTGTATTACTGTGCCAGA 297
Db 238 TTCTCCCTGAACCTGAGCTGTGTGACCGCGGACACGCGGTGTATTACTGTGCCAGG 297
Qy 298 GATTGGGCCCCAAATAGCTGGAAACACGCTAGGCTTCTGGGGCCAGGGAGTCTGTGTACC 357
Db 298 GGGAGCTACGGGGGCTACTACTACGGTATGGAGCTCTGGGGCCAGGGGACCAACCGTACC 357
Qy 358 GTCTCCTCA 366
Db 358 GTCTCCTCA 366

RESULT 15

US-09-017-628-9
; Sequence 9, Application US/09017628
; Patent No. 5990287
; GENERAL INFORMATION:
; APPLICANT: HOSOKAWA, Saiko

APPLICANT: TAGAWA, Toshiaki
APPLICANT: HIRAKAWA, Yoko
APPLICANT: ITO, No. 5990287ihiko
APPLICANT: NAGAIKE, Kazuhito
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
CELL SURFACE ANTIGEN OF CANCER CELL MEMBRANE
FILE REFERENCE: 177/527361KH
CURRENT APPLICATION NUMBER: US/09/017,628
CURRENT FILING DATE: 1998-02-02
EARLIER APPLICATION NUMBER: 08/360,125
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 366
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Hybridoma producing human antibody 1-3-1
US-09-017-628-9

Query Match 65.0%; Score 237.8; DB 2; Length 366;
Best Local Similarity 81.6%; Pred. No. 1.5e-62;
Matches 301; Conservative 0; Mismatches 62; Indels 6; Gaps 2;
Qy 1 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 60
Db 1 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 60
Qy 61 ACCTGCGCTGTCTGTGGTGGTCTCTCAGCAGTAGTA---ACTGGTGGACCTGGATCCGC 117
Db 61 ACCTGCACTGTCTGTGGTGGTCTCCATCAGCAGTAGTAGTACTACTGGGGCTGGATCCGC 120
Qy 118 CAGCCCCCAGGGAAGGGACTGGAGTGGATTGGAGCTATCTCTGGTGGTGGGGCCACC 177
Db 121 CAGCCCCCAGGGAAGGGGCTGGAGTGGATTGGAGTATCTATTATA---GTGGGAGCACC 177
Qy 178 AACTACAAACCGTCCCTCAAGAGTCGAGTCATCATTTTCAAGACACGTCCTCAAGAACCCAG 237
Db 178 TACTACAAACCGTCCCTCAAGAGTCGAGTCATCATTTTCAAGACACGTCCTCAAGAACCCAG 237
Qy 238 TTCTCCCTGAACCTGAACCTGTGTGACCGCGGACACGCGCGGTGTATTACTGTGCCAGA 297
Db 238 TTCTCCCTGAAGCTGAGCTGTGTGACCGCGGACACGCGGTGTATTACTGTGCCAGG 297
Qy 298 GATTGGGCCCCAAATAGCTGGAAACACGCTAGGCTTCTGGGGCCAGGGAGTCTGTGTACC 357
Db 298 GGGAGCTACGGGGGCTACTACTACGGTATGGAGCTCTGGGGCCAGGGGACCAACCGTACC 357
Qy 358 GTCTCCTCA 366
Db 358 GTCTCCTCA 366

Search completed: December 29, 2003, 21:48:28
Job time : 41.2876 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 1465.44 Seconds
(without alignments)
9875.644 Million cell updates/sec

Title: US-09-019-441-4_COPY_58_411

Perfect score: 354

Sequence: 1 GAGGTGACGCTGGTGGAGTC.....TCCTGGTCACCGTCTCCTCA 354

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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5: gb_ov.*

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8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	338.2	95.5	19040	6	BD075127 Method fo
2	255.2	72.1	463	9	AF173920 Macaca mu
3	254.6	71.9	463	9	AF173919 Macaca mu
4	253	71.5	463	9	AF173918 Macaca mu
5	252.4	71.3	429	9	AF416355 Papio cyn
6	250.4	70.7	458	6	BD015540 Human mon
7	250.4	70.7	458	6	BD094918 Human mon
8	246.6	69.7	462	9	AF173921 Macaca mu
9	244.8	69.2	714	9	AF173921 Macaca mu
10	244	68.9	364	6	BD161780 Method fo
11	244	68.9	364	6	BD167727 High effi
12	243.2	68.7	348	9	AB063673 Homo sapi
13	242.4	68.5	348	9	U00491 Human immun
14	242.2	68.4	429	9	HS03894 Human rheum
15	242.2	68.4	667	9	HS03894 Human rheum
16	241.8	68.3	462	9	AF173923 Macaca mu
17	241.6	68.2	714	9	AF173923 Macaca mu
18	241.6	68.2	714	9	AF173923 Macaca mu
19	241.6	68.2	714	9	AF173923 Macaca mu
20	241.6	68.2	714	9	AF173923 Macaca mu
21	240	67.8	714	9	AF173923 Macaca mu
22	240	67.8	720	6	AX740176 Sequence
23	240	67.8	720	6	AX740176 Sequence
24	240	67.8	720	6	AX740176 Sequence
25	239.8	67.7	405	9	HUMIGHADC
26	239.2	67.6	348	9	AF231396 Homo sapi
27	239.2	67.6	363	9	AF231396 Homo sapi
28	239.2	67.6	365	9	AF231396 Homo sapi
29	238.6	67.4	462	9	HUMIGHVAB
30	238.4	67.3	714	9	AF173922 Macaca mu
31	237.6	67.1	348	9	AF173922 Macaca mu
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33	237.6	67.1	372	9	AF173922 Macaca mu
34	237.4	67.1	376	9	AF173922 Macaca mu
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36	237	66.9	742	6	BD161779 Method fo
37	236.2	66.7	437	9	HUMIGHVAK
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39	236	66.7	360	9	AF173922 Macaca mu
40	236	66.7	360	9	AF173922 Macaca mu
41	236	66.7	527	9	AF173922 Macaca mu
42	236	66.7	534	9	AF173922 Macaca mu
43	235.8	66.6	376	9	AF173922 Macaca mu
44	235.6	66.6	342	9	AF173922 Macaca mu
45	235.4	66.5	342	9	AF173922 Macaca mu

ALIGNMENTS

RESULT 1
BD075127

LOCUS

DEFINITION

BD075127

Method for integrating genes at specific sites in mammalian cells

via homologous recombination and vectors for accomplishing the

same.

ACCESSION

BD075127.1

VERSION

BD075127.1

KEYWORDS

JP 2001516221-A/3.

SOURCE

unidentified

ORGANISM

unclassified.

REFERENCE

1 (bases 1 to 19040)

Reff.M.E., Barnett,R.S. and McLachlan,K.R.

Methd for integrating genes at specific sites in mammalian cells

TITLE

Method for integrating genes at specific sites in mammalian cells

19040 bp DNA linear PAT 27-AUG-2002

via homologous recombination and vectors for accomplishing the same

Patent: JP 2001516221-A 3 25-SEP-2001;

IDSC PHARMACEUTICALS CORP

OS Unidentified

PN JP 2001516221-A/3

PD 25-SEP-2001

PF 09-MAR-1998 JP 1998540539

PR 14-MAR-1997 US 08/819866 13-FEB-1998 US 09/023715 PI

MITCHELL E REFF, RICHARD SENCE BARNETT, KAREN RETTA MCLACHLAN PC

C12N15/90, C12N15/85, C12Q1/68, C12N5/10, C12N15/13, PC

C07K16/28,

PC C12N15/12, C07K14/705, G01N33/53, C12N15/62, C07K19/00 CC

Strandedness: Single;

CC Topology: Linear;

CC Method for integrating genes at specific sites in mammalian

CC cells via

CC homologous recombination and vectors for accomplishing the CC

Same

FH Key Location/Qualifiers

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FT Location/Qualifiers

1..19040

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/mol_type="genomic DNA"

/db_xref="taxon:32644"

BASE COUNT 4707 a 4976 c 4835 g 4522 t

ORIGIN

Query Match 95.5%; Score 338.2; DB 6; Length 19040;

Best Local Similarity 98.9%; Pred. No. 1e-81; 3; Indels 1; Gaps 1;

Matches 351; Conservative 0; Mismatches 0; TGGCAAGCCCTGGGGGTCCTCGAGACTC 60

9493 GAGGTGCAGCTGGTGGAGTCTGGGGGCGCTTGGCAAGCCCTGGGGGTCCTCGAGACTC 9552

61 TGGTCGCGAGCTCCGGGTTGAGTTACCTTCAATACTACTACAGACTGGGTCGCG 120

9553 TCCTCGCGAGCTCCGGGTTGAGTTACCTTCAATACTACTACAGACTGGGTCGCG 9612

121 CAGGCTCCAGGCGAGGCGTGGAGTGGTCTCAGCTATTAGTAGTGGTGGTATCCCA 180

9613 CAGGCTCCAGGCGAGGCGTGGAGTGGTCTCAGCTATTAGTAGTGGTGGTATCCCA 9672

181 TGGTACGAGACTCCGTTGAAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACA 240

9673 TGGTACGAGACTCCGTTGAAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACA 9732

241 CTGTTTCTTCAATGAACAGCTGAGCTGAGGACAGCGGTGCTATTACTGTGCGAGC 300

9733 CTGTTTCTTCAATGAACAGCTGAGCTGAGGACAGCGGTGCTATTACTGTGCGAGC 9792

301 TTGACTACAGGCTGTGACTCCTGGGGCCAGGAGTCTGTTGTCACCGTCTCTCA 354

9793 TTGACTACAGGCTGTGACTCCTGGGGCCAGGAGTCTGTTGTCACCGTCTCTCA 9847

RESULT 2

AF173920

LOCUS Macaca mulatta immunoglobulin heavy chain variable segment

DEFINITION precursor (IGHV) gene, partial cds.

ACCESSION AF173920

VERSION AF173920.1 GI:9587772

KEYWORDS

SOURCE Macaca mulatta (rhesus monkey)

ORGANISM Macaca mulatta

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

Cercopithecoidea; Macaca.

REFERENCE 1 (bases 1 to 463)

AUTHORS Helmut, E.P., Letvin, N.L. and Margolin, D.H.

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

2 (bases 1 to 463)

Margolin, D.H.

Direct Submission

Submitted (02-AUG-1999) Viral Pathogenesis Division, Beth Israel

Deaconess Medical Center, Research East 113, PO Box 15732, Boston,

MA 02215, USA

FEATURES

Location/Qualifiers

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/organism="Macaca mulatta"

/mol_type="genomic DNA"

/db_xref="taxon:9544"

/tissue_type="kidney"

/germline

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/gene="IGHV"

/note="similar to human immunoglobulin heavy chain

variable segments of the VH3 family; synonyms: IgVH, Ig

VH, VH"

join(1..46,150..>463)

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/codon_start=1

/product="immunoglobulin heavy chain variable segment

precursor"

/protein_id="AAF89376.1"

/db_xref="GI:9587773"

/translation="MFGLSWFLVALLKGVCQVQLVSGGGLAKPGGSLRLSCAAS

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NSLRADETATYCAKDTV"

47..149

/gene="IGHV"

457..>463

/gene="IGHV"

/functions="putative recombinant recognition sequence

(heptamer)"

BASE COUNT 103 a 91 c 151 g 118 t

ORIGIN

Query Match 72.1%; Score 255.2; DB 9; Length 463;

Best Local Similarity 93.6%; Pred. No. 6.1e-59;

Matches 279; Conservative 0; Mismatches 13; Indels 6; Gaps 1;

Qy 1 GAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAGCCCTGGGGGTCCTCGAGACTC 60

161 GAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAGCCCTGGGGGTCCTCGAGACTC 220

Qy 61 TGGTCGCGAGCTCCGGGTTGAGTTACCTTCAATACTACTACAGACTGGGTCGCG 120

221 TCCTGCGAGCTCCG-----GATTCACCTTCAGTACTACTACATGGAGCTGGGTCGCG 274

Qy 121 CAGGCTCCAGGCGAGGCGCTGGAGTGGTCTCAGCTATTAGTAGTGGTGGTATCCCA 180

275 CAGGCTCCAGGCGAGGCGCTGGAGTGGTCTCAGCTATTAGTAGTGGTGGTATCCCA 334

Qy 181 TGGTACGAGACTCCGTTGAAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACA 240

335 TGGTACGAGACTCCGTTGAAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACA 394

Qy 241 CTGTTTCTTCAATGAACAGCTGAGCTGAGGACAGCGGTGCTATTACTGTGCGGA 298

395 CTGTATCTTCAATGAACAGCTGAGCTGAGGACAGCGGTGCTATTACTGTGCGGA 452

RESULT 3

AF173919

LOCUS Macaca mulatta immunoglobulin heavy chain variable segment

DEFINITION precursor (IGHV) gene, partial cds.

ACCESSION AF173919


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|||||
275 CAGGCTCAGGAAGGGCTGGAGTGGCTCTCAGCTATTAGTATGGTGGTAGCACA 334
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181 TGGTACGAGACTCCGTTGAAGGCGAGATTCACCATCTCCAGAGAAACGCAACACACA 240
|||||
335 TGGTACGAGACTCCGTTGAAGGCGAGATTCACCATCTCCAGAGAAACGCAACACACA 394
|||||
241 CTGTTCTTCAATGAACAGCTGAGAGCTGAGGACAGGCTGTCTATTACTGTGCGAG 299
|||||
395 CTGTATCTTCAATGAACAGCTGAGAGCTGAGGACAGGCTGTCTATTACTGTGCGAG 453
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RESULT 5
AF416355 429 bp mRNA linear PRI 27-MAR-2002
LOCUS Papio cynocephalus anubis clone VH3-d3 immunoglobulin heavy chain
DEFINITION variable region mRNA, partial cds.
ACCESSION AF416355
VERSION AF416355.1 GI:19744271
KEYWORDS Papio anubis (olive baboon)
SOURCE Papio anubis
ORGANISM Papio anubis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Papio.
REFERENCE 1 (bases 1 to 429)
Scnicariello,F., Jayashankar,L. and Attanasio,R.
Baboon immunoglobulin variable region heavy chains: identification
of genes homologous to members of the human IGHV1-IGHV7 subgroups
Immunogenetics 53 (10-11), 815-820 (2002)
JOURNAL MEDLINE 21850437
PUBMED 11862381
REFERENCE 2 (bases 1 to 429)
Scnicariello,F., Jayashankar,L. and Attanasio,R.
Direct Submission
AUTHORS Submitted (04-SEP-2001) Department of Biology, Georgia State
University, PO BOX 4010, Atlanta, GA 30302, USA
JOURNAL Location/Qualifiers
FEATURES
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1..429
/codon_start=1
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/protein_id="AAL96421.1"
/db_xref="GI:19744272"
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GFTSDYIMDVRQAPGKLEWVRKINTGWTWADSVKGRFTISRNANKNTLYLQWN
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BASE COUNT 87 a 107 c 141 g 94 t
ORIGIN

Query Match 71.3%; Score 252.4; DB 9; Length 429;
Best Local Similarity 87.2%; Pred. No. 3.6e-58;
Matches 319; Conservative 0; Mismatches 26; Indels 21; Gaps 3;

QY 1 GAGGTGACGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGCTCCCTGAGACTC 60
DB 58 GAGGTGACGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGCTCCCTGAGACTC 117
QY 61 TGGTGCAGCCTCCGGGTTGAGTTTACCTTCAATAACTACTACATGAGACTGGGTCGCG 120
DB 118 TCCTGCGCAGCTCCG-----GATTACCTTCAGTGACTACTACATGAGACTGGGTCGCG 171
QY 121 CAGGCTCCAGGCGAGGCGCTGGAGTGGGCTCTCAGCTATTAGTAGTGGTATCCCA 180
DB 172 CAGGCTCCAGGCGAGGCGCTGGAGTGGGCTCTCAGCTATTAGTAGTGGTATCCCA 228
QY 181 TGGTACGAGACTCCGTTGAAGGCGAGATTCACCATCTCCAGAGAAACGCAACACACA 240
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Db 229 TGGTACGAGACTCCGTTGAAGGCGGCTTCCATCCTCCAGAGAAACGCAACACACA 288
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DB 289 CTGTATCTTCAATGAACAGCTGAGAGCTGAGGACAGGCTGTCTATTACTGTGCGAGA 348
QY 300 -----CTTGACTACAGGGTCTGACTCTCTGGGGCCAGGAGTCTCTGGTCCACGCTC 348
DB 349 GATCGAAGGACAGTAACCTGGGGGTTGACTACTGGGCCAGGAGTCTCTGGTCCACGCTC 408
QY 349 TCCTCA 354
DB 409 TCCTCA 414
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RESULT 6
BD015540 458 bp DNA linear PAT 27-AUG-2002
LOCUS Human monoclonal antibody against TGF-beta-II receptor and
DEFINITION medicinal use thereof.
ACCESSION BD015540
VERSION BD015540.1 GI:22556677
KEYWORDS JP 2001206899-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 458)
Sakamoto,S. and Kamada,M.
Human monoclonal antibody against TGF-beta-II receptor and
medicinal use thereof
Patent: JP 2001206899-A 2 31-JUL-2001;
JOURNAL JAPAN TOBACCO INC
COMMENT OS Homo sapiens (human)
PN JP 2001206899-A/2
PD 31-JUL-2001
PF 08-NOV-2000 JP 2000340216
PI SHINJI SAKAMOTO,NASAFUMI KAMADA
PC C07K16/28,A61K39/395,A61P1/16,A61P9/04,A61P9/10,A61P9/10, PC
A61P11/00,
PC A61P13/12,A61P17/00,A61P17/02,A61P17/04,A61P17/06,A61P19/02,
PC A61P43/00,
PC C12N5/10,C12N15/02//C12P21/08
CC Human monoclonal antibody against TGF-beta-II receptor and CC
thereof medicinal use
CC therof
FT Key Location/Qualifiers
CDS 1..458
Location/Qualifiers
1..458
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 92 a 121 c 139 g 106 t
ORIGIN

Query Match 70.7%; Score 250.4; DB 6; Length 458;
Best Local Similarity 83.9%; Pred. No. 1.3e-57;
Matches 297; Conservative 0; Mismatches 51; Indels 6; Gaps 1;

QY 1 GAGGTGACGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGCTCCCTGAGACTC 60
DB 58 GAGGTGACGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGCTCCCTGAGACTC 117
QY 61 TGGTGCAGCCTCCGGGTTGAGTTTCACTTCAATAACTACTACATGAGACTGGGTCGCG 120
DB 118 TCCTGTCAGCCTCTG-----GATTACCTTCAGTAGCTTTAGCATGAACCTGGGTCGCG 171
QY 121 CAGGCTCCAGGCGAGGCGCTGGAGTGGGCTCTCAGTATTAGTAGTGGTATCCCA 180
DB 172 CAGGCTCCAGGCGAGGCGCTGGAGTGGGCTCTCAGTATTAGTAGTGGTATCCCA 231
QY 181 TGGTACGAGACTCCGTTGAAGGCGAGATTCACCATCTCCAGAGAAACGCAACACACA 240
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232 TACTACACAGACTCAGTGAAGGCGGATTACCATCTCCAGAGACAACGCCAAGAACTCA 291
241 CTGTTTCTTCAATGAACAGCTGAGAGCTGAGACACAGCGTGTCTATTACTGTGGCAGC 300
292 CTGTATCTGCAATGAACAGCTGAGAGCGGAGACACAGCGTGTCTATTACTGTGGCAGA 351
301 TTGACTACAGGCTGTGACTCTCTGGGGCCAGGAGTCTCTGGTCAACCGTCTCTCTCA 354
352 GGGTACTGGGGTTTGACTACTGGGGCCAGGAGAACCTGTGTCACCGTCTCTCTCA 405

RESULT 7
BD094918 458 bp DNA linear PAT 27-AUG-2002
LOCUS Human monoclonal antibody for human TGF-beta type II receptor and
DEFINITION pharmaceutical use thereof.
ACCESSION BD094918
VERSION BD094918.1 GI:22640506
KEYWORDS WO 0136642-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 458)
AUTHORS Sakamoto, S. and Kamada, M.
TITLE Human monoclonal antibody for human TGF-beta type II receptor and
pharmaceutical use thereof
JOURNAL Patent: WO 0136642-A 2 25-MAY-2001;
JAPAN TOBACCO INC, SHINJI SAKAMOTO, MASAFUMI KAWADA
COMMENT OS Homo sapiens (human)
PN WO 0136642-A/2
PD 25-MAY-2001
PF 17-NOV-2000 WO 2000JP008129
PR 18-NOV-1999 JP 99P 328681.08-NOV-2000 JP OOP 340216 PI
SHINJI SAKAMOTO, MASAFUMI KAWADA
PC C12N15/13, C07K16/28, C12N5/16, A61K39/395, A61P13/12,
A61P11/00,
PC A61P11/00, A61P9/08, A61P9/10, A61P17/06, A61P17/04, A61P17/02, PC
A61P19/02.
PC A61P29/00
CC Human monoclonal antibody for human TGF-beta type II receptor
and
CC pharmaceutical use thereof
FH Key Location/Qualifiers
FT CDS (1)..(456).
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BASE COUNT 92 a 121 c 139 g 106 t
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Query Match 70.7%; Score 250.4; DB 6; Length 458;
Best Local Similarity 83.9%; Pred. No. 1.3e-57;
Matches 297; Conservative 0; Mismatches 51; Indels 6; Gaps 1;

1 GAGGTGACGTGTGGAGTCTGGGGCGGCTTGCAAGAGCTGGGGGTCCTGAGACTC 60
58 GAGGTGACGTGTGGAGTCTGGGGCGGCTTGCAAGAGCTGGGGGTCCTGAGACTC 117
61 TGGTGGCGAGCTCGGGTTCAGTTTCACTTCAATACTACTAGTGGTGGTCCGC 120
118 TCCTGTGACGCTCTG-----GATTACCTTCAGTAGCTTTAGCATGAACTGGTCCGC 171
121 CAGGCTCCAGGCGAGGCGCTGGAGTGGGTCTCAGTATTAGTAGTGGTATGCCACA 180
172 CAGGCTCCAGGAGAGGCGTGGAGTGGGTCTATCCATCATTAGTAGTAGTATCAT 231
181 TGGTACGACAGCTCCGTGAAGGGGAGATTACCATCTCCAGAGAGAACGCCAACACA 240
232 TACTACACAGACTCAGTGAAGGCGGATTACCATCTCCAGAGACAACGCCAAGAACTCA 291

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241 CTGTTTCTTCAATGAACAGCTGAGAGCTGAGGACACAGCGTGTCTATTACTGTGGCAGC 300
292 CTGTATCTGCAATGAACAGCTGAGAGCGGAGACACAGCGTGTCTATTACTGTGGCAGA 351
301 TTGACTACAGGCTGTGACTCTCTGGGGCCAGGAGTCTCTGGTCAACCGTCTCTCTCA 354
352 GGGTACTGGGGTTTGACTACTGGGGCCAGGAGAACCTGTGTCACCGTCTCTCTCA 405

RESULT 8
AF173921 462 bp DNA linear PRI 31-JUL-2000
LOCUS Macaca mulatta immunoglobulin heavy chain variable segment
DEFINITION precursor (IGHV) gene, partial cds.
ACCESSION AF173921
VERSION AF173921.1 GI:9587774
KEYWORDS
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
REFERENCE 1 (bases 1 to 462)
AUTHORS Helmut, E.F., Letwin, N.L. and Margolin, D.H.
TITLE Germline repertoire of the immunoglobulin V(H)3 family in rhesus
monkeys
JOURNAL Immunogenetics 51 (7), 519-527 (2000)
MEDLINE 20367631
PUBMED 10912503
REFERENCE 2 (bases 1 to 462)
AUTHORS Margolin, D.H.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-1999) Viral Pathogenesis Division, Beth Israel
Deaconess Medical Center, Research East 113, PO Box 15732, Boston,
MA 02215, USA
FEATURES
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/tissue_type="kidney"
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/gene="IGHV"
/notes="similar to human immunoglobulin heavy chain
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VH, VH"
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misc_feature
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(heptamer)"
BASE COUNT 100 a 91 c 153 g 118 t
ORIGIN
Query Match 69.7%; Score 246.6; DB 9; Length 462;
Best Local Similarity 91.6%; Pred. No. 1.4e-56;
Matches 274; Conservative 0; Mismatches 19; Indels 6; Gaps 1;

1 GAGGTGACGTGTGGAGTCTGGGGCGGCTTGCGCAAGCTGGGGGTCCTGAGACTC 60

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Db      160 GAGGTGAGCTGGTGGAGTCTGGGGCGGCTTGCCAAAGCCTGGGGGTCCTCGAGACTC 219
Qy      61 TGGTGGCAGCCTCGGGTTCAGGTTCACTTCAATAAATCACTACATGAGTGGTCCGC 120
Db      220 TCCTGGCAGCCTCTG-----GATTCACTTCACTAGTACTACATGAGTGGTCCGC 273
Qy      121 CAGGCTCCAGGCGAGGGCTGGAGTGGTCTCAGTATTAGTACTAGTGGTATCCACA 180
Db      274 CAGGCTTCCAGGGAAGGGCTGGAGTGGTCTCAGTATTAGTACTAGTGGTATCCACA 333
Qy      181 TGGTACGAGACTCCGTTGAAGGCGAGATTACCATCTCCAGAGAAAGCGCAACACACA 240
Db      334 TGGTACGAGACTCCGTTGAAGGCGAGATTACCATCTCCAGAGAAAGCGCAACACACA 393
Qy      241 CTGTTTCTTCAATGAACAGCCTGAGAGCTGAGACACGGTGTCTATTACTGTGGCAG 299
Db      394 CTGTATCTTCAATGAGCAGCTGAGAGCTGAGACACGGCGGTATTACTGTGGCAG 452

RESULT 9
HSA6119      714 bp      mRNA      linear      PRI 18-NOV-1998
LOCUS      Homo sapiens mRNA for A4 anti-IFN-G scFv recombinant antibody,
DEFINITION      partial.
ACCESSION      AJ006119
VERSION      AJ006119.1 GI:3152373
KEYWORDS      recombinant antibody.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS      Pini, A., Viti, F., Santucci, A., Carnemolla, B., Zardi, L., Neri, P. and
TITLES      Neri, D.
      Design and use of a phage display library. Human antibodies with
      subnanomolar affinity against a marker of angiogenesis eluted from
      a two-dimensional gel
JOURNAL      J. Biol. Chem. 273 (34), 21769-21776 (1998)
MEDLINE      98371014
PUBMED      9705314
REFERENCE      2 (bases 1 to 714)
AUTHORS      Viti, F.
TITLES      Direct Submission
JOURNAL      Submitted (12-MAY-1998) Viti F., Molecular Biology and Biophysics,
      ETH (Swiss Federal Institute of Technology), ETH Hoenggerberg,
      CH-8093 Zuerich, SWITZERLAND
FEATURES      Location/Qualifiers
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BASE COUNT      150 a      189 c      224 g      151 t
ORIGIN
Query Match      69.2%; Score 244.8; DB 9; Length 714;
Best Local Similarity      83.4%; Pred. No. 4.2e-56;
Matches 292; Conservative 0; Mismatches 52; Indels 6; Gaps 1;

Qy      1 GAGGTGAGCTGGTGGAGTCTGGGGCGGCTTGCCAAAGCCTGGGGGTCCTCGAGACTC 60
Db      1 GAGGTGAGCTGGTGGAGTCTGGGGCGGCTTGCTGACAGCTGGGGGTCCTCGAGACTC 60
Qy      61 TGGTGGCAGCCTCGGGTTCAGGTTCACTTCAATAAATCACTACATGAGTGGTCCGC 120

Db      160 GAGGTGAGCTGGTGGAGTCTGGGGCGGCTTGCCAAAGCCTGGGGGTCCTCGAGACTC 219
Qy      61 TGGTGGCAGCCTCGGGTTCAGGTTCACTTCAATAAATCACTACATGAGTGGTCCGC 120
Db      220 TCCTGGCAGCCTCTG-----GATTCACTTCACTAGTACTACATGAGTGGTCCGC 273
Qy      121 CAGGCTCCAGGCGAGGGCTGGAGTGGTCTCAGTATTAGTACTAGTGGTATCCACA 180
Db      274 CAGGCTTCCAGGGAAGGGCTGGAGTGGTCTCAGTATTAGTACTAGTGGTATCCACA 333
Qy      181 TGGTACGAGACTCCGTTGAAGGCGAGATTACCATCTCCAGAGAAAGCGCAACACACA 240
Db      334 TGGTACGAGACTCCGTTGAAGGCGAGATTACCATCTCCAGAGAAAGCGCAACACAGC 294
Qy      241 CTGTTTCTTCAATGAACAGCCTGAGAGCTGAGACACGGTGTCTATTACTGTGGCAGC 300
Db      235 CTGTATCTTCAATGAACAGCCTGAGAGCGGAGACACGGCGGTATATTACTGTGGGAAA 294
Qy      301 TTGACTACAGGCTGCTGACTCTCGGGCGCAGGGAGTCTCGTACCGCTCTC 350
Db      295 CGTGTCTCTCGGTTTGACTACTTGGGCGCAGGGAACCGTGTGTCACCGTCTC 344

RESULT 10
BD161780      364 bp      DNA      linear      PAT 17-JAN-2003
LOCUS      Method for screening high-efficiency antibody.
DEFINITION      BD161780
ACCESSION      BD161780
VERSION      BD161780.1 GI:27867538
KEYWORDS      JP 2002174635-A/164.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 364)
AUTHORS      Kaneko, K.
TITLES      Method for screening high-efficiency antibody
JOURNAL      Patent: JP 2002174635-A 164 21-JUN-2002;
      JAPAN SCIENCE AND TECHNOLOGY CORP, PRESIDENT OF NATIONAL CENTER OF
      NEU TECHNOLOGY, HEALTH LABOUR AND WELFARE
COMMENT      OS Homo sapiens (human)
      PN JP 2002174635-A/164
      PD 21-JUN-2002
      PF 07-DEC-2000 JP 2000373259
      PI KIYOTOSHI KANEKO
      PC G01N33/53.C12N15/09.C12P21/08.C12Q1/68.C12N15/00 CC Method
      for screening high-efficiency antibody FH Key
      Location/Qualifiers
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      /db_xref="taxon:9606"
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BASE COUNT      73 a      90 c      114 g      75 t      12 others
ORIGIN
Query Match      68.9%; Score 244; DB 6; Length 364;
Best Local Similarity      82.0%; Pred. No. 7.1e-56;
Matches 287; Conservative 0; Mismatches 57; Indels 6; Gaps 1;

Qy      1 GAGGTGAGCTGGTGGAGTCTGGGGCGGCTTGCCAAAGCCTGGGGGTCCTCGAGACTC 60
Db      9 GAGGTGAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCTGGGGGTCCTCGAGACTC 68
Qy      61 TGGTGGCAGCCTCGGGTTCAGGTTCACTTCAATAAATCACTACATGAGTGGTCCGC 120
Db      69 TCCTGTGAGCCTCTG-----GATTCACTTCACTAGTACTAGTGGTATCCACA 122
Qy      121 CAGGCTCCAGGCGAGGGCTGGAGTGGTCTCAGTATTAGTACTAGTGGTATCCACA 180
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Qy      181 TGGTACGAGCTCCGTTGAAGGCGAGATTACCATCTCCAGAGAAAGCGCAACACACA 240

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Db 183 TACTACGAGACTCCGTGAGGCGCGTTACCATCTCCAGAGACAAATTCAGAACACG 242
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Db 243 CTGTATCTGCAATGAACAGCTCAGAGCTCAGACACGCGGTATATTACTGTGCCAAA 302
Qy 301 TTGACTACAGGCTGTGACTCTCTGGGGCCAGGAGTCTCTGTGCACCGTCTC 350
Db 303 NNNNNNNNNNTTGTACTACTGGGCGCAGGAACCTGTGTACCGTCTC 352

RESULT 11
BD167727
LOCUS BD167727 364 bp DNA linear PAT 17-JAN-2003
DEFINITION High efficiency screening method for antibodies.
ACCESSION BD167727
VERSION BD167727.1 GI:27873539
KEYWORDS WO 0242774-A/164.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 364)
AUTHORS Kaneko,K.
TITLE High efficiency screening method for antibodies
JOURNAL Patent: WO 0242774-A 164 30-MAY-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP. JAPAN AS REPRESENTED BY
PRESIDENT O KAZUHIKO KATAYAMA PSCHIATRY MINISTRY OF HEALTH LABOUR
AND WELFARE, KIYOTOSHI KANEKO
OS Homo sapiens (human)
PN WO 0242774-A/164
PD 30-MAY-2002
PF 05-JUN-2001 WO 2001JP004732
PR 24-NOV-2000 JP OOP 358539
PI KIYOTOSHI KANEKO
PC G01N33/531
CC High efficiency screening method for antibodies FH Key
Location/Qualifiers
FT source 1..364 /organism="Homo sapiens (human)"
FT Location/Qualifiers
1..364
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/mol_type="genomic DNA"
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BASE COUNT 73 a 90 c 114 g 75 t 12 others
ORIGIN

Query Match 68.9%; Score 244; DB 6; Length 364;
Best Local Similarity 82.0%; Pred. No. 7.1e-56;
Matches 287; Conservative 0; Mismatches 57; Indels 6; Gaps 1;

Qy 1 GAGTGCAGCTGTGGAGTCTGGGGCGGCTTGCAAGCCTGGGGGTCCCTGAGACTC 60
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Qy 61 TGGTGGCAGCTCCGGTTCAGGTTACCTTCAATACTACTACATGAGTGGTCCGC 120
Db 69 TCCTGTGCAGCTCTG-----GATTACCTTTAGCAGCTATGCGATGAGTGGTCCGC 122

Qy 121 CAGGCTCCAGGCGAGGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTATCCACACA 180
Db 123 CAGGCTCCAGGAGAGGGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTATCCACACA 182

Qy 181 TGGTACGAGACTCCGTGAAGGGCAGATTACCATCTCCAGAGAGAACGCCAACACACA 240
Db 183 TACTACGAGACTCCGTGAAGGGCGGTTTACCATCTCCAGAGACAAATTCAGAACACG 242

Qy 241 CTGTTTCTTCAATGAACAGCTCAGAGCTCAGACACGCGTGTCTATTACTGTGCCAGC 300
Db 243 CTGTATCTGCAATGAACAGCTCAGAGCTCAGACACGCGGTATATTACTGTGCCAAA 302

Qy 301 TTGACTACAGGCTGTGACTCTCTGGGGCCAGGAGTCTCTGTGCACCGTCTC 350

Db 303 NNNNNNNNNNTTGTACTACTGGGCGCAGGAACCTGTGTACCGTCTC 352

RESULT 12
AB063673
LOCUS AB063673 348 bp mRNA linear PRI 02-JUL-2002
DEFINITION Homo sapiens IGH mRNA for immunoglobulin heavy chain VHDJ region, partial cds, clone:H23.
ACCESSION AB063673
VERSION AB063673.1 GI:21668547
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M., Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J., Miura,K. and Kurosawa,Y.
TITLE Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional genomics
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 348)
AUTHORS Kurosawa,Y.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University; Kutsukake-cho, Toyosake 470-1192, Japan (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387) Please visit our web site URL:http://www.fujita-hu.ac.jp/immunity/.

FEATURES
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79 a 83 c 109 g 77 t

BASE COUNT 79 a 83 c 109 g 77 t
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Query Match 68.7%; Score 243.2; DB 9; Length 348;
Best Local Similarity 83.1%; Pred. No. 1.2e-55;
Matches 291; Conservative 0; Mismatches 53; Indels 6; Gaps 1;

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Qy 61 TGGTGGCAGCTCCGGTTCAGGTTCACTTCAATACTACTACATGAGTGGTCCGC 120
Db 61 TCCTGTGCAGCTCTG-----GATTACCTTCAGTAGTTATGAATGAATGGTCCGC 114

Qy 121 CAGGCTCCAGGCGAGGCGTGGAGTGGGTCTCAGCTATTAGTAGTGGTATCCACACA 180
Db 115 CAGGCTCCAGGGAAGGGCTGGAGTGGGTTCATACATTTAGTAGTAGTACCATTA 174

Qy 181 TGGTACGAGACTCCGTGAAGGGCAGATTACCATCTCCAGAGAGAACGCCAACACACA 240

Db 175 TACTACGAGACTCTGTGAAGGCGGATTACCATCTCCAGAGACAGCCAGAACTCA 234
Qy 241 CTGTTCTTCAATGAACAGCCTGAGAGCTGAGACACGCTGTCTATTACTGTGCGAGC 300
Db 235 CTGTATCTGCAATGAACAGCCTGAGAGCCGAGACACGCTGTCTATTACTGTGCGAGA 294
Qy 301 TTGACTACAGGCTGTGACTCTCTGGGGCCAGGGAGTCTGTGTCACCGTCTC 350
Db 295 GGTTGGGGAACCTTGACTACTGTGGGGCCAGGGAACCTGTGTCACCGTCTC 344

RESULT 13
U00491 348 bp mRNA linear PRI 08-MAY-1994
LOCUS Human immunoglobulin heavy chain variable region (clone Amulc3-3)
DEFINITION mRNA, partial cds.
ACCESSION U00491
VERSION U00491.1 GI:392577
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 348)
AUTHORS Huang, C. and Stollar, B.D.
TITLE A majority of Ig H chain cDNA of normal human adult blood lymphocytes resembles cDNA for fetal Ig and natural autoantibodies
JOURNAL J. Immunol. 151 (10), 5290-5300 (1993)
MEDLINE 94044753
PUBMED 8228225
REFERENCE 2 (bases 1 to 348)
AUTHORS Stollar, B.D.
TITLE Direct Submission
JOURNAL Submitted (10-AUG-1993) Stollar B.D., Tufts University, Biochemistry, 136 Harrison Ave., Boston, MA 02111, USA

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91 a 118 c 134 g 86 t

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Matches 292; Conservative 0; Mismatches 56; Indels 6; Gaps 1;
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Db 1 GAGGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGTACAGCCTGGGGGTCCCTGAGACTC 60
Qy 61 TGGTGGCAGCTCCGGGTTCAGGTTCACCTCACTACTACGATCGATGGTGGTCCGC 120
Db 61 TCCTGTGAGCCTC-----TAGATTCACCTTTAGCAGCTATGCCATGAGTGGGTCCGC 114
Qy 121 CAGGCTCCAGGCGAGGGCTGGAGTGGGTCTCACCTATTAGTAGTGGTGGTATCCCA 180
Db 115 CAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGCTATCAGTGTAGTGGTAGCACA 174

Qy 181 TGTAGCAGACTCCGTGAAGGSCAGATTACCATCTCCAGAGAGAACGCAACACACA 240
Db 175 TACTACGAGACTCCGTGAAGGCGGTTACCATCTCCAGAGACAAATCCAGACACG 234
Qy 241 CTGTTCTTCAATGAACAGCCTGAGAGCTGAGGACACGCGTGTCTATTACTGTGCGAGC 300
Db 235 CTGTATCTGCAATGAACAGCCTGAGAGCCGAGACACGCGCTATATTACTGTGCGATG 294
Qy 301 TTGACTACAGGCTGTGACTCTCTGGGGCCAGGGAGTCTGTGTCACCGTCTCCTCA 354
Db 295 GTGGGAGCTTCCCATGACTACTGTGGGGCCAGGGAACCTGTGTCACCGTCTCCTCA 348

RESULT 14
HSHA3D1IG 429 bp mRNA linear PRI 15-FEB-1999
LOCUS Homo sapiens rearranged Humigha3d1 gene encoding IgG heavy chain
DEFINITION variable region.
ACCESSION X59703
VERSION X59703.1 GI:32012
KEYWORDS heavy chain; IgG; immunoglobulin; J-segment; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 429)
AUTHORS Olee, T., Lu, E.W., Huang, D.F., Soto-Gil, R.W., Defetos, M., Kozin, P., Carson, D.A. and Chen, P.P.
TITLE Genetic analysis of self-associating immunoglobulin G rheumatoid factors from two rheumatoid synovia implicates an antigen-driven response
JOURNAL J. Exp. Med. 175 (3), 831-842 (1992)
MEDLINE 92158804
PUBMED 1740665
REFERENCE 2 (bases 1 to 429)
AUTHORS Tsaiwei, O.
TITLE Direct Submission
JOURNAL Submitted (17-JAN-1992) O. Tsaiwei, Department of Medicine - 0663, University of California, San Diego La Jolla, California 92093-0663, USA

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91 a 118 c 134 g 86 t

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Best Local Similarity 84.0%; Pred. No. 2.2e-55;
Matches 300; Conservative 0; Mismatches 48; Indels 9; Gaps 2;
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Qy 61 TGGTCGCGAGCTCCGGGTTTCAGGTTTACCTTCAATTAACACTACTACATGAGTGGGTCCGC 120
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 Db 61 TCCTGTGCGAGCTCTG-----GATTCACCTTCAGTAACATAGATGAATGGGTCCGC 114
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 Qy 241 CTGTTTCTTCAATGAACAGAGCTCAGAGCTCAGAGACAGGCTGTCTATTACTGTGCG--- 297
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RESULT 15
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 DEFINITION Human rheumatoid factor D1 IgG heavy chain VH3 region rearranged.
 ACCESSION U03894
 VERSION U03894.1 GI:485719
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 20 to 532)
 Defetos, M., Olee, T., Carson, D.A. and Chen, P.P.
 Defining the genetic origins of three rheumatoid synovium-derived
 IgG rheumatoid factors
 J. Clin. Invest. 93 (6), 2545-2553 (1994)
 JOURNAL 94259815
 MEDLINE 8200991
 PUBMED
 REFERENCE 2 (bases 1 to 667)
 Chen, P.P.
 Direct Submission
 TITLE Submitted (01-DEC-1993) Pojen P. Chen, Medicine, University of
 JOURNAL California San Diego, 9500 Gilman Dr., La Jolla, CA 92093-0663, USA
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 Best Local Similarity 84.0%; Pred. No. 2.1e-55;
 Matches 300; Conservative 0; Mismatches 48; Indels 9; Gaps 2;
 Qy 1 GAGGTGCGAGCTCTGGAGTCTGGGGCGGCTTGGCAAGAGCTGGGGGTCCCTGAGACTC 60
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 Db 239 GAGGTGCGAGCTCTGGAGTCTGGGGGAGGCTTGGTACAGCTGGGGGTCCCTGAGACTC 298
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 Qy 61 TGGTGGCGAGCTCCGGGTTTCAGGTTTCACTTCAATAACTACTACATGAGACTGGGTCCGC 120
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 Db 299 TCCTGTGCGAGCTCTG-----GATTCACCTTCAGTAACATATAGCATGAATGGGTCCGC 352
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 Qy 121 CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCAGTATTAAGTAGTAGTGGTATCCACA 180
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 Db 353 CAGGCTCCAGGGAAGGGGCTGGAGTGGGTTTCATACATTAGTAGTAGTAGTATCCATA 412
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 Qy 181 TGGTACGCGAGCTCCGTGAAGGGCAGATTCCACCATCTCCAGAGAGACGCCAACACACA 240
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 Db 413 TACTACGCGAGACTCTGTGAAGGGCCGATTCCACCATCTCCAGAGACAATGCCAAGAACTCA 472
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 Qy 241 CTGTTTCTTCAATGAACAGCTTGAGAGCTGAGACACGCTGTCTATTACTGTGCG--- 297
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 Db 473 CTGTATCTGCAATGAACAGCTTGAGAGCCGAGGACACGCTGTGTATTACTGTGCGAGA 532
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 Qy 298 AGCTTGACTACAGGTTTGTACTCTCTGGGGCCAGGGAGTCTCTGTCACCGTCTCCTCA 354
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 Db 533 AGCGGATACAGAGGGGGCGAGTACTGGGGCCAGGGAACCTGGTCAACCGTCTCCTCA 589
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 1531.8 Seconds
(without alignments)
5616.780 Million cell updates/sec

Title: US-09-019-441-4_COPY_58_411

Perfect score: 354

Sequence: 1 GAGGTGAGCTGGTGGAGTC.....TCCTGGTCACCGTCTCTCA 354

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hcc:*
9: gb_est1:*
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16: em_estom:*
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25: em_gss_rtd:*
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27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	241.4	68.2	406	9 AW401971	AW401971 UI-HF-BK0
2	239.2	67.6	1138	13 BX379829	BX379829 BX379829
3	239.2	67.6	1201	13 BX417408	BX417408 BX417408
4	235.8	66.6	613	12 BM007475	BM007475 603616742

5	232.8	65.8	447	9	AW402793	AW402793 UI-HF-BK0
6	231.4	65.4	511	9	AW402613	AW402613 UI-HF-BK0
7	230.2	65.0	471	9	AW403220	AW403220 UI-HF-BK0
8	227.6	64.3	1164	10	BF974771	BF974771 602245420
9	225.2	63.6	443	9	AW401428	AW401428 UI-HF-BK0
10	224.8	63.5	582	9	AW401386	AW401386 UI-HF-BK0
11	224.4	63.4	648	10	BG340670	BG340670 602462250
12	223.2	63.1	429	9	AJ547930	AJ547930 AJ547930
13	223.2	63.1	920	13	BQ708458	BQ708458 AGENCOURT
14	222	62.7	920	13	BQ711467	BQ711467 AGENCOURT
15	221.6	62.6	456	9	AW403059	AW403059 UI-HF-BK0
16	221.4	62.5	894	10	BG684839	BG684839 602636557
17	221.2	62.5	481	14	CA397706	CA397706 CS94F03.Y
18	219.8	62.1	908	10	BG686881	BG686881 602650867
19	219.4	62.0	440	9	AW408304	AW408304 UI-HF-BK0
20	219.4	62.0	687	10	BG397964	BG397964 602439484
21	219.4	62.0	879	10	BG759748	BG759748 602711146
22	219.4	62.0	1004	13	BQ711355	BQ711355 AGENCOURT
23	219	61.9	889	13	BX357384	BX357384 BX357384
24	218.4	61.7	942	13	BQ710859	BQ710859 AGENCOURT
25	217.8	61.5	740	10	BG757947	BG757947 602714983
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27	217.8	61.5	875	13	BQ706723	BQ706723 AGENCOURT
28	217.8	61.5	968	13	BQ706746	BQ706746 AGENCOURT
29	217.8	61.5	1069	12	BM914329	BM914329 AGENCOURT
30	217	61.3	840	10	BG756031	BG756031 602716521
31	216.8	61.2	510	9	AW403707	AW403707 UI-HF-BK0
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33	215.8	61.0	618	12	BM713479	BM713479 UI-E-EJO-
34	215.6	60.9	911	13	BQ712666	BQ712666 AGENCOURT
35	215.6	60.9	916	13	BQ708408	BQ708408 AGENCOURT
36	215.4	60.8	890	13	BQ709879	BQ709879 AGENCOURT
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38	215.2	60.8	487	9	AW403882	AW403882 UI-HF-BK0
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41	214.2	60.5	957	13	BQ894558	BQ894558 AGENCOURT
42	213.6	60.3	962	13	BQ707926	BQ707926 AGENCOURT
43	213.6	60.3	988	13	BQ712092	BQ712092 AGENCOURT
44	213	60.2	868	12	BG771903	BG771903 602721715
45	212.6	60.1	494	10	BG745545	BG745545 602723942

ALIGNMENTS

RESULT 1
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DEFINITION IMAGE:3054342 5', mRNA sequence.
ACCESSION AW401971
VERSION AW401971.1 GI:6920657
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 406)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

	Location/Qualifiers	
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ORIGIN		
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	Best Local Similarity 82.2%; Pred. No. 3.2e-52;	
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Db	173 CAGGCTCCAGGGAAGGGCTGGAGTGGGTTTCATACATTAGTAGTAGTGTGATACCATA 232	
Qy	181 TGGTACCCAGACTCCGTGAAGGGCAGATTACCATCTCCAGAGNAGACGCCAACACACA 240	
Db	233 TACTACGCAGACTCTGTGAAGGGCCGAGTACCACATCTCCAGAGACAAAGCCNAGAAGTCA 292	
Qy	241 CTGPTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCCAGC 300	
Db	293 CTGTATCTGCANATGAACAGCCTGAGAGCCGAGAGACACGGCTGTTTATTACTGTGCGAGT 352	
Qy	301 TTGACTACAGGGTCTGACTCTGGGGCCAGGGAGTCTGTGTCACCGTCTCCTCA 354	
Db	353 CAATATTAACAACAGCTGGTACTGGGGCCAGGAAACCTGTGTCAACCGTCTCCTCA 406	

[illegible]

```

Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/invitrogen Corporation 1600
Paraday Avenue Genoscope sequence ID : CS0DI040C080P1.
FEATURES
    source                1..1138
                            /organism="Homo sapiens"
                            /mol_type="mRNA"
                            /db_xref="taxon:9606"
                            /clone="CS0DI040YE16"
                            /tissue_types="PLACENTA COT 25-NORMALIZED"
                            /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                            /notes="1st strand cDNA was primed with a NotI-oligo(dT)
                                primer. Five prime end enriched, double-strand cDNA was
                                digested with Not I and cloned into the Not I and EcoR V
                                sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      250 a      323 c      329 g      225 t      11 others
ORIGIN
    Query Match      67.6%; Score 239.2; DB 13; Length 1138;
    Best Local Similarity 81.9%; Pred. No. 1.7e-51;
    Matches 290; Conservative 0; Mismatches 58; Indels 6; Gaps 1;

Qy 1 GAGTGCAGCTGTGTGAGTCTGGGGCGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC 60
Db 186 GAGTGCAGCTGTGTGAGTCTGGGGGAGGCGCTGTGCAAGCTGGGGGGTCCCTGAGACTC 245

Qy 61 TGTGTGGCAGCTCCGGGTTTCAGGTTTCACCTTCAATAACTACTACATGGAAGTGGTCCGC 120
Db 246 TCTGTGCAGCCCTCTG-----GATTACCTTCAGTAGCTATTAACTGAAGAACTGGTCCGC 299

Qy 121 CAGGCTCCAGGCGAGGGGCTGGAGTGGGTCTCAGCTATTAGTAGTAGTGTGTATCCACACA 180
Db 300 CAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCATCCATTAGTAATAGTGGTGTACATA 359

Qy 181 TGTGTACGACATCTCCGTGAAGGGGAGATTCCACCATCTCCAGAGAGAAACGCCAACACACA 240
Db 360 TACTACGACACTCAGTGAAGGGGCCGGATCACCATTCTCCAGAGACAAACGCCAAGAACTCA 419

Qy 241 CTGTTTCTTCAAAATGAACAGCCTTGAGAGCTGGAGACACGGCTGCTCTATTACTGTGCGAGC 300
Db 420 CTGTATCTGCAATGAACAGCCTTGAGAGCGAGGACACGGCTGTGTATTACTGTGCGAGA 479

Qy 301 TTGACTACAGGGTCTGACTCTCTGGGGCCAGGGAGTCTCTGGTCAACGGTCTCCTCA 354
Db 480 GGGGGGTACCGGTATGACAGTCTGGGGCCAGGGACACCGTCAACGGTCTCCTCCA 533

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RESULT 3
BX4117408
LOCUS
DEFINITION
1201 bp mRNA linear EST 13-MAY-2003
BX4117408 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE009Y115
5-PRIME, mRNA sequence.
BX4117408
ACCESSION
VERSION
BX4117408.1 GI:30650401
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7198.r For
more information about this cluster, see
[http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DE009AE08QP1&cluster=7198.r](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DE009AE08QP1&cluster=7198.r). Contact :
Peng Liang Email : fliang@lifetech.com URL :

ncsp://www.genoscope.cns.fr/177000000/ncsp/cgi-bin/cluster.cgi?seq=CS0E009AE080P1&cluster=7198.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :

found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: M13 Forward.

FEATURES

Location/Qualifiers
 1. .447
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3054608"
 /tissue_type="lymph"
 /cell_type="germinal center B cells"
 /cell_line="MGC85"
 /lab_host="DH10B (LTI)"
 /clone_lib="NIH MGC 36"
 /notes="Vector: p773-Pac; Site 1: NotI; Site 2: Eco RI;
 Constructed from size fractionated cytoplasmic mRNA
 (0.5-1.5kb). Directionally cloned. Cells provided by Louis
 M. Staudt, Ph.D. Library preparation by Maria de Fatima
 Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
 97 a 110 c 137 g 103 t

BASE COUNT
 ORIGIN

Query Match 65.8%; Score 232.8; DB 9; Length 447;
 Best Local Similarity 80.8%; Pred. No. 5.6e-50;
 Matches 286; Conservative 0; Mismatches 62; Indels 6; Gaps 1;
 Qy 1 GAGTGCAGCTGTGGAGTCTGGGGGGCTTGGCAAGCCTGGGGGTCCTCGAGACTC 60
 Db 95 GAGGTGCAGTGTGGAGTCTGGGGGGAGCCCTGGTCAAGCCTGGGGGTCCTCGAGACTC 154
 Qy 61 TGGTGCAGGCTCGGGTTCAGGTTCCAGTTCACTTCAATTAACCTACTACTGAGTGGTCCGC 120
 Db 155 TCCTGTGAGCCTCTGGATTGAG-----CTTCAATAGCTACATCAATGAGTGGTCCGC 208
 Qy 121 CAGGCTCCAGGCGAGGGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTGGTATCCACACA 180
 Db 209 CAGGCTCCAGGCGAGGGCTGGAGTGGGTCTCATTCTATCTAGTGGTGGTATCTACATA 268
 Qy 181 TGGTACGAGACTCGTGAAGGGGAGATTACCATCTCCAGAGAGAGCGCAACACACA 240
 Db 269 TATTACGAGACTCAGTGAAGGGGCGATTACCATCTCCAGAGAGAGCGCAACAGACTCA 328
 Qy 241 CTGTTCTTCAATGAACAGCTGAGAGCTGAGAGCTGAGAGACGGCTGTCTATTACTGTCCGAGC 300
 Db 329 CTGATCTGCAATGAACAGCTGAGAGCTGAGAGCGGCTGTGTTATTACTGTCCGAGCA 388
 Qy 301 TTGACTACAGGCTCTGACTCTCTGGGGCCAGGGAGTCTTGGTCAACCGTCTCTCTCA 354
 Db 389 GATTGTCTCATGTGAGCTCTGGGGCAAGGGACCGGTACCGTCTCTCTCA 442

RESULT 6

AW402613 511 bp mRNA linear EST 16-FEB-2000
 LOCUS
 DEFINITION UI-HF-BK0-aax-g-05-0-UI.r1 NIH MGC_36 Homo sapiens cDNA clone
 IMAGE:3055305 5', mRNA sequence.
 ACCESSION AW402613 GI:6921317
 VERSION
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC <http://mgi.nci.nih.gov/>.
 1 (bases 1 to 511)

National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab

cDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: M13 Forward.

FEATURES

Location/Qualifiers
 1. .511
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3055305"
 /tissue_type="lymph"
 /cell_type="germinal center B cells"
 /cell_line="MGC85"
 /lab_host="DH10B (LTI)"
 /clone_lib="NIH MGC 36"
 /notes="Vector: p773-Pac; Site 1: NotI; Site 2: Eco RI;
 Constructed from size fractionated cytoplasmic mRNA
 (0.5-1.5kb). Directionally cloned. Cells provided by Louis
 M. Staudt, Ph.D. Library preparation by Maria de Fatima
 Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
 104 a 131 c 151 g 125 t

BASE COUNT
 ORIGIN

Query Match 65.4%; Score 231.4; DB 9; Length 511;
 Best Local Similarity 81.8%; Pred. No. 1.4e-49;
 Matches 297; Conservative 0; Mismatches 51; Indels 15; Gaps 2;
 Qy 1 GAGTGCAGCTGTGGAGTCTGGGGGGCTTGGCAAGCCTGGGGGTCCTCGAGACTC 60
 Db 71 GAGGTGCAGTGTGGAGTCTGGGGGGAGGTTTGGTACAGCCTGGAGGTCCTCGAGACTC 130
 Qy 61 TGGTGCAGCCTCGGGTTCAGGTTCCAGTTCACTTCAATTAACCTACTACTGAGTGGTCCGC 120
 Db 131 TCCTGTGTAGCCTCTG-----GATTCACTTTAGTAGTTATGAATGAATGGTCCGC 184
 Qy 121 CAGGCTCCAGGCGAGGGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTGGTATCCACACA 180
 Db 185 CAGGCTCCAGGCGAGGGCTGGAGTGGGTCTTACATATTAGTAGTGGTGGTATCCATA 244
 Qy 181 TGGTACGAGACTCGGTGAAGGGCAGATTCCATCTCCAGAGAGAGCGCAACACACA 240
 Db 245 TTCTACGAGACTCTGTGAAGGGCCGATTCCATCTCCAGAGAGAGCGCAACAGACTCA 304
 Qy 241 CTGTTCTTCAATGAACAGCCTGAGAGCTGAGAGCTGAGAGACGGCTGTCTATTACTGTCCGAGC 300
 Db 305 CTGTATCTGCAATGAACAGCCTGAGAGCGGAGAGACAGGCTGTATTACTGTCCGAGA 364
 Qy 301 TTGACTACAGGG-----TCTGACTCTCTGGGGCCAGGGAGTCTCTGGTCAACCGTCTCC 351
 Db 365 CTCAATAGTGGAGACTACTTTTGTGACTACTGGGGCCAGGGAGACCTGTGTCACCGTCTCC 424
 Qy 352 TCA 354
 Db 425 TCA 427

RESULT 7

AW403220 471 bp mRNA linear EST 16-FEB-2000
 LOCUS
 DEFINITION UI-HF-BK0-aax-h-04-0-UI.r1 NIH MGC_36 Homo sapiens cDNA clone
 IMAGE:3055710 5', mRNA sequence.
 ACCESSION AW403220 GI:6922096
 VERSION
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC <http://mgi.nci.nih.gov/>.
 1 (bases 1 to 471)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: M13 forward.

FEATURES

Location/Qualifiers
 1..471
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3055710"
 /tissue_type="lymph"
 /cell_type="germinal center B cells"
 /cell_line="MGC85"
 /lab_host="DH10B (LTI)"
 /clone_lib="NIH MGC 36"
 /note="Vector: pMT3-Pac; Site 1: NotI; Site 2: Eco RI;
 Constructed from size fractionated cytoplasmic mRNA
 (0.5-1.5kb). Directionally cloned. Cells provided by Louis
 M. Staudt, Ph.D. Library preparation by Maria de Fatima
 Bonaldo, Ph.D. and M. Rento Soares, Ph.D."

BASE COUNT 98 a 127 c 143 g 103 t

ORIGIN

Query Match 65.0%; Score 230.2; DB 9; Length 471;
 Best Local Similarity 81.3%; Pred. No. 2.7e-49;
 Matches 300; Conservative 0; Mismatches 48; Indels 21; Gaps 2;
 Qy 1 GAGTGCAGCTGGTGGAGTCTGGGGGGCGCTTGGCAAAGCTGGGGGGTCCCTGAGACTC 60
 Db 76 GAGGTGCAGCTGGTGGAGTCTGGGGGGCGCTTGGCAAAGCTGGGGGGTCCCTGAGACTC 135
 Qy 61 TGGTGGCAGCTCGGGTTCAGGTTACCTTCAATTAATCACTACTACATGAGTGGTCCGC 120
 Db 136 TCCTGTGCAGCTCTG-----GATTACCTTCACTAGCAGTATGAACTGGGTCCGC 189
 Qy 121 CAGGCTCAGGGCAGGGCTGGAGTGGGTCTCACTATTAGTAGTGGTGGTATCCACACA 180
 Db 190 CAGGCTCAGGAGAGGGCTGGAGTGGGTCTCACTATTAGTAGTGGTGGTATCCACACA 249
 Qy 181 TGGTACGAGACTCCGTGAAGGGCAGATTCACTATCTCCAGAGAGAACGCCAACACACA 240
 Db 250 TACTACGAGACTCAGTGAAGGGCGGATTCACTATCTCCAGAGAGAACGCCAACACTCA 309
 Qy 241 CTGTTTCTTCAATGAACAGCTGAGAGCTGAGACACGGCTGTCTATTACTGTGCG--- 297
 Db 310 CTGTATCTGCAATGAACAGCTGAGAGCTGAGAGCGGCTGTGTATTACTGTGCGAGA 369
 Qy 298 -----AGCTTCACTACAGGGTCTCACTCTCTGGGGCCAGGGAGTCTCTGGTCACC 345
 Db 370 GCCCATAGTACAGCTGGCCAGGCAGCACTACTTGGGGCCAGGGAGTCTCTGGTCACC 429
 Qy 346 GTCTCTCTCA 354
 Db 430 GTCTCTCTCA 438

RESULT 8

BF974771
 LOCUS 602245420P1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4336541 5',
 DEFINITION mRNA sequence.
 ACCESSION BF974771
 VERSION BF974771.1 GI:12341986
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE

1 (bases 1 to 1164)
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

Plate: LLC1209 row: g column: 06

High quality sequence stop: 696.

FEATURES

Location/Qualifiers
 1..1164
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4336541"
 /tissue_type="primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 48"
 /note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH MGC Library."

BASE COUNT 284 a 313 c 330 g 236 t

ORIGIN

Query Match 64.3%; Score 227.6; DB 10; Length 1164;
 Best Local Similarity 81.0%; Pred. No. 1.8e-48;
 Matches 298; Conservative 0; Mismatches 49; Indels 21; Gaps 2;
 Qy 2 AGGTGCAGCTGGTGGAGTCTGGGGGGCGCTTGGCAAAGCTGGGGGGTCCCTGAGACTCT 61
 Db 122 AGGTGCAGCTGGTGGAGTCTGGGGGGCGCTTGGCAAAGCTGGGGGGTCCCTGAGACTCT 181
 Qy 62 GGTGCGCAGCTCCGGGTTTCAGGTTTCACTTCAATTAATACTACTAGTGGTCCGCC 121
 Db 182 CCTGTGCAGCTCTG-----GATTCACTTCACTAGTACTACTATGAGTGGATCCGCC 235
 Qy 122 AGGCTCCAGGGCAGGGCTGGAGTGGGTCTCAGGTATTAGTAGTGGTATCCCAT 181
 Db 236 AGGCTCCAGGGCAGGGCTGGAGTGGGTCTCAGGTATTAGTAGTGGTATCCCAT 295
 Qy 182 GGTACGCAGACTCCGTGAAGGGCAGATTCACTATCTCCAGAGAGAACGCCAACACAC 241
 Db 296 GCTACGCAGACTCTGTGAAGGGCGGATTCACTATCTCCAGAGAGAACGCCAACACTAC 355
 Qy 242 TGTTCCTTCAAAATGAACAGCTGAGAGCTGAGACACGGCTGTCTATTACTGTGCGAG-- 299
 Db 356 TGTATCTGCAATGAACAGCTGAGAGCTGAGAGCGGCGGTGTATTACTGTGCGAGAG 415
 Qy 300 -----CTTGACTACAGGGTCTGACTCTCTGGGGCCAGGGAGTCTCTGGTCACCG 346
 Db 416 ATCAGAGGAACAACACAGCTGGTAGATTTTGACTACTTGGGGCCAGGGAAACCTGTGTACCG 475
 Qy 347 TCTCTCTCA 354
 Db 476 TCTCTCTCA 483

RESULT 9

AW401428

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LOCUS      AW401428      443 bp      mRNA      linear      EST 16-FEB-2000
DEFINITION UI-HF-BK0-aad-b-02-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
IMAGE:3053139 5', mRNA sequence.
ACCESSION  AW401428
VERSION    AW401428.1 GI:6920011
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 443)
            NIH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished
            Contact: Robert Strausberg, Ph.D.
            Email: cgabbs@mail.nih.gov
            Eco RI site shown at the beginning of the sequence.
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: M.B. Soares Lab
            cDNA Library Arrayed by: M.B. Soares Lab
            DNA Sequencing by: M.B. Soares Lab
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.
FEATURES   Location/Qualifiers
            source
            1..443
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                /mol_type="mRNA"
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                /clone="IMAGE:3053139"
                /tissue_type="lymph"
                /cell_type="germinal center B cells"
                /lab_host="DH10B (LTI)"
                /clone_lib="NIH MGC 36"
                /note="Vector: pTZ19-Pac; Site 1: NotI; Site 2: Eco RI;
                Constructed from size fractionated cytoplasmic mRNA
                (0.5-1.5kb). Directionally cloned. Cells provided by Louis
                M. Staudt, Ph.D. Library preparation by Maria de Fatima
                Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 93 a 116 c 131 g 103 t
ORIGIN
Query Match 63.6%; Score 225.2; DB 9; Length 443;
Best Local Similarity 80.6%; Pred. No. 5.2e-48;
Matches 295; Conservative 0; Mismatches 53; Indels 18; Gaps 2;
QY 1 GAGGTGACGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCTCGAGACTC 60
DB 82 GAGGTGACGCTGGTGGAGTCTGGGGGAGGCGTGGTCAAGCCTGGGGGTCCTCGAGACTC 141
QY 61 TGGTGGCAGCTCCGGGTTGAGGTTCACCTTCAATAACTACTACATGAGTGGGTCCGC 120
DB 142 TCCTGTGAGCTCTG-----GATTACCTTCACTATACATGAGTGGGTCCGC 195
QY 121 CAGGCTCAGGCGAGGCGTGGAGTGTCTCAGTATAGTAGTGGTATCCCAACA 180
DB 196 CAGGCTCAGGCGAGGCGTGGAGTGGGTCTCATCATGAGTGGTGGTACTTACATA 255
QY 181 TGGTACGAGACTCCGTCAGGCGAGATTCCACATCTCCAGAGAGACGCCCAACAACA 240
DB 256 TACTACGAGACTCAGTGAAGGCGGATTCACCATCTCCAGAGACAGCCCAAGACTCA 315
QY 241 CTGTTTCTTCAATGAACAGCTGAGAGCTGAGGACACGGGTGTCTATTACTGTGGAGC 300
DB 316 CTGATCTCGCATGACAGCTGAGAGCGGAGACACCGGTGTCTATTACTGTGGAGA 375
QY 301 TTGACTACAGG-----TCTGACTCTCGGGCGAGGAGTCTCGGTACCGTCC 348
DB 376 GGAGTTCCCATGGTTTCAGTTCTACTTTTGACTACTGGGGCGAGGAAACCTGTGTCACCGTC 435
QY 349 TCCTCA 354

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Db 436 TCCTCA 441
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AW401386      582 bp      mRNA      linear      EST 16-FEB-2000
DEFINITION UI-HF-BK0-aau-b-03-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
IMAGE:3055324 5', mRNA sequence.
ACCESSION  AW401386
VERSION    AW401386.1 GI:6920168
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 582)
            NIH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished
            Contact: Robert Strausberg, Ph.D.
            Email: cgabbs@mail.nih.gov
            Eco RI site shown at the beginning of the sequence.
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: M.B. Soares Lab
            cDNA Library Arrayed by: M.B. Soares Lab
            DNA Sequencing by: M.B. Soares Lab
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.
FEATURES   Location/Qualifiers
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                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:3055324"
                /tissue_type="lymph"
                /cell_type="germinal center B cells"
                /cell_line="MGC85"
                /lab_host="DH10B (LTI)"
                /clone_lib="NIH MGC 36"
                /note="Vector: pTZ19-Pac; Site 1: NotI; Site 2: Eco RI;
                Constructed from size fractionated cytoplasmic mRNA
                (0.5-1.5kb). Directionally cloned. Cells provided by Louis
                M. Staudt, Ph.D. Library preparation by Maria de Fatima
                Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 117 a 155 c 169 g 141 t
ORIGIN
Query Match 63.5%; Score 224.8; DB 9; Length 582;
Best Local Similarity 80.8%; Pred. No. 7.4e-48;
Matches 291; Conservative 0; Mismatches 57; Indels 12; Gaps 2;
QY 1 GAGGTGACGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCTCGAGACTC 60
DB 132 GAAGAACATCTGGTGGAGTCTGGGGGAGCCCTTGGTACAGCTGGAGGTCCCTGAGACTC 191
QY 61 TGGTGGCAGCTCCGGGTTGAGGTTCACCTTCAATAACTACTACATGAGTGGGTCCGC 120
DB 192 TCCTGTGAGCTCTG-----GATTACCTTCACTATACATGAGTGGTGGTCCGC 245
QY 121 CAGGCTCAGGCGAGGCGTGGAGTGGGTCTCAGTATAGTAGTGGTATCCCAACA 180
DB 246 CAGGCTCAGGCGAGGCGTGGAGTGGGTTCATACATTAGTAGTGGTGGTATCCATA 305
QY 181 TGGTACGAGACTCCGTTGAAGGCGAGATTCCACATCTCCAGAGAGACGCCCAACAACA 240
DB 306 TACTACGAGACTCTGTGAAGGCGGCTTCCATCTCCAGAGACACGCCCAAGACTCC 365
QY 241 CTGTTTCTTCAATGAACAGCTGAGAGCTGAGAGACAGGCTGTCTATTACTGTGGC--- 297
DB 366 CTGTTTCTGAGATGAACAGCTTGAAGCGGAGGACACGCGTGTATTACTGTGCGAAA 425

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Qy 298 ---AGCTTGACTCAGGGTCTGACTCCTGGGGCCAGGGAGTCTCTGGTCAACCGTCTCCTCA 354
Db 426 GCTATTGTGCTGTGAGCTTGTGCTGTGGGGCCAGGGACCTGTGTCAACCGTCTCCTCA 485

RESULT 11
LOCUS BG340670
DEFINITION 602462250F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4574941 5',
mRNA sequence.
ACCESSION BG340670
VERSION BG340670.1 GI:13147108
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 648)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L10M1285 row: d column: 14
High quality sequence stop: 648.
Location/Qualifiers
1. 648
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4574941"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_libs="NIH MGC 48"
/notes="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected 500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
2 others
BASE COUNT 148 a 178 c 188 g 132 t
ORIGIN
Query Match 63.4%; Score 224.4; DB 10; Length 648;
Best Local Similarity 81.4%; Pred. No. 9.7e-48;
Matches 288; Conservative 0; Mismatches 56; Indels 10; Gaps 2;

Qy 1 GAGGTGACGCTGTGGAGTCTGGGGCGGGCTTGGCAAGCCTGGGGGTCCTCGAGACTC 60
Db 82 GAGGTGACGCTGTGGAGTCTGGGGCGGGCTTGGTACAGCCTGGGGGTCCTCGAGACTC 141
Qy 61 TGGTGGCAGCCTCGGGTTGAGTTACCTTCAATACTACTACATGAGTGGTGGTCCGC 120
Db 142 TCCTGTGAGGCTCTG-----GATTACACTTTAGCAGCTATGCCATGAGTGGTGGTCCGC 195
Qy 121 CAGGCTCCAGGCGAGGGCTGAGTGGGTCTCAGCTATTAGTAGTGGTGGTATCCCCACA 180
Db 196 CAGGCTCCAGGGAAGGGGCTGAGTGGGTCTCAGCTATTAGTGGTGGTGGTAGACA 255
Qy 181 TGGTACGAGACTCCGTGAAGGGCAGATTACCATCTCCAGAGAGAACGCCCAACAACA 240
Db 256 TACTACGAGACTCCGTGAAGGGCGGTTACCATCTCCAGAGACATTCAGAGACACG 315

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Qy 241 CTGTTTCTTCAATGAACAGCTGAGAGCTGAGGACACGCTGTCTATTACTGTGGAGC 300
Db 316 CTGTAICTGAATGAACAGCTGAGAGCCGAGGACACGCGCTATATTACTGTGGAGC 375

Qy 301 TTGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCTCTGTCAACCGTCTCCTCA 354
Db 376 ---CACCCGGTGATGGCTGACTGGGGCCAGGAACCTGTGTCAACCGTCTCCTCA 425

RESULT 12
AJ547930
LOCUS AJ547930 MTAPHEU Medicago truncatula cDNA clone mtaehac110006d09,
mRNA sequence.
ACCESSION AJ547930
VERSION AJ547930.1 GI:28611644
KEYWORDS EST.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
1 (bases 1 to 429)
REFERENCE 1 Nyamuren, O., Colditz, F., Rosendahl, S., Bekel, T., Meyer, F., Kuester
AUTHORS H., Franken, P. and Krajinski, F.
TITLE First insights into the pathogenic interaction formed between the
omycete Aphanomyces euteiches and legumes using the model plant
Medicago truncatula
JOURNAL Unpublished
COMMENT Contact: Krajinski F
LG Molekulargenetik
Herrenhaeuser Str. 2 D-30419 Hannover, Germany.
Location/Qualifiers
1. 429
/organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:3880"
/clone="mtaehac110006d09"
/tissue_type="root"
/dev_stage="6 days after inoculation with Aphanomyces
euteiches zoospores"
/clone_libs="MTAPHEU"
/notes="Vector: pGEM-T; Site 1: EcoRI; genotype A17; Total
RNA was isolated from roots harvested 6 days after
inoculation with Aphanomyces euteiches zoospores. cDNA was
prepared from total RNA using the SMART PCR cDNA system
(Clontech). This cDNA was used as tester in Suppression
Subtractive Hybridization (SSH). The SSH-cDNA fragments
were generated using the SSH-adaptor sequences
ctaatacgaactactataggctcggcgccggccggcagggt and
ctaatacgaactactaggcgctggcgccggcagggt (Clontech) and
ligated after Suppression Subtractive Hybridization into
the pGEM-Teasy vector (Promega). Plasmids containing cDNA
inserts were propagated in E. coli TOP 10F' cells
(Invitrogen)."
BASE COUNT 92 a 109 c 140 g 88 t
ORIGIN
Query Match 63.1%; Score 223.2; DB 9; Length 429;
Best Local Similarity 80.1%; Pred. No. 1.7e-47;
Matches 277; Conservative 0; Mismatches 63; Indels 6; Gaps 1;

Qy 1 GAGGTGAGTGTGTGAGTCTGGGGCGGGCTTGGCAAGCCTGGGGGTCCTCGAGACTC 60
Db 90 GAGGTGAGTGTGTGAGTCTGGGGCGGGCTTGGTCCAGCCTGGGAGGTCCTCGAGACTC 149
Qy 61 TGGTGGCAGCCTCCGGTTCAGTTCACCTTCAATACTACTACATGAGTGGTGGTCCGC 120
Db 150 TCCTGTGAGGCTCTG-----GATTACACCTTTAGCAGCTAGGCTAGCTGGTCCGC 203
Qy 121 CAGGCTCCAGGCGAGGGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTGGTATCCCCACA 180

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|||||
204 CAGGCTCAGGAGGAGGCTGGAGTGGTCTCAGCTATTAGTGGTGGTGGTAGCACA 263
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181 TGGTACGAGACTCCGTTGAAGGCGAGATTCAACCACTCCAGAGAGAAAGCGCAACACACA 240
|||
264 TACTACGAGACTCCGTTGAAGGCGGTTTCAACCATCTCCAGAGACAATTCACAGAACACG 323
|||
241 CTGTTCTTCAATGAACAGCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 300
|||
324 CTGTATCTGCAAAATGAACAGCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCAAGA 383
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301 TTGACTACAGGCTGACTCTCTGGGCGCAGGAGTCTCTGTGTCACCG 346
|||
384 GGGAAATCCGCGGAGGAGTGGGGCCCAAGTACCCTTGGTCACCG 429
|||

RESULT 13
B0708458 920 bp mRNA linear EST 16-JUL-2002
LOCUS
DEFINITION AGENCOURT_7976428 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214426
5', mRNA sequence.
ACCESSION B0708458
VERSION B0708458.1 GI:21847357
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 920)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM2381 row: 1 column: 11
High quality sequence stop: 649.
FEATURES
Location/Qualifiers
1..920
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6214426"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/notes="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
BASE COUNT 189 a 272 c 259 g 200 t
ORIGIN
Query Match 63.1%; Score 223.2; DB 13; Length 920;
Best Local Similarity 80.6%; Pred. No. 2.3e-47;
Matches 290; Conservative 0; Mismatches 58; Indels 12; Gaps 2;

QY 1 GAGGTGACGTGGTGGAGTCTGGGGCGGCTTGGCAAGCCCTGGGGGTCCCTGAGACTC 60
DB 121 GAGGTGCGGCTGGTGGAGTCTGGGGAGGCTTGGTACAGCCCTGGGGGACCCCTGAGACTC 180
QY 61 TGGTCCGAGCCTCCCGGTTGAGGTTACCTTCAATAACTACTACATGACTGGTGGTCCGC 120
DB 181 TCCTGTGAGCCTCTG-----GATTCACTTTAGCACTATGCGATGACCTGGGTCCGC 234

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121 CAGGCTCCAGGCGAGGCGTGGAGTGGTCTCAGCTATTAGTGGTGGTGGTAGCACA 180
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235 CAGCTCCAGGAAAGGGGCTGGAGTGGTCTCAGCTATTAGTGGTGGTGGTAGCACA 294
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181 TGGTACGAGACTCCGTTGAAGGCGAGATTCAACCATCTCCAGAGAGAAAGCGCAACACACA 240
|||
295 TACTACGAGACTCCGTTGAAGGCGGTTTCAACCATCTCCAGAGACAATTCACAGAACACG 354
|||
241 CTGTTCTTCAATGAACAGCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGA-- 298
|||
355 CTGTATCTGCAAAATGAACAGCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAAA 414
|||
299 ---GCTTGACTACAGGCTGACTCTCTGGGCGCAGGAGTCTCTGGTCCGCTCTCTCA 354
|||
415 GAAGGACTTCGAGACTCTGACTGCTGGGGCGAGGAAACGAGGTCAACCGTCTCTCA 474
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RESULT 14
B0711467 920 bp mRNA linear EST 16-JUL-2002
LOCUS
DEFINITION AGENCOURT_8484867 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6300988
5', mRNA sequence.
ACCESSION B0711467
VERSION B0711467.1 GI:21850366
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 920)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM2516 row: c column: 05
High quality sequence stop: 587.
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6300988"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/notes="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
BASE COUNT 187 a 286 c 252 g 194 t 1 others
ORIGIN
Query Match 62.7%; Score 222; DB 13; Length 920;
Best Local Similarity 80.1%; Pred. No. 4.7e-47;
Matches 293; Conservative 0; Mismatches 55; Indels 18; Gaps 2;

QY 1 GAGGTGACGTGGTGGAGTCTGGGGCGGCTTGGCAAGCCCTGGGGGTCCCTGAGACTC 60
DB 110 GAGGTGACGTGGTGGAGTCTGGGGAGGCTTGGTACAGCCCTGGGGGACCCCTGAGACTC 169
QY 61 TGGTCCGAGCCTCCCGGTTTCAAGTTCACCTTCAATAACTACTACATGAGTGGTCCGC 120

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[illegible]

RESULT 15
 AW403059
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

AW403059 456 bp mRNA linear EST 16-FEB-2000
 UI-HF-BK0-aa1-f-10-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
 IMAGE:3054090 5', mRNA sequence.
 AW403059
 AW403059.1 GI:6921885
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 456)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 CDNA Library Preparation: M.B. Soares Lab
 CDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
www.bio.llnl.gov/bbrp/image/image.html

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seq primer: 5' to 3' forward:
Location/Qualifiers
1. .456
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3054090"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_lib="NIH MGC 36"
/note="Vector: pT773-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5Kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT      103 a      104 c      139 g      110 t
ORIGIN

Query Match      62.6%; Score 221.6; DB 9; Length 456;
Best Local Similarity 82.9%; Pred. No. 4.5e-47;
Matches 267; Conservative 0; Mismatches 49; Indels 6; Gaps 1;

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QY	1	GAGTGCAGCTGTGTGGAGTCTGTGGGGCGGCTTGGCAAAGCCTTGGGGGTTCCTTGAGACTC	50
Db	109	GAGGTGCAGCTGTGTGGAGTCTGTGGGGAGGCTTGGTACAGCCTGGAGGGTCCCTTGAGACTC	168
QY	61	TGGTGGCAGCCTCCGGGTTCAGGTTCACTTCACCTCAATAACTACTACATGCACTGGGTCCGC	120
Db	169	TCCTGTGCAGCCTCTG-----GATTCAACCTTCAGTAGTTATGGAATGAACCTGGGTCCGC	222
QY	121	CAGGCTCCAGGGCAGGGCGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTGMATCCCA	180
Db	223	CAGGCTCCAGGGAAGGGCTGGAGTGGGTTTCATCATTAGTAGTGGTAGTACCATA	282
QY	181	TGGTACGCAGACTCCGTGAAGGGCAGATTCCCATCTCCAGAGAGAACCCCAACAACA	240
Db	283	TACTACGCAGACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCA	342
QY	241	CTGTTTCTTTCAAATGAACAGCCTGAGAGCTGAGGAACGGCTGTCTATTACTGTGTGGAGC	300
Db	343	CTGTATCTGCAATGAAGAGCCTGAGAGCGGAGACCGCTGTTTATTACTGTGTGCAGC	402
QY	301	TTGACTACAGGGTCTGACTCCT	322
Db	403	CATATAGCAGCAGCTGACGACT	424

Search completed: December 29, 2003, 21:44:18
Job time : 1535.8 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 154.453 Seconds
(without alignments)
6187.013 Million cell updates/sec

Title: US-09-019-441-4_COPY_58_411

Perfect score: 354

Sequence: 1 GAGTGCAGCTGGTGGAGTC.....TCCTGGTCACCGTCCTCTCA 354

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq 19Jun03:*

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- 2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
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- 23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
- 24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
- 25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	354	100.0	411	19 AAV33310	Anti-human CD23 5E
2	349.2	98.6	19035	19 AAV61794	Traget plasmid Man
3	250.4	70.7	458	22 AAH41153	Human coding seque
4	244	68.9	348	24 AAL39119	Antibody screening
5	244	68.9	364	24 ABK99213	DNA sequence for a
6	244	68.9	364	24 ABK99213	Antibody screening
7	240	67.8	720	20 AAX36070	DNA encoding a sin
8	240	67.8	720	25 ABZ76706	Human serum albumi

9	238.4	67.3	348	24 AAD46290	Human KDR (VEGFR-2
10	238.4	67.3	348	25 ABT23325	VEGF binding relat
11	237	66.9	742	24 ABK99212	DNA sequence for a
12	237	66.9	742	24 AAL39103	Antibody screening
13	236.8	66.9	742	24 AAD46292	Human KDR (VEGFR-2
14	236.8	66.9	348	25 ABT23327	VEGF binding relat
15	235.2	66.4	348	24 AAD46294	Human KDR (VEGFR-2
16	235.2	66.4	348	25 ABT23329	VEGF binding relat
17	235.2	66.4	1710	22 AAS22533	Human cDNA encodin
18	235.2	66.4	1721	22 AAS22530	Human cDNA encodin
19	234.2	66.2	348	22 AAS03478	DNA encoding anti-
20	233.4	65.9	351	24 AAL43586	Dig3 antibody heav
21	231.8	65.5	720	24 ABK6789	DNA encoding monoc
22	230.4	65.1	348	22 AAS03513	DNA encoding anti-
23	230.4	65.1	738	21 AA255614	Internalising anti-
24	229.8	64.9	462	25 ABZ22306	S. pneumoniae pps-
25	229.6	64.9	348	22 AAS03461	DNA encoding anti-
26	229.4	64.8	351	24 ABK90972	Human antibody hea
27	228.4	64.5	4026	24 ABK81191	DNA encoding immu
28	227.2	64.2	349	22 AAS03504	DNA encoding anti-
29	225.4	63.7	351	24 ABA92717	Fibronectin isofo
30	225.4	63.7	722	21 AA228986	Anti-murine CTLA-4
31	225.4	63.7	729	21 AA228997	Anti-murine CTLA-4
32	223.4	63.1	681	22 AAH30055	TRO005 heavy chain
33	223.2	63.1	354	22 AAS03470	DNA encoding anti-
34	222	62.7	497	25 ABZ70910	Anti-TRAIL-R antib
35	220.8	62.4	660	22 AAS13367	Human cDNA encodin
36	220.8	62.4	908	24 ABA91388	Anti-Bacillus anth
37	220.6	62.3	354	18 AAT72127	CEA-specific antib
38	220	62.1	354	18 AAT72128	CEA-specific antib
39	219.8	62.1	348	22 AAS03446	DNA encoding anti-
40	219.4	62.0	311	23 ABA46318	Human liver single
41	219.4	62.0	311	24 AAS20923	Human genome-deriv
42	219.4	62.0	743	16 AAQ78986	Human immunoglobul
43	219.2	61.9	348	18 AAT72130	CEA-specific antib
44	219.2	61.9	354	22 AAH47513	Anti-IL-18 antibod
45	219	61.9	411	19 AAV24243	Chimeric antibody

ALIGNMENTS

RESULT 1
AAV33310
ID AAV33310 standard; DNA; 411 BP.

XX AAV33310;

AC AAV33310;

DT 25-MAR-2003 (updated)

DT 18-NOV-1998 (first entry)

XX Anti-human CD23 588 monoclonal antibody heavy chain variable region DNA.

XX Anti-human CD23 588 monoclonal antibody; heavy chain variable region;

KW human CD23; IGB; FcER1/CD23; gamma-1 constant region;

KW gamma-3 constant region; allergy; inflammation; autoimmune disease;

KW allergic rhinitis; conjunctivitis; autoimmune haemolytic anaemia; ss.

XX Macaca fascicularis

XX Key Location/Qualifiers

PH Key 1..411

FT CDS /tag= a

FT /product= "anti-human CD23 588 heavy chain variable

FT region"

FT /note= "CDS does not contain a stop codon"

FT sig_peptide 1..57

FT /tag= b

FT mat_peptide 58..411

FT /tag= c

FT misc_feature 148..168

FT /tag= d

FT /note= "encodes CDR 1 region"

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FT misc_feature 211..261
FT /*tag= e
FT /note= "encodes CDR 2 region"
FT 358..378
FT /*tag= f
FT /note= "encodes CDR 2 region"
FT
FT
XX WO9837099-A1.
XX
XX 27-AUG-1998.
XX
XX 17-FEB-1998; 98WO-US02253.
XX
XX 20-FEB-1997; 97US-0803085.
XX 05-FEB-1998; 98US-0019441.
XX
XX (IDEC-) IDEC PHARM CORP.
XX (SEK) SEIKAGAKU CORP.
XX
XX Klotzer WS, Nakamura T, Reff ME;
XX
XX WPI; 1998-467495/40.
XX P-PSDB; AAW70380.
XX
XX New anti-human CD23 monoclonal antibody - used for inhibiting IgE
XX expression to treat or prevent allergic, inflammatory and
XX auto-immune conditions
XX
XX Example 1; Pages 108-110; 146pp; English.
XX
XX The present sequence represents a DNA sequence encoding the heavy
XX chain variable region of primate monoclonal antibody anti-human CD23 5E8.
XX The invention provides primate monoclonal antibodies which specifically
XX bind human CD23, the low affinity receptor for IgE (FcεRI/CD23),
XX and comprise either of a human gamma-1 or human gamma-3 constant region
XX that binds to human Fc gamma receptors and inhibits IgE expression.
XX The monoclonal antibodies of the invention are claimed to be useful
XX for inhibiting induced IgE production for treating or preventing
XX allergic, inflammatory and autoimmune conditions e.g. allergic rhinitis
XX conjunctivitis, autoimmune haemolytic anaemia, etc.
XX (Updated on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 411 BP; 80 A; 102 C; 130 G; 99 T; 0 other;
XX
XX Query Match 100.0%; Score 354; DB 19; Length 411;
XX Best Local Similarity 100.0%; Pred. No. 3e-90;
XX Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 GAGGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCCTGAGACTC 60
Db |||||
OY 58 GAGGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCCTGAGACTC 117
Db |||||
OY 61 TGGTGGCGAGCTCGGGTTCAGGTTTCACTTCAATTAATACTACTGAGTGGGTCCGC 120
Db |||||
OY 118 TGGTGGCGAGCTCGGGTTCAGGTTTCACTTCAATTAATACTACTGAGTGGGTCCGC 177
Db |||||
OY 121 CAGGCTCCAGGCGAGGGCTGGAGTGGTCTCAAGTATAGTAGTGGTGGTATCCACA 180
Db |||||
OY 178 CAGGCTCCAGGCGAGGGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTGGTATCCACA 237
Db |||||
OY 181 TGGTACGAGACTCGTGAAGGCGAGATTACCATCTCCAGAGAGAGCCCAACACACA 240
Db |||||
OY 238 TGGTACGAGACTCGTGAAGGCGAGATTACCATCTCCAGAGAGAGCCCAACACACA 297
Db |||||
OY 241 CTGTTTCTTCAATGAACAGCTCAGAGCTGAGGACAGCGTGTCTATTACTGTGGCAGC 300
Db |||||
OY 298 CTGTTTCTTCAATGAACAGCTCAGAGCTGAGGACAGCGTGTCTATTACTGTGGCAGC 357
Db |||||
OY 301 TTGACTACAGGCTGTGACTCTCTGGGGCCAGGGAGTCTTGGTCAACGTTCTCTCA 354
Db |||||
OY 358 TTGACTACAGGCTGTGACTCTCTGGGGCCAGGGAGTCTTGGTCAACGTTCTCTCA 411
Db |||||
```

```
RESULT 2
AAV61794
ID AAV61794 standard; DNA; 19035 BP.
XX
XX AAV61794;
AC
XX
XX 07-JUN-1999 (first entry)
DT
XX
XX Traget plasmid Mandy containing anti-CD23 gene.
DE
XX
XX Mandy; target plasmid; gene integration; gene amplification;
KW homologous recombination; vector; neomycin phosphotransferase;
KW neo gene; selectable marker; immunoglobulin; CD23; 5E8; human; ss.
XX
XX Chimeric - Mus sp.
OS Chimeric - Escherichia coli.
OS Chimeric - Baculovirus.
OS Chimeric - Cytomegalovirus.
OS Chimeric - Rhesus macaque polyoma virus.
OS Chimeric - Photinus sp.
OS Chimeric - Salmonella typhimurium.
OS Chimeric - Homo sapiens.
XX
XX Key Location/Qualifiers
FT misc_feature 361 /*tag= a
FT /note= "this base represents a nucleotide missing
FT from the sequence given in the
FT specification. It is included to
FT maintain the nucleotide numbering in the
FT specification for this sequence"
FT
FT misc_feature 721 /*tag= b
FT /note= "this base represents a nucleotide missing
FT from the sequence given in the
FT specification. It is included to
FT maintain the nucleotide numbering in the
FT specification for this sequence"
FT
FT misc_feature 2941 /*tag= c
FT /note= "this base represents a nucleotide missing
FT from the sequence given in the
FT specification. It is included to
FT maintain the nucleotide numbering in the
FT specification for this sequence"
FT
FT misc_feature 3301 /*tag= d
FT /note= "this base represents a nucleotide missing
FT from the sequence given in the
FT specification. It is included to
FT maintain the nucleotide numbering in the
FT specification for this sequence"
FT
FT misc_feature 4261 /*tag= e
FT /note= "this base represents a nucleotide missing
FT from the sequence given in the
FT specification. It is included to
FT maintain the nucleotide numbering in the
FT specification for this sequence"
FT
FT misc_feature 4621..4622 /*tag= f
FT /note= "these bases represent nucleotides missing
FT from the sequence given in the
FT specification. They are included to
FT maintain the nucleotide numbering in the
FT specification for this sequence"
FT
FT misc_feature 8161 /*tag= g
FT /note= "this base represents a nucleotide missing
FT from the sequence given in the
FT specification. It is included to
FT maintain the nucleotide numbering in the
FT specification for this sequence"
FT
FT
```

FT misc_feature 8521..8522
 FT /*tag= h
 FT /note= "these bases represent nucleotides missing
 FT from the sequence given in the
 FT specification. They are included to
 FT maintain the nucleotide numbering in the
 FT specification for this sequence"

FT misc_feature 12061
 FT /*tag= i
 FT /note= "this base represents a nucleotide missing
 FT from the sequence given in the
 FT specification. It is included to
 FT maintain the nucleotide numbering in the
 FT specification for this sequence"

FT misc_feature 12421
 FT /*tag= j
 FT /note= "these bases represent nucleotides missing
 FT from the sequence given in the
 FT specification. They are included to
 FT maintain the nucleotide numbering in the
 FT specification for this sequence"

FT misc_feature 13381
 FT /*tag= k
 FT /note= "this base represents a nucleotide missing
 FT from the sequence given in the
 FT specification. It is included to
 FT maintain the nucleotide numbering in the
 FT specification for this sequence"

FT misc_feature 14641..14642
 FT /*tag= l
 FT /note= "these bases represent nucleotides missing
 FT from the sequence given in the
 FT specification. They are included to
 FT maintain the nucleotide numbering in the
 FT specification for this sequence"

FT misc_feature 15001..15002
 FT /*tag= m
 FT /note= "these bases represent nucleotides missing
 FT from the sequence given in the
 FT specification. They are included to
 FT maintain the nucleotide numbering in the
 FT specification for this sequence"

FT misc_feature 15961..15962
 FT /*tag= n
 FT /note= "these bases represent nucleotides missing
 FT from the sequence given in the
 FT specification. They are included to
 FT maintain the nucleotide numbering in the
 FT specification for this sequence"

FT misc_feature 16321..16322
 FT /*tag= o
 FT /note= "these bases represent nucleotides missing
 FT from the sequence given in the
 FT specification. They are included to
 FT maintain the nucleotide numbering in the
 FT specification for this sequence"

XX MO9841645-A1.
 XX
 XX 24-SEP-1998.
 XX
 XX 09-MAR-1998; 98WO-US03935.
 XX
 PR 13-FEB-1998; 98US-0023715.
 PR 14-MAR-1997; 97US-0819866.
 XX
 XX (IDEC-) IDEC PHARM CORP..
 XX
 XX Barnett RS, McLachlan KR, Reff ME;
 XX
 XX WPI, 1998-521229/44.
 XX
 XX Site specific integration of DNA in mammals for expressing, e.g.

PT immunoglobulins - comprises homologous recombination using
 PT selectable marker and target plasmids.
 XX
 PS Example 1; Fig 10; 114pp; English.
 XX
 CC This is the nucleotide sequence of novel target plasmid Mandy.
 CC The plasmid includes an inactivated murine dihydrofolate reductase
 CC (DHFR) gene, the Escherichia coli beta-galactosidase gene,
 CC baculovirus DNA, a cassette comprising the promoter and enhancer
 CC elements from cytomegalovirus and SV40 virus, the E. coli
 CC beta-glucuronidase (GUS) gene, firefly luciferase gene, an
 CC inactivated Salmonella typhimurium histidinol dehydrogenase (HisD)
 CC gene and transposon Tns neomycin phosphotransferase (neo) gene
 CC sequences, in a pBR-derived backbone, and also an anti-human CD23
 CC IgG receptor human gamma-1 monoclonal antibody 5E8 gene. The
 CC invention provides a novel method for integrating a desired
 CC exogenous DNA at a target site within the genome of a mammalian
 CC cell via homologous recombination. This involves transfecting the
 CC cell with a 'marker plasmid' such as Desmond (see AAV61792), which
 CC contains a unique sequence that is foreign to the mammalian cell
 CC genome and which provides a substrate for homologous recombination,
 CC followed by transfection with a 'target plasmid', such as Mandy
 CC or Molly (see AAV61793), containing a sequence which provides for
 CC homologous recombination with the unique sequences contained in
 CC the marker plasmid, and further comprising a desired DNA that is
 CC to be integrated into the mammalian cells, typically an
 CC immunoglobulin or other secreted mammalian glycoprotein. The
 CC homologous recombination system utilises the neo gene as a
 CC dominant selectable marker. The neo gene is split into 3 exons.
 CC Exon 3 is present on the marker plasmid and becomes integrated
 CC into the host cell genome upon integration of the marker plasmid
 CC into the mammalian cells. Exons 1 and 2 are present on the
 CC targeting plasmid, and are separated by an intron into which at
 CC least one gene of interest is cloned. Homologous recombination
 CC of the targeting vector with the integrated marking vector results
 CC in correct splicing of all 3 exons of the neo gene and expression
 CC of a functional neo protein. The method is applicable to all
 CC mammalian cells, and can be used to express any type of recombinant
 CC protein. The use of a triply spliced selectable marker means that
 CC all selected colonies arise from homologous recombination. In
 CC addition, the number of colonies that need to be screened to
 CC identify high producer clones is reduced. An amplifiable gene can
 CC be inserted on integration of the marking vector, so that when a
 CC gene is targeted to this site, the gene is further enhanced by gene
 CC amplification.
 XX
 SQ Sequence 19035 BP; 4705 A; 4968 C; 4822 G; 4519 T; 21 other;
 Query Match 98.6%; Score 349.2; DB 19; Length 19035;
 Best Local Similarity 99.2%; Pred. No. 2e-88;
 Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTGCAGCTGTGTGAGTCTGGGGCGGCTTGGCAAAGCCTGGGGGTCCCTGAGACTC 60
 DB 9489 GAGGTGAGTGTGTGAGTCTGGGGCGGCTTGGCAAAGCCTGGGGGTCCCTGAGACTC 9548
 QY 61 TGGTGCAGCTCCCGGTTTCACTTCAATAACTACTACATGAGCTGGGTCCGC 120
 DB 9549 TCCTGCGAGCTCCCGGTTTCACTTCAATAACTACTACATGAGCTGGGTCCGC 9508
 QY 121 CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTATCCACA 180
 DB 9609 CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTATCCACA 9668
 QY 181 TGGTACGCGAGCTCCGTGAAGGCGAGATTCAACATCTCCAGAGAGAACGCCAACACACA 240
 DB 9669 TGGTACGCGAGCTCCGTGAAGGCGAGATTCAACATCTCCAGAGAGAACGCCAACACACA 9728
 QY 241 CTGTTTCTTCAATGAACAGCTGAGAGCTGAGGACACCGCTGTCTATTACTGTGGAGC 300
 DB 9729 CTGTTTCTTCAATGAACAGCTGAGAGCTGAGGACACCGCTGTCTATTACTGTGGAGC 9788
 QY 301 TTCACTACAGGGTCTGACTCTCTGGGGCCAGGGAGTCTCTGGTCAACCGTCTCTCTCA 354

Db 9789 TTGACTACAGGCTCTGACTCTCTGGGCGAGGAGTCTCTGGTTCACCGTCTCTCA 9842
 |||||
 RESULT 3
 AAH41153
 ID AAH41153 standard; DNA; 458 BP.
 XX
 AC AAH41153;
 XX
 DT 22-AUG-2001 (first entry)
 XX
 DE Human coding sequence SEQ ID 3.
 XX
 KW Human; antiarthritic; cardiant; monoclonal antibody; keloid; arthritis;
 KW Tumour Growth Factor-beta II receptor; TGF-beta II receptor; atopy;
 KW signal transduction inhibition; tissue fibrosis; atherosclerosis; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200136642-A1.
 XX
 PD 25-MAY-2001.
 XX
 PF 17-NOV-2000; 2000WO-JP08129.
 XX
 PR 18-NOV-1999; 99JP-0328681.
 PR 08-NOV-2000; 2000JP-0340216.
 XX
 PA (NISR) JAPAN TOBACCO INC.
 XX
 PI Sakamoto S, Kamada M;
 XX
 DR WPI; 2001-343825/36.
 DR P-PSDB; AAB99111.
 XX
 PT Human monoclonal antibodies recognizing human TGF-beta II receptor,
 PT useful for treating TGF-beta associated diseases such as tissue
 PT fibrosis -
 XX
 PS Example 12; Page 94-95; 118pp; Japanese.
 XX
 CC The present invention relates to novel human monoclonal antibodies. The
 CC antibodies can bind to human Tumour Growth Factor-beta (TGF-beta) II
 CC receptor, resulting in the inhibition of the signal transduction of human
 CC TGF-beta into cells. The antibodies can be used for the prevention and
 CC treatment of diseases associated with the production of TGF-beta, such as
 CC tissue fibrosis in the lung, liver, skin, kidney or other tissues,
 CC atherosclerosis, atopy, keloid and arthritis. The present sequence was
 CC used in the present invention.
 XX
 SQ Sequence 458 BP; 92 A; 121 C; 139 G; 106 T; 0 other;
 Query Match 70.7%; Score 250.4; DB 22; Length 458;
 Best Local Similarity 83.9%; Pred. No. 5.6e-61;
 Matches 297; Conservative 0; Mismatches 51; Indels 6; Gaps 1;
 QY 1 GAGGTGCAGCTGGTGGAGTCTCTGGGCGGCTTGGCAAGCTTGGGGGTCCTCGAGACTC 60
 DB 58 GAGGTGCAGCTGGTGGAGTCTCTGGGCGGCTTGGCAAGCTTGGGGGTCCTCGAGACTC 117
 QY 61 TGGTGGCAGCTCCGGGTTGAGTTTCACTTCAATTAATACTACTAGTGGTGGTCCG 120
 DB 118 TCCTGTGAGGCTCTG-----GATTCACCTTCACTTGTAGTGGTGGTCCG 171
 QY 121 CAGGCTCCAGGCGCAGGGGCTGGAGTGGGTCTCACTATTAGTAGTGGTGGTCCACACA 180
 DB 172 CAGGCTCCAGGAGGAGGGCTGGAGTGGGTCTCATCTCATTCATTAGTAGTAGTACATA 231
 QY 181 TGGTACGAGACTCCGTGAAGGCGAGATTCCACATCTCCAGAGAACGCCCAACACACA 240
 DB 232 TACTACAGACTCAGTGAAGGGCGGATTCCATCTCCAGAGAACGCCCAAGAACTCA 291

QY 241 CTGTTTCTTCAATGAACAGCCTGAGAGCTGAGGACACAGCCTCTCTATTACTGTGGAGC 300
 DB 292 CTGTAICTGCAATGAACAGCCTGAGAGCCGAGGACACAGCCTGTGTATTACTGTGGAGA 351
 QY 301 TTGACTACAGGCTCTGACTCTCTGGGCGCAGGAGTCTCTGGTACCGTCTCTCTCA 354
 DB 352 GGGTACTCTGGGGTTTGACTACTCTGGGCGCAGGAAACCTCTGGTACCGTCTCTCTCA 405
 RESULT 4
 AAL39119
 ID AAL39119 standard; DNA; 348 BP.
 XX
 AC AAL39119;
 XX
 DT 02-SEP-2002 (first entry)
 XX
 DE Antibody screening method related DNA VH (DP-47).
 XX
 KW Screening antibody; 2-D electrophoresis; plural protein; protein spot;
 KW antibody library; proteomics; ds.
 XX
 OS Unidentified.
 XX
 PN WO200242774-A1.
 XX
 PD 30-MAY-2002.
 XX
 PF 05-JUN-2001; 2001WO-JP04732.
 XX
 PR 24-NOV-2000; 2000JP-0358539.
 XX
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 PA (NINA-) JAPAN NAT CENT NEUROLOGY & PSYCHIATRY.
 XX
 PI Kaneko K;
 XX
 DR WPI; 2002-471742/50.
 DR P-PSDB; AAO21548.
 XX
 PT Screening an antibody using 2-D electrophoresis on plural proteins in
 PT samples for separating individual protein spots to react with an
 PT antibody library useful in proteomics and other biological sciences -
 XX
 PS Disclosure; Fig 1; 78pp; Japanese.
 XX
 CC The invention relates to a novel method for screening an antibody,
 CC comprising performing 2-D electrophoresis on plural proteins in a sample.
 CC Individual protein spots are separated by reacting them with an antibody
 CC library and then replicating the bound antibodies before reacting them
 CC with the spot proteins again. The method is useful for screening an
 CC antibody specific for a target protein, e.g. from a phage antibody
 CC library, which is useful in proteomics for studying various protein and
 CC complementary deoxyribonucleic acid (cDNA) expression libraries as well
 CC as gene functions, and in other biological and medical sciences. This
 CC polynucleotide is a DNA sequence relating to the antibody screening
 CC method of the invention.
 XX
 SQ Sequence 348 BP; 71 A; 84 C; 108 G; 73 T; 12 other;
 Query Match 68.9%; Score 244; DB 24; Length 348;
 Best Local Similarity 82.0%; Pred. No. 3.3e-59;
 Matches 287; Conservative 0; Mismatches 57; Indels 6; Gaps 1;
 QY 1 GAGGTGCAGCTGGTGGAGTCTGGGCGGCTTGGCAAGCTTGGGGGTCCTCGAGACTC 60
 DB 1 GAGGTGCAGCTGGTGGAGTCTGGGCGGAGGCTTGTACAGCTTGGGGGTCCTCGAGACTC 60
 QY 61 TGGTGGCAGCTCCGGGTTGAGTTTCACTTCAATTAATACTACTAGTGGTGGTCCG 120
 DB 61 TCCTGTGAGGCTCTG-----GATTCACCTTGTAGCAGCTATGCCAGTGGTGGTCCG 114
 QY 121 CAGGCTCCAGGCGCAGGGGCTGGAGTGGGTCTCACTATTAGTAGTGGTGGTATCCACACA 180

Db 115 CAGGCTCCAGGAAGGGCTGAGTGGGTCTCAGCTATTAGTGGTGGTAGCACA 174
Qy 181 TGGTACGAGACTCCGTGAAGGGCAGATTACCATCTCCAGAGAGACGCCAACACACA 240
Db 175 TACTACGAGACTCCGTGAAGGGCGGTTCACCATCTCCAGAGACAAATTCAGAACACG 234
Qy 241 CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGACACGGCTGTCTATTACTGTGCGAGC 300
Db 235 CTGTATCTGCAATGAACAGCCTGAGAGCCGAGACACGGCGGTATATTACTGTGCGAAA 294
Qy 301 TTGACTACAGGGTCTGACTCTCGGGCCAGGAGTCTCTGTGTCACCGTCTC 350
Db 295 NNNNNNNNNNTTGTACTCTGGGGCCAGGAACCCCTGGTCAACCGTCTC 344

RESULT 5

ABK99213
ID ABK99213 standard; DNA; 364 BP.

XX AC ABK99213;

DT 21-OCT-2002 (first entry)

XX DNA sequence for antibody DP47 heavy chain variable region.

XX Sequence arrayed library; SAL; ss; antibody library;

KW protein identification; DP47; DPR22.

XX Homo sapiens.

OS JP2002174635-A.

PN 21-JUN-2002.

XX 07-DEC-2000; 2000JP-0373259.

XX 07-DEC-2000; 2000JP-0373259.

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA (KOKU-) KOKURITSU SEISHIN SHINKEI CENT SOCHO.

XX WPI; 2002-579732/62.

DR P-PSDB; ABG69320.

XX Screening of an antibody used for the identification of an objective
PT protein in high efficiency -

XX Example 8; Page 38; 43pp; Japanese.

XX The invention relates to screening an antibody against a specific protein
CC in an objective structure sample containing a protein group in high
CC efficiency, comprising reacting an objective structure sample containing
CC a protein group or a portion containing an objective protein in the
CC sample with an antibody library, recovering the antibody combined with
CC the protein, replicating the recovered antibody and reacting it with the
CC objective protein at least once. The method is used for the
CC identification of an objective protein. The present sequence is a
CC DNA sequence for an antibody chain (derived from the DP47 heavy chain,
CC the DP47 light chain or a combination of the two) used in the method of
CC the invention.

XX Sequence 364 BP; 73 A; 90 C; 114 G; 75 T; 12 other;

Qy Query Match 68.9%; Score 244; DB 24; Length 364;

Db Best Local Similarity 82.0%; Pred. No. 3.4e-59;

XX Matches 287; Conservative 0; Mismatches 57; Indels 6; Gaps 1;

Qy 1 CAGGTGACGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCTCCCTGAGACTC 60

Db 9 CAGGTGACGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGTCTCCCTGAGACTC 68

Qy 61 TGGTGGCAGCCTCCGGGTTTCAGGTTTACCTTCAATTAATACTACTACATGAGTGGTCCGC 120

Db 69 TCCTGTGACGCTCTG-----GATTACACCTTTAGCAGCTATGCCATGAGCTGGGTCCGC 122
Qy 121 CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTGGTATCCACACA 180
Db 123 CAGGCTCCAGGGAGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTGGTGGTAGCACA 182
Qy 181 TGGTACGACGACTCCGTGAAGGGCAGATTACCATCTCCAGAGAGAACGCCAACACACA 240
Db 183 TACTACGACGACTCCGTGAAGGGCGGTTCACCATCTCCAGAGACAAATTCAGAACACG 242
Qy 241 CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGACACGGCTGTCTATTACTGTGCGAGC 300
Db 243 CTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCGGTATATTACTGTGCGAAA 302
Qy 301 TTGACTACAGGGTCTGACTCTCGGGCCAGGAGTCTCTGTGTCACCGTCTC 350
Db 303 NNNNNNNNNNTTGTACTCTGGGGCCAGGAACCCCTGGTCAACCGTCTC 352

RESULT 6

AAL39104
ID AAL39104 standard; DNA; 364 BP.

XX AC AAL39104;

DT 02-SEP-2002 (first entry)

XX Antibody screening method related DNA SEQ ID No 164.

XX Screening antibody; 2-D electrophoresis; plural protein; protein spot;
KW antibody library; proteomics; ds.

XX Unidentified.

XX WO200242774-A1.

PN 30-MAY-2002.

XX 05-JUN-2001; 2001WO-JP04732.

XX 24-NOV-2000; 2000JP-0358539.

XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.

PA (NINA-) JAPAN NAT CENT NEUROLOGY & PSYCHIATRY.

XX Kaneko K;

XX WPI; 2002-471742/50.

XX Screening an antibody using 2-D electrophoresis on plural proteins in
PT samples for separating individual protein spots to react with an
PT antibody library useful in proteomics and other biological sciences -
XX Example 8; Page 73; 78pp; Japanese.

XX The invention relates to a novel method for screening an antibody,
CC comprising performing 2-D electrophoresis on plural proteins in a sample.
CC Individual protein spots are separated by reacting them with an antibody
CC library and then replicating the bound antibodies before reacting them
CC with the spot proteins again. The method is useful for screening an
CC antibody specific for a target protein, e.g. from a phage antibody
CC library, which is useful in proteomics for studying various protein and
CC complementary deoxyribonucleic acid (cDNA) expression libraries as well
CC as gene functions, and in other biological and medical sciences. This
CC polynucleotide is a DNA sequence relating to the antibody screening
CC method of the invention.

XX Sequence 364 BP; 73 A; 90 C; 114 G; 75 T; 12 other;

Qy Query Match 68.9%; Score 244; DB 24; Length 364;

Db Best Local Similarity 82.0%; Pred. No. 3.4e-59;

XX Matches 287; Conservative 0; Mismatches 57; Indels 6; Gaps 1;

Qy 1 GAGTGCAGCTGTGGAGTCTGGGGGGGGCTTGGCAAGCCCTGGGGGGTCCCTGAGACTC 60
Db 9 GAGTGCAGCTGTGGAGTCTGGGGGGGGCTTGGTACAGCCCTGGGGGGTCCCTGAGACTC 68
Qy 61 TGGTCCGAGCTCCGGGTTTCAGGTTTCCACCTTCAATAACTACTACATGGACTGGGTCGCG 120
Db 69 TCCTGTGAGGCTCTG-----GATTTCACCTTTAGCAGCTATGCCATGAGCTGGTCCGCG 122
Qy 121 CAGGCTCCAGGGCAGGGGCTGGAGTGGGCTCTCAGCTATTAGTAGTGGTGGTATCCACCA 180
Db 123 CAGGCTCCAGGAAGGGGCTGGAGTGGGCTCTCAGCTATTAGTGGTGGTGGTAGCACA 182
Qy 181 TGGTACGAGACTCCGTGAAGGGGAGATTACCATCTCCAGAGAGAACGCCCAACACACA 240
Db 183 TACTACGAGACTCCGTGAAGGGGCTTCAACCATCTCCAGAGACAAATTCGAAGAACAG 242
Qy 241 CTGTTTCTTCAAAATGAACAGCTCAGAGCTCAGGACAGCGGTGCTATTACTGTGCGAGC 300
Db 243 CTGTATCTGCAAAATGAACAGCTCAGAGCCGAGGACAGCGCCGTATATTACTGTGCGAAA 302
Qy 301 TTGACTACAGGCTCTGACTCTCTGGGGCCAGGGAGTCTCTGGTCAACCGTCTC 350
Db 303 NNNNNNNNNNTTGACTACTTGGGGCCAGGGAACCCCTGGTCAACCGTCTC 352

RESULT 7
AAX36070
ID AAX36070 standard; DNA; 720 BP.
XX AC AAX36070;
XX DT 15-JUL-1999 (first entry)
XX DE DNA encoding a single chain antibody (ScFv).
XX KW Screening; functional polypeptide; ligand; non-functional;
XX KW enrichment; single chain antibody; ScFv; ss.
XX OS Unidentified.
XX PN WO9920749-A1.
XX PD 29-APR-1999.
XX PF 20-OCT-1998; 98WO-GB031135.
XX PR 21-NOV-1997; 97US-0065729.
XX PR 20-OCT-1997; 97GB-0022131.
XX PR 13-NOV-1997; 97US-0065428.
XX PA (MEDI-) MEDICAL RES COUNCIL.
XX PI Tomlinson I, Winter G;
XX DR WPI; 1999-288302/24.
XX DR P-PSDB; AAY02472.

PT Screening for functional polypeptides which bind a ligand
XX Disclosure; Fig 2; 67pp; English.
XX

CC The specification describes a method for screening for functional
CC polypeptides which bind a ligand. The method comprises contacting a
CC repertoire of polypeptides with a generic ligand, and then screening
CC selected functional polypeptides with a target ligand. The method
CC permits the removal from a chosen repertoire of polypeptides, those
CC which are non-functional, e.g. as a result of the introduction of
CC frame-shift mutations, stop codons, folding mutants or expression
CC mutants which would be or are incapable of binding to any target
CC ligand. The method also permits the enrichment of a chosen repertoire
CC of polypeptides for those polypeptides which are functional, well folded
CC and highly expressed. The polypeptides obtained can be used in

CC diagnostic, prophylactic and therapeutic procedures. The present
CC sequence encodes the single chain antibody (ScFv) that forms the basis
CC of a library according to the invention.
XX SQ Sequence 720 BP; 168 A; 181 C; 214 G; 157 T; 0 other;
Query Match 67.8%; Score 240; DB 20; Length 720;
Best Local Similarity 82.6%; Pred. No. 5.5e-58;
Matches 289; Conservative 0; Mismatches 55; Indels 6; Gaps 1;
Qy 1 GAGTGCAGCTGTGGAGTCTGGGGGGGGCTTGGCAAGCCCTGGGGGGTCCCTGAGACTC 60
Db 1 GAGTGCAGCTGTGGAGTCTGGGGGGGGCTTGGTACAGCCCTGGGGGGTCCCTGAGACTC 60
Qy 61 TGGTCCGAGCTCCGGGTTTCAGGTTTCCACCTTCAATAACTACTACATGGACTGGGTCGCG 120
Db 61 TCCTGTGAGGCTCTG-----GATTTCACCTTTAGCAGCTATGCCATGAGCTGGTCCGCG 114
Qy 121 CAGGCTCCAGGGCAGGGGCTGGAGTGGGCTCTCAGCTATTAGTAGTGGTGGTATCCACCA 180
Db 115 CAGGCTCCAGGAAGGGGCTGGAGTGGGCTCTCAGCTATTAGTGGTGGTGGTAGCACA 174
Qy 181 TGGTACGAGACTCCGTGAAGGGGAGATTACCATCTCCAGAGAGAACGCCCAACACACA 240
Db 175 TACTACGAGACTCCGTGAAGGGGCTTCAACCATCTCCAGAGACAAATTCGAAGAACAG 234
Qy 241 CTGTTTCTTCAAAATGAACAGCTCAGAGCTCAGGACAGCGGTGCTATTACTGTGCGAGC 300
Db 235 CTGTATCTGCAAAATGAACAGCTCAGAGCCGAGGACAGCGCCGTATATTACTGTGCGAAA 294
Qy 301 TTGACTACAGGCTCTGACTCTCTGGGGCCAGGGAGTCTCTGGTCAACCGTCTC 350
Db 295 AGTTATGGTCTCTTTGACTACTTGGGGCCAGGGAACCCCTGGTCAACCGTCTC 344

RESULT 8
ABZ76706
ID ABZ76706 standard; DNA; 720 BP.
XX AC ABZ76706;
XX DT 01-MAY-2003 (first entry)
XX DE Human serum albumin antibody related DNA #1.
XX KW Ligand; human serum albumin; HSA; antibody; cytostatic; anti-HIV;
XX KW anti-inflammatory; antianaemic; immunosuppressive; neuroprotective;
XX KW dual-specific ligand; cancer; HIV infection; hepatitis; rubella;
XX KW anaemia; inflammation; autoimmune disorder; multiple sclerosis;
XX KW Crohn's disease; myasthenia gravis; gene; ds.
XX OS Homo sapiens.
XX OS Synthetic.
XX PH Key Location/Qualifiers
XX CDS 1..720
XX FT /*tag= a
XX FT /partial
XX FT /product= "HSA antibody amino acid sequence"
XX FT /note= "no start or stop codons given"
XX PN WO2003002609-A2.
XX PD 09-JAN-2003.
XX PF 28-JUN-2002; 2002WO-GB03014.
XX PR 28-JUN-2001; 2001GB-0015841.
XX PA (MEDI-) MEDICAL RES COUNCIL.
XX PI Winter G, Ignatovich O, Tomlinson I;
XX


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DR WPI; 2003-210246/20.
DR P-PSDB; ABP95997.
XX
XX Dual-specific ligand having immunoglobulins with binding specificity to
PT different antigens or epitopes, useful for treating, preventing or
PT diagnosing diseases, e.g. cancer, HIV infection, inflammations, or
PT myasthenia gravis
XX
XX Example 1; Fig 1; 84pp; English.
XX
XX The present invention describes a dual-specific ligand (I) comprising:
CC (a) a first single immunoglobulin variable domain with a binding
CC specificity to a first antigen or epitope; and (b) a second complementary
CC immunoglobulin single variable domain with a binding activity to a second
CC antigen or epitope. The binding domains are mutually complementary, and
CC the first and second domains lack mutually complementary domains that
CC share the same specificity. (I) has cytostatic, anti-HIV, antianaemic,
CC antiinflammatory, immunosuppressive and neuroprotective activities. The
CC dual-specific ligand is useful for treating, preventing or diagnosing
CC diseases, e.g. cancer, HIV infection, hepatitis, rubella, anaemia,
CC inflammations or autoimmune disorders (e.g. multiple sclerosis, Crohn's
CC disease or myasthenia gravis). The dual-specific ligand may be used to
CC recruit cytotoxic T-cells to a cancer cell. The dual-specific ligand is
CC also useful for monitoring the efficacy of drugs, as well as for
CC monitoring toxicity. The present sequence encodes a human serum albumin
CC (HSA) related antibody sequence, which is used in an example from the
CC present invention.
XX
XX Sequence 720 BP; 168 A; 181 C; 214 G; 157 T; 0 other;
XX
XX Query Match 67.8%; Score 240; DB 25; Length 720;
XX Best Local Similarity 82.6%; Pred. No. 5.5e-58;
XX Matches 289; Conservative 0; Mismatches 55; Indels 6; Gaps 1;
XX
Qy 1 GAGTGCAGCTGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCTGAGACTC 60
Db 1 GAGTGCAGCTGTGGAGTCTGGGGCGGCTTGGTACAGCCTGGGGGTCCTGAGACTC 60
Qy 61 TGGTGGCAGCCTCGGGTTCAGGTTCCACCTTCAATTAAGTACTACATGAGTGGTCCGC 120
Db 61 TCGTGTGAGCCTCTG-----GATTCACTTTAGCAGCTATGCTGAGTGGTCCGC 114
Qy 121 CAGGCTCCAGGCGAGGCTGGAGTGGGTCTCAGTATTAGTAGTGGTGTATCCACACA 180
Db 115 CAGGCTCCAGGCGAGGCTGGAGTGGGTCTCAGTATTAGTAGTGGTGTATCCACACA 174
Qy 181 TGGTACGAGACTCCGTGAAGGGCAGATTACCATCTCCAGAGAGAACGCCAACACACA 240
Db 175 TACTACGAGACTCCGTGAAGGGCGGTTACCATCTCCAGAGAGAACGCCAACACAGC 234
Qy 241 CTGTTTCTTCAATGACAGCCTGAGAGCTGAGACAGGCTGTCTATTACTGTGGAGC 300
Db 235 CTGTATCTGCAATGAAACAGCCTGAGAGCGGAGACAGCGCGGTATTACTGTGGAAA 294
Qy 301 TTGACTACAGGCTGACTCTCTGGGGCGAGGAGTCTCTGGTCAACCGTCTC 350
Db 295 AGTTATGGTCTTTGACTACTGGGGCGAGGAGACCTGTGTCACCGTCTC 344
XX
XX RESULT 9
XX AAD46290
XX ID AAD46290 standard; DNA; 348 BP.
XX
XX AC AAD46290;
XX
XX 27-DEC-2002 (first entry)
XX
XX Human KDR (VEGFR-2) Fab heavy chain (VH) DNA from D2C6 clone.
XX
XX Human; tumour; vascular endothelial growth factor receptor; metastasis;
XX epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC;
XX breast; VEGFR; heart; EGFR; therapy; invasiveness; heavy chain; gene;
XX VH; ds.

```

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XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..348
XX /tag= a
XX /product= "Human KDR (VEGFR-2) Fab heavy chain (VH)
XX protein"
XX /note= "CDS does not include start and stop codon"
XX /partial
XX
XX WO200270008-A1.
XX
XX 12-SEP-2002.
XX
XX 04-MAR-2002; 2002WO-US06762.
XX
XX 02-MAR-2001; 2001US-0798689.
XX
XX (IMCL-) IMCLONE SYSTEMS INC.
XX (ROCK/) ROCKWELL P.
XX (GOLD/) GOLDSTEIN N I.
XX
XX WPI; 2002-691738/74.
XX
XX P-PSDB; AAE28870.
XX
XX Inhibiting tumor growth in humans involves administering vascular
XX endothelial growth factor receptor antagonists in combination with
XX radiation, chemotherapeutic agents, or epidermal growth factor receptor
XX antagonists -
XX
XX Example 9; Page 121-122; 151pp; English.
XX
XX The invention relates to a method of inhibiting tumour growth which
XX involves administering, vascular endothelial growth factor receptor
XX (VEGFR) antagonists in combination with radiation, chemotherapeutic
XX agent, or epidermal growth factor receptor (EGFR) antagonist. The method
XX is useful for inhibiting tumour growth in a human, where the tumour (e.g.
XX tumour of the breast, heart, lung, small intestine, colon, spleen, bone,
XX kidney, bladder, head and neck, ovary, prostate, brain, pancreas, skin,
XX bone marrow, blood, thymus, uterus, testicles, cervix or liver) over
XX expresses VEGFR. It is also useful for inhibiting growth of colon tumour
XX or non-small cell lung carcinoma (NSCLC) and tumour overexpressing EGFR.
XX It is preferably useful for treating subjects with both solid tumours,
XX preferably high vascular tumours and non-solid tumours. The inhibition
XX or reduction of tumour growth includes prevention or inhibition of the
XX progression of tumour, including cancerous and non-cancerous tumours,
XX where the progression of tumours includes the invasiveness, metastasis,
XX recurrence and increase in size of the tumour. The present sequence is
XX human KDR (VEGFR-2) Fab antibody heavy chain DNA.
XX
XX Sequence 348 BP; 82 A; 85 C; 105 G; 76 T; 0 other;
XX
XX Query Match 67.3%; Score 238.4; DB 24; Length 348;
XX Best Local Similarity 82.3%; Pred. No. 1.3e-57;
XX Matches 288; Conservative 0; Mismatches 56; Indels 6; Gaps 1;
XX
Qy 1 GAGTGCAGCTGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCTGAGACTC 60
Db 1 GAGTGCAGCTGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCTGAGACTC 60
Qy 61 TGGTGGCAGCCTCCGGGTTTCAGGTTTCACCTTCAATTAAGTACTACATGAGTGGTCCGC 120
Db 61 TCGTGTGAGCCTCTG-----GATTCACTTTAGTACTAGTAGTGGTGTATCCACACA 180
Qy 121 CAGGCTCCAGGCGAGGCTGGAGTGGGTCTCAGTATTAGTAGTGGTGTATCCACACA 180
Db 115 CAGGCTCCAGGCGAGGCTGGAGTGGGTCTCAGTATTAGTAGTGGTGTATCCACACA 174
Qy 181 TGGTACGAGACTCCGTGAAGGGCAGATTACCATCTCCAGAGAGAACGCCAACACACA 240
Db 175 TACTACGAGACTCCGTGAAGGGCGGTTACCATCTCCAGAGAGAACGCCAACAGACTCA 234

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QY 241 CTGTTTCTTCAATGACAGCCTGAGAGCTGAGGACACGCTGTCTATTACTGTGCGAGC 300
DB 235 CTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGCTGTGTATTACTGTGCGAGA 294
QY 301 TTGACTACAGGCTCTGACTCTCTGGGGCCAGGGAGTCTCTGTGTCACCGTCTC 350
DB 295 GTCACAGATGCTTTTGATATCTGGGGCCAGGGACATGTCACCGTCTC 344

RESULT 10
ABT23325
ID ABT23325 standard; DNA; 348 BP.
AC ABT23325;
XX
XX
DT 01-MAY-2003 (first entry)
DE VEGF binding related DNA SEQ ID No 75.
XX
XX Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;
KW leukaemia cell; vascular endothelial growth factor; tumour;
KW bispecific antigen-binding protein; human; gene; ds.
XX
XX Homo sapiens.
XX
XX WO2003002144-A1.
XX
XX 09-JAN-2003.
XX
XX 26-JUN-2002; 2002WO-US20332.
XX
XX 26-JUN-2001; 2001US-301299P.
XX
XX (IMCL-) IMCLONE SYSTEMS INC.
XX
XX Zhu Z;
XX
XX WPI; 2003-201468/19.
XX
XX P-PSDB; ABJ26763.
XX
XX New bispecific antibodies having antigen-binding sites specific for a
XX first vascular endothelial growth factor (VEGF) receptor and for a
XX second VEGF receptor, useful for inhibiting migration of leukemia
XX cells, or for treating tumors -
XX
XX Disclosure; Page 70; 98pp; English.
XX
XX The invention relates to a novel antibody having a first antigen binding
XX site specific for a first vascular endothelial growth factor (VEGF)
XX receptor and a second antigen-binding site specific for a second VEGF
XX receptor. The bispecific antigen-binding proteins block activation of the
XX VEGF receptor and are useful for reducing or inhibiting VEGF-induced
XX cellular functions such as mitogenesis of vascular endothelial cells
XX and migration of leukaemia cells. The antibodies are useful for treating
XX tumours and for in vivo or in vitro for investigative and diagnostic
XX methods. This polynucleotide sequence represents a human DNA sequence
XX relating to the bispecific antibodies that bind to the VEGF receptors of
XX the invention.
XX
XX Sequence.348 BP; 82 A; 85 C; 105 G; 76 T; 0 other;
XX
XX Query Match 67.3%; Score 238.4; DB 25; Length 348;
XX Best Local Similarity 82.3%; Pred. No. 1.3e-57;
XX Matches 288; Conservative 0; Mismatches 56; Indels 6; Gaps 1;
QY 1 GAGGTGACAGCTGGTGGAGTCTGGGGGGCTTGCAAGCCTGGGGGTCTCTGAGACTC 60
DB 1 GAGGTGACAGCTGGTGGAGTCTGGGGGGAGGCTGTGTCAGCCTGGGGGTCTCTGAGACTC 60
QY 61 TGGTGGCGAGCCTCCGGGTTCCAGGTTTACCTTCAATTAACACTACTACATGAGTGGTCCGC 120
DB 61 TCCTGTGCAGCCTCTG-----GATTACCTTTCAGTAGCTATAGCATGAATGAGTGGTCCGC 114
```

```
QY 121 CAGGCTCCAGGGCAGGGGCTGGAGTGGTCTCACGTATTAGTAGTAGTGGTATCCACA 180
DB 115 CAGGCTCCAGGGAGAGGGGCTGGAGTGGTCTCATTCATTAGTAGTAGTAGTACATA 174
QY 181 TGGTACGCGAGACTCCCTGGAAGGCGAGTTCACCATCTCCAGAGAGAACGCCACAACACA 240
DB 175 TACTACGCGAGACTCAGTGAAGGGCCGATTCCACCATCTCCAGAGAGAACGCCACAAGACTCA 234
QY 241 CTGTTTCTTCAATGAACAGCCTGAGAGCTGAGGACACGCTCTTATTACTGTGCGAGC 300
DB 235 CTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGCTGTGTATTACTGTGCGAGA 294
QY 301 TTGACTACAGGCTCTGACTCTCTGGGGCCAGGGAGTCTCTGTGTCACCGTCTC 350
DB 295 GTCACAGATGCTTTTGATATCTGGGGCCAGGGACATGTCACCGTCTC 344

RESULT 11
ABK99212
ID ABK99212 standard; DNA; 742 BP.
XX
XX AC ABK99212;
XX
XX 21-OCT-2002 (first entry)
XX
XX DNA sequence for antibody DP47VH/DPKS22VL.
XX
XX Sequence arrayed library; SAL; ss; antibody library;
XX protein identification; DP47; DPK22.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX JP2002174635-A.
XX
XX 21-JUN-2002.
XX
XX 07-DEC-2000; 2000JP-0373259.
XX
XX 07-DEC-2000; 2000JP-0373259.
XX
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX (KOKU-) KOKURITSU SEISHIN SHINKAI CENT SOCHO.
XX
XX WPI; 2002-579732/62.
XX
XX Screening of an antibody used for the identification of an objective
XX protein in high efficiency -
XX
XX Example 8; Page 38; 43pp; Japanese.
XX
XX The invention relates to screening an antibody against a specific protein
XX in an objective structure sample containing a protein group in high
XX efficiency, comprising reacting an objective structure sample containing
XX a protein group or a portion containing an objective protein in the
XX sample with an antibody library, recovering the antibody combined with
XX the protein, replicating the recovered antibody and reacting it with the
XX objective protein at least once. The method is used for the
XX identification of an objective protein. The present sequence is a
XX DNA sequence for an antibody chain (derived from the DP47 heavy chain,
XX the DPK22 light chain or a combination of the two) used in the method of
XX the invention.
XX
XX Sequence 742 BP; 152 A; 186 C; 225 G; 155 T; 24 other;
XX
XX Query Match 66.9%; Score 237; DB 24; Length 742;
XX Best Local Similarity 80.6%; Pred. No. 3.9e-57;
XX Matches 283; Conservative 0; Mismatches 62; Indels 6; Gaps 1;
QY 1 GAGGTGACAGTGGTGGAGTCTGGGGGGCGGCTTGCAAGCCTGGGGGTCTCTGAGACTC 60
DB 9 GAGGTGACAGTGGTGGAGTCTGGGGGGAGGTTTGGTACAGCCTGGGGGTCTCTGAGACTC 68
```

QY 61 TGGTGCAGCAGCTCCGGTTTCAGGTTCCACCTTCAATAACTACTACATGAGTGGTCCGC 120
 DB 69 TCCTGTGCAGCCCTCG-----GATTCACTTTAGTAGTTATGTCATGAGTGGTCCGC 122
 QY 121 CAGGCTCCAGGCGAGGGCTGGAGTGGGTCTCAGGTATTAGTAGTAGTGGTATCCACA 180
 DB 123 CAAGCTCCAGGGAAGGGCTGGAGTGGGTCTCTGCTATTAGTGGAGTGGTGGTAGACA 182
 QY 181 TGGTACGCAGACTCCGTTGAAGGCGAGATTCCACCATCTCCAGAGAGAACGCCACAACA 240
 DB 183 TATTATGACAGACTCTGTGAAGGCGGATTCCACCATCTCCAGAGACAATCTCAAGAACCC 242
 QY 241 CTGTTTCTTCAATGAACAGCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 300
 DB 243 CTGTATCTGCAATGAACAGTCTGAGAGCCGAGGACACGCCGTATATTACTGTGCGAAA 302
 QY 301 TTGACTACAGGTTCTGACTCTCTGGGGCCAGGGAGTCTGTGTCACCGTCTCC 351
 DB 303 NNNNNNNNNNTTGTACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCC 353

RESULT 12

AAL39103
 ID AAL39103 standard; DNA; 742 BP.

XX AC AAL39103;

DT 02-SEP-2002 (first entry)

XX Antibody screening method related DNA SEQ ID No 163.

DE Screening antibody; 2-D electrophoresis; plural protein; protein spot;
 KW antibody library; proteomics; ds.

XX Unidentified.

XX WO200242774-A1.

XX 30-MAY-2002.

XX 05-JUN-2001; 2001WO-JP04732.

XX 24-NOV-2000; 2000JP-0358539.

XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.

PA (NINA-) JAPAN NAT CENT NEUROLOGY & PSYCHIATRY.

XX Kaneko K;

XX WPI; 2002-471742/50.

XX Screening an antibody using 2-D electrophoresis on plural proteins in
 PT samples for separating individual protein spots to react with an
 PT antibody library useful in proteomics and other biological sciences -

XX Example 8; Page 72; 78pp; Japanese.

XX The invention relates to a novel method for screening an antibody,
 CC comprising performing 2-D electrophoresis on plural proteins in a sample.
 CC Individual protein spots are separated by reacting them with an antibody
 CC library and then replicating the bound antibodies before reacting them
 CC with the spot proteins again. The method is useful for screening an
 CC antibody specific for a target protein, e.g. from a phage antibody
 CC library, which is useful in proteomics for studying various protein and
 CC complementary deoxyribonucleic acid (cDNA) expression libraries as well
 CC as gene functions, and in other biological and medical sciences. This
 CC polynucleotide is a DNA sequence relating to the antibody screening
 CC method of the invention.

XX Sequence 742 BP; 152 A; 186 C; 225 G; 155 T; 24 other;

XX Query Match 66.9%; Score 237; DB 24;

XX Best Local Similarity 80.6%; Pred. No. 3.9e-57; Length 742;

Matches 283; Conservative 0; Mismatches 62; Indels 6; Gaps 1;
 QY 1 GAGGTGCAGCTGTGGAGTCTGGGGCGGCTTGGCAAGGCTGGGGGTCCCTGAGACTC 60
 DB 9 GAGGTGCAGCTGTGGAGTCTGGGGGAGGTTTGGTACAGCTGGGGGTCCCTGAGACTC 68
 QY 61 TGGTGCAGCAGCTCCGGTTTCAGGTTTCACTTCAATAACTACTACATGAGTGGTCCGC 120
 DB 69 TCCTGTGCAGCCCTCG-----GATTCACTTTAGTAGTTATGTCATGAGTGGTCCGC 122
 QY 121 CAGGCTCCAGGCGAGGGCTGGAGTGGGTCTCAGGTATTAGTAGTAGTGGTATCCACA 180
 DB 123 CAAGCTCCAGGGAAGGGCTGGAGTGGGTCTCTGCTATTAGTGGAGTGGTGGTAGACA 182
 QY 181 TGGTACGCAGACTCCGTTGAAGGCGAGATTCCACCATCTCCAGAGAGAACGCCACAACA 240
 DB 183 TATTATGACAGACTCTGTGAAGGCGGATTCCACCATCTCCAGAGACAATCTCAAGAACCC 242
 QY 241 CTGTTTCTTCAATGAACAGCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 300
 DB 243 CTGTATCTGCAATGAACAGTCTGAGAGCCGAGGACACGCCGTATATTACTGTGCGAAA 302
 QY 301 TTGACTACAGGTTCTGACTCTCTGGGGCCAGGGAGTCTGTGTCACCGTCTCC 351
 DB 303 NNNNNNNNNNTTGTACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCC 353

RESULT 13

AAD46292
 ID AAD46292 standard; DNA; 348 BP.

XX AC AAD46292;

DT 27-DEC-2002 (first entry)

XX Human KDR (VEGFR-2) Fab heavy chain (VH) DNA from DIH4 clone.

XX Human; tumour; vascular endothelial growth factor receptor; metastasis;
 KW epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC;
 KW breast; VEGFR; heart; EGFR; therapy; invasiveness; heavy chain; gene;
 XX VH; ds.

XX Homo sapiens.

PH Key Location/Qualifiers
 FT CDS 1..348

FT /*tag= a /product= "Human KDR (VEGFR-2) Fab heavy chain (VH)

FT /protein"

FT /note= "CDS does not include start and stop codon"

FT /partial

XX WO200270008-A1.

XX 12-SEP-2002.

XX 04-MAR-2002; 2002WO-US06762.

XX 02-MAR-2001; 2001US-0798689.

XX (IMCL-) IMCLONE SYSTEMS INC.

PA (ROCK/) ROCKWELL P.

PA (GOLD/) GOLDSTEIN N I.

XX WPI; 2002-691738/74.

DR P-PSDB; AAE28870.

XX Inhibiting tumor growth in humans involves administering vascular
 PT endothelial growth factor receptor antagonists in combination with
 PT radiation, chemotherapeutic agents, or epidermal growth factor receptor
 PT antagonists -

XX Example 12; Page 124-125; 151pp; English.

XX CC The invention relates to a method of inhibiting tumour growth which
 CC involves administering, vascular endothelial growth factor receptor
 CC (VEGFR) antagonists in combination with radiation, chemotherapeutic
 CC agent, or epidermal growth factor receptor (EGFR) antagonist. The method
 CC is useful for inhibiting tumour growth in a human, where the tumour (e.g.
 CC tumour of the breast, heart, lung, small intestine, colon, spleen, bone,
 CC kidney, bladder, head and neck, ovary, prostate, brain, pancreas, skin,
 CC bone marrow, blood, thymus, uterus, testicles, cervix or liver) over
 CC expresses VEGFR. It is also useful for inhibiting growth of colon tumour
 CC or non-small cell lung carcinoma (NSCLC) and tumour overexpressing EGFR.
 CC It is preferably useful for treating subjects with both solid tumours,
 CC preferably high vascular tumours and non-solid tumours. The inhibition
 CC or reduction of tumour growth includes prevention or inhibition of the
 CC progression of tumour, including cancerous and non-cancerous tumours,
 CC where the progression of tumours includes the invasiveness, metastasis,
 CC recurrence and increase in size of the tumour. The present sequence is
 CC human KDR (VEGFR-2) Fab antibody heavy chain DNA.
 XX SQ Sequence 348 BP; 82 A; 86 C; 104 G; 76 T; 0 other;
 Query Match 66.9%; Score 236.8; DB 24; Length 348;
 Best Local Similarity 82.0%; Pred. No. 3.6e-57;
 Matches 287; Conservative 0; Mismatches 57; Indels 6; Gaps 1;
 QY 1 GAGGTGAGCTGGTGGAGTCTGGGGGGCGCTTGGCAAGCCTGGGGGGTCCCTGAGACTC 60
 DB 1 GAGGTCCAGCTGGTGGAGTCTGGGGGGAGCGCTGGTCAAGCTGGGGGGTCCCTGAGACTC 60
 QY 61 TGGTGGCAGCTCCGGGTTTCAGGTTTCACTTCAATTAACACTACATGAGTGGTGGTCCGC 120
 DB 61 TCCTGTGAGCCTCTGGATTCA-----CCTTCACTAGCTATAGCATGAATGGTGGTCCGC 114
 QY 121 CAGGCTCCAGGGCAGGGGCTGGAGTGGTCTCAGCTATTAGTAGTGGTGGTATCCCA 180
 DB 115 CAGGCTCCAGGGAAGGGCTGGAGTGGTCTCATCCATTAGTAGTAGTATTACATA 174
 QY 181 TGGTACGAGACTCCGTGAAGGGCAGATTCCACATCTCCAGAGAGAGCCCAACACACA 240
 DB 175 TACTACGAGACTCAGTGAAGGGCCGATTCCACATCTCCAGAGAGAGCCCAAGACTCA 234
 QY 241 CTGTTTCTTCAAATGAACAGCTCAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 300
 DB 235 CTGTATCTGCAATGAACAGCTGAGAGCCGAGAGCCGAGGACACGGCTGTATTACTGTGCGAGA 294
 QY 301 TTGACTACAGGGTCTGACTCTCTGGGGCCAGGGAGTCTCTGTGTCACCGTCTC 350
 DB 295 GTCACAGATGCTTTTGATATCTGGGGCCAAAGGGACAATGGTCAACCGTCTC 344
 RESULT 14
 ABT23327
 ID ABT23327 standard; DNA; 348 BP.
 XX AC ABT23327;
 XX 01-MAY-2003 (first entry)
 XX VEGF binding related DNA SEQ ID No 79.
 XX Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;
 KW leukaemia cell; vascular endothelial growth factor; tumour;
 KW bispecific antigen-binding protein; human; gene; ds.
 XX Homo sapiens.
 XX WO2003002144-A1.
 XX 09-JAN-2003.
 XX 26-JUN-2002; 2002WO-US20332.
 XX 26-JUN-2001; 2001US-301299P.

XX PA (IMCL-) IMCLONE SYSTEMS INC.
 XX PI Zhu Z;
 XX DR WPI; 2003-201468/19.
 XX PT New bispecific antibodies having antigen-binding sites specific for a
 PT first vascular endothelial growth factor (VEGF) receptor and for a
 PT second VEGF receptor, useful for inhibiting migration of leukemia
 PT cells, or for treating tumors -
 XX Disclosure; Page 72; 98pp; English.
 XX The invention relates to a novel antibody having a first antigen binding
 CC site specific for a first vascular endothelial growth factor (VEGF)
 CC receptor and a second antigen-binding site specific for a second VEGF
 CC receptor. The bispecific antigen-binding proteins block activation of the
 CC VEGF receptor and are useful for reducing or inhibiting VEGF-induced
 CC cellular functions such as mitogenesis of vascular endothelial cells
 CC and migration of leukaemia cells. The antibodies are useful for treating
 CC tumours and for in vivo or in vitro for investigative and diagnostic
 CC methods. This polynucleotide sequence represents a human DNA sequence
 CC relating to the bispecific antibodies that bind to the VEGF receptors of
 CC the invention.
 XX SQ Sequence 348 BP; 82 A; 86 C; 104 G; 76 T; 0 other;
 Query Match 66.9%; Score 236.8; DB 25; Length 348;
 Best Local Similarity 82.0%; Pred. No. 3.6e-57;
 Matches 287; Conservative 0; Mismatches 57; Indels 6; Gaps 1;
 QY 1 GAGGTGAGCTGGTGGAGTCTGGGGGGCGCTTGGCAAGCCTGGGGGGTCCCTGAGACTC 60
 DB 1 GAGGTCCAGCTGGTGGAGTCTGGGGGGAGCGCTGGTCAAGCTGGGGGGTCCCTGAGACTC 60
 QY 61 TGGTGGCAGCTCCGGGTTTCAGGTTTCACTTCAATTAACACTACATGAGTGGTGGTCCGC 120
 DB 61 TCCTGTGAGCCTCTGGATTCA-----CCTTCACTAGCTATAGCATGAATGGTGGTCCGC 114
 QY 121 CAGGCTCCAGGGCAGGGGCTGGAGTGGTCTCAGTATTAGTAGTGGTGGTATCCCA 180
 DB 115 CAGGCTCCAGGGAAGGGCTGGAGTGGTCTCATCCATTAGTAGTAGTATTACATA 174
 QY 181 TGGTACGAGACTCCGTGAAGGGCAGATTCCACATCTCCAGAGAGAGCCCAACACACA 240
 DB 175 TACTACGAGACTCAGTGAAGGGCCGATTCCACATCTCCAGAGAGAGCCCAAGACTCA 234
 QY 241 CTGTTTCTTCAAATGAACAGCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 300
 DB 235 CTGTATCTGCAATGAACAGCTGAGAGCCGAGAGCCGAGGACACGGCTGTATTACTGTGCGAGA 294
 QY 301 TTGACTACAGGGTCTGACTCTCTGGGGCCAGGGAGTCTCTGTGTCACCGTCTC 350
 DB 295 GTCACAGATGCTTTTGATATCTGGGGCCAAAGGGACAATGGTCAACCGTCTC 344
 RESULT 15
 AAD46294
 ID AAD46294 standard; DNA; 348 BP.
 XX AC AAD46294;
 XX 27-DEC-2002 (first entry)
 XX Human KDR (VEGFR-2) Fab heavy chain (VH) DNA from D2H2 clone.
 XX Human; tumour; vascular endothelial growth factor receptor; metastasis;
 KW epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC;
 KW breast; VEGFR; heart; EGFR; therapy; invasiveness; heavy chain; gene;
 XX VH; ds.
 XX Homo sapiens.

XX Key Location/Qualifiers
FH 1..348
FT /*tag= a
FT /product= "Human KDR (VEGFR-2) Fab heavy chain (VH)
FT /protein"
FT /notes= "CDS does not include start and stop codon"
FT /partial
XX WO200270008-A1.
XX
XX 12-SEP-2002.
XX
XX 04-MAR-2002; 2002WO-US06762.
XX
XX 02-MAR-2001; 2001US-0798689.
XX
XX (IMCL-) IMCLONE SYSTEMS INC.
XX (ROCK/) ROCKWELL P.
XX (GOLD/) GOLDSTEIN N I.
XX
XX WPI; 2002-691738/74.
XX P-PSDB; AAE28873.
XX
XX Inhibiting tumor growth in humans involves administering vascular
PT endothelial growth factor receptor antagonists in combination with
PT radiation, chemotherapeutic agents, or epidermal growth factor receptor
PT antagonists -
XX
XX Example 12; Page 126; 151pp; English.
XX
XX The invention relates to a method of inhibiting tumour growth which
CC involves administering, vascular endothelial growth factor receptor
CC (VEGFR) antagonists in combination with radiation, chemotherapeutic
CC agent, or epidermal growth factor receptor (EGFR) antagonist. The method
CC is useful for inhibiting tumour growth in a human, where the tumour (e.g.
CC tumour of the breast, heart, lung, small intestine, colon, spleen, bone,
CC kidney, bladder, head and neck, ovary, prostate, brain, pancreas, skin,
CC bone marrow blood, thymus, uterus, testicles, cervix or liver) over
CC expresses VEGFR. It is also useful for inhibiting growth of colon tumour
CC or non-small cell lung carcinoma (NSCLC) and tumour overexpressing EGFR.
CC It is preferably useful for treating subjects with both solid tumours,
CC preferably high vascular tumours and non-solid tumours. The inhibition
CC or reduction of tumour growth includes prevention or inhibition of the
CC progression of tumour, including cancerous and non-cancerous tumours;
CC where the progression of tumours includes the invasiveness, metastasis,
CC recurrence and increase in size of the tumour. The present sequence is
CC human KDR (VEGFR-2) Fab antibody heavy chain DNA.
XX
XX Sequence 348 BP; 82 A; 85 C; 105 G; 76 T; 0 other;
SQ

Query Match 66.4%; Score 235.2; DB 24; Length 348;
Best Local Similarity 81.7%; Pred. No. 1e-56;
Matches 286; Conservative 0; Mismatches 58; Indels 6; Gaps 1;
Qy 1 GAGGTGAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCTGGGGGTCCCTGAGACTC 60
Db 1 GAAGTGAGCTGGTGGAGTCTGGGGGAGGCTGGTCAAGCTGGGGGTCCCTGAGACTC 60
Qy 61 TGGTGGCGAGCCTCCGGGTTTCAAGTTTCAATTAATCTACATGAGCTGGGTCCGC 120
Db 61 TCCTGTGCAGCCTCTGAATCA-----CCTTCAGTAGCTATAGCATGAATGGTCCGC 114
Qy 121 CAGGCTCCAGGCGAGGGGCTGGAGTGGGTCTCAGTATTAGTAGTAGTGGTATCCACA 180
Db 115 CAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCATCCATTAGTAGTAGTATTACATA 174
Qy 181 TGGTACCAGACTCCGTGAAGGGGAGATTCCACCATCTCCAGAGAGACGCCAACACACA 240
Db 175 TACTACGAGACTCAGTGAAGGGGCGGATTCCACCATCTCCAGAGACAAACCGAGGACTCA 234
Qy 241 CTGTTTCTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGGAGC 300

Db 235 CTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACACGCGCTGTGTATTACTGTGCGAGA 294
Qy 301 TTGACTACAGGGTCTGACTCTCTGGGGCCAGGGAGTCTCTGTGTACCGTCTC 350
Db 295 GTCAACAGATGCTTTTGATATCTGGGGCCAGGAGCAATGGTCACCGTCTC 344

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OM nucleic - nucleic search, using sw model

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SUMMARIES

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4	220.6	62.3	354	2	US-08-652-816A-21
5	220	62.1	354	2	US-08-652-816A-22
6	219.4	62.0	743	3	US-08-545-809A-48
7	219.2	61.9	348	2	US-08-652-816A-24
8	218.4	61.7	715	3	US-08-545-809A-11
9	217.8	61.5	519	3	US-08-545-809A-21
10	215.6	60.9	432	1	US-08-026-320A-1
11	215.6	60.9	892	4	US-09-273-839A-11
12	214.6	60.6	747	4	US-10-039-785-65
13	213.6	60.3	514	3	US-08-545-809A-23
14	212.2	59.9	351	2	US-08-428-197-35
15	212.2	59.9	351	5	PCT-US93-10555-35
16	211	59.6	345	2	US-08-428-197-41
17	211	59.6	345	5	PCT-US93-10555-41
18	210.4	59.4	294	2	US-08-428-197-47
19	210.4	59.4	294	5	PCT-US93-10555-47
20	210.2	59.4	381	3	US-09-240-274-96
21	208.8	59.0	354	2	US-08-958-201-1
22	207.6	58.6	360	2	US-08-958-201-9
23	206.6	58.4	649	3	US-08-545-809A-64
24	206.2	58.2	903	4	US-09-273-839A-12
25	206.2	58.2	913	4	US-09-273-839A-10
26	205.6	58.1	360	2	US-08-958-201-7
27	204.2	57.7	5925	4	US-09-315-926A-78

28	203.2	57.4	393	1	US-08-259-372A-3	Sequence 3, Appl
29	203.2	57.4	393	1	US-08-468-671-3	Sequence 3, Appl
30	202.4	57.2	369	2	US-08-428-197-37	Sequence 37, Appl
31	202.4	57.2	369	5	PCT-US93-10555-37	Sequence 37, Appl
32	202.2	57.1	366	2	US-08-958-201-5	Sequence 5, Appl
33	201.8	57.0	724	3	US-08-545-809A-53	Sequence 53, Appl
34	200.2	56.6	376	5	PCT-US93-12501-2	Sequence 2, Appl
35	200.2	56.6	514	3	US-08-545-809A-20	Sequence 20, Appl
36	199.2	56.3	393	3	US-09-240-274-97	Sequence 97, Appl
37	199.2	56.3	930	4	US-09-079-029-6	Sequence 6, Appl
38	197.8	55.9	357	1	US-07-988-925-23	Sequence 23, Appl
39	197.8	55.9	357	2	US-08-362-780-23	Sequence 23, Appl
40	197.6	55.8	372	2	US-08-428-197-43	Sequence 43, Appl
41	197.6	55.8	372	5	PCT-US93-10555-43	Sequence 43, Appl
42	197.6	55.8	640	3	US-08-545-809A-9	Sequence 9, Appl
43	197.4	55.8	360	2	US-08-428-197-19	Sequence 19, Appl
44	197.4	55.8	360	2	US-08-428-197-21	Sequence 21, Appl
45	197.4	55.8	360	5	PCT-US93-10555-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-08-803-085-4
; Sequence 4, Application US/08803085
; Patent No. 6011138
; GENERAL INFORMATION:
; APPLICANT: REEF, Mitchell E.
; APPLICANT: KLOETZER, William S.
; APPLICANT: NAKAMURA, Takehiko
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES AND USE THEREOF AS THERAPEUTICS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/803,085
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 411 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..411
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 58..411
US-08-803-085-4

Query Match 100.0%; Score 354; DB 3; Length 411;

Best Local Similarity 100.0%; Pred. No. 8.8e-101; Indels 0; Gaps 0;
Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGCAAAAGCTGGGGGTCCTGAGACTC 60
DB 58 GAGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGCAAAAGCTGGGGGTCCTGAGACTC 117

QY 61 TGGTCCGAGCTCCGGGTTGAGTTCACTTCAATTAATCTACATGAGTGGTCCGC 120
DB 118 TGGTCCGAGCTCCGGGTTGAGTTCACTTCAATTAATCTACATGAGTGGTCCGC 177

QY 121 CAGGCTCAGGGCAGGGCTGGAGTGGTCTCACTATTAGTAGTGGTGTGATCCACCA 180
DB 178 CAGGCTCAGGGCAGGGCTGGAGTGGTCTCACTATTAGTAGTGGTGTGATCCACCA 237

QY 181 TGGTACGAGCTCCGTTGAAGGCGAGATTACCATCTCCAGAGAGAAAGCCCAACACCA 240
DB 238 TGGTACGAGCTCCGTTGAAGGCGAGATTACCATCTCCAGAGAGAAAGCCCAACACCA 297

QY 241 CTGTTTCTTCAATGAACAGCTGAGAGCTGAGGACAGGCTGTCTATTACTGTGGAGC 300
DB 298 CTGTTTCTTCAATGAACAGCTGAGAGCTGAGGACAGGCTGTCTATTACTGTGGAGC 357

QY 301 TTGACTACAGGCTGACTCTCTGGGGCAGGGAGTCTGTGTCACCGTCTCTCTCA 354
DB 358 TTGACTACAGGCTGACTCTCTGGGGCAGGGAGTCTGTGTCACCGTCTCTCTCA 411

RESULT 2

US-09-343-485A-3
; Sequence 3, Application US/09343485A
; Patent No. 6413777
; GENERAL INFORMATION:
; APPLICANT: REPE, MITCHELL R.
; APPLICANT: BARNETT, RICHARD S.
; APPLICANT: MCILACHLAN, KAREN R.
; TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT SPECIFIC SITES IN
; TITLE OF INVENTION: MAMMALIAN CELLS VIA HOMOLOGOUS RECOMBINATION AND
; TITLE OF INVENTION: VECTORS FOR ACCOMPLISHING THE SAME
; FILE REFERENCE: 037003-0275807
; CURRENT APPLICATION NUMBER: US/09/343,485A
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/023,715
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 08/819,866
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 19040
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; OTHER INFORMATION: referred to as "Mandy"

US-09-343-485A-3

Query Match 95.5%; Score 338.2; DB 4; Length 19040;
Best Local Similarity 98.9%; Pred. No. 3.8e-95;
Matches 351; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 GAGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGCAAAAGCTGGGGGTCCTGAGACTC 60
DB 9493 GAGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGCAAAAGCTGGGGGTCCTGAGACTC 9552

QY 61 TGGTCCGAGCTCCGGGTTGAGTTCACTTCAATTAATCTACATGAGTGGTCCGC 120
DB 9553 TCCTGGGAGAGCTCCGGGTTGAGTTCACTTCAATTAATCTACATGAGTGGTCCGC 9612

QY 121 CAGGCTCAGGGCAGGGCTGGAGTGGTCTCACTATTAGTAGTGGTGTGATCCACCA 180
DB 9613 CAGGCTCAGGGCAGGGCTGGAGTGGTCTCACTATTAGTAGTGGTGTGATCCACCA 9672

QY 181 TGGTACGAGACTCCCTGAAGGCGAGATTACCATCTCCAGAGAGAAAGCCCAACACCA 240
DB 9673 TGGTACGAGACTCCCTGAAGGCGAGATTACCATCTCCAGAGAGAAAGCCCAACACCA 9732

QY 241 CTGTTTCTTCAATGAACAGCTGAGAGCTGAGGACAGGCTGTCTATTACTGTGGAGC 300
DB 9733 CTGTTTCTTCAATGAACAGCTGAGAGCTGAGGACAGGCTGTCTATTACTGTGGAGC 9792

QY 301 TTGACTACAGGCTCTGACTCTCTGGGGCAGGGAGTCTGTGTCACCGTCTCTCTCA 354
DB 9793 TTGACTACAGGCTCTGACTCTCTGGGGCAGGGAGTCTGTGTCACCGTCTCTCTCA 9847

RESULT 3

US-09-273-839A-9
; Sequence 9, Application US/09273839A
; Patent No. 6329156
; GENERAL INFORMATION:
; APPLICANT: Cirino, Nick M
; APPLICANT: Jackson, Paul J
; APPLICANT: Lehnert, Bruce E
; TITLE OF INVENTION: Disruption of Anthrax Toxin Binding to Cell Surface
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: S-89,662
; CURRENT APPLICATION NUMBER: US/09/273,839A
; CURRENT FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 9
; LENGTH: 908
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-273-839A-9

Query Match 62.4%; Score 220.8; DB 4; Length 908;

Best Local Similarity 80.1%; Pred. No. 3.3e-59;
Matches 290; Conservative 0; Mismatches 57; Indels 15; Gaps 2;

QY 2 AGGTGAGCTGGTGGAGTCTGGGGGCGGCTTGCAAAAGCTGGGGGTCCTGAGACTCT 61
DB 104 AGGTCAACTTAAGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCTGAGACTCT 163

QY 62 GGTGCGCAGCTCCGGGTTTCACTTCAATTAATTAATTAATTAATTAATTAATTAAT 121
DB 164 CTTGTGAGCTCTG-----GATTCACTTACAGCAGTATGATGATGATGATGATGAT 217

QY 122 AGGCTCCAGGCGAGGGCTGGAGTGGTCTCAGTATTAGTAGTAGTAGTAGTAGTAGTAG 181
DB 218 AGGCTCCAGGCGAGGGCTGGAGTGGTCTCAGTATTAGTAGTAGTAGTAGTAGTAGTAG 277

QY 182 GGTACGCGAGCTCCGTGAGGGCAGATTCACTTCACTTCACTTCACTTCACTTCACTTCA 241
DB 278 ACTACGCGAGCTCAGTGAAGGGCAGATTCACTTCACTTCACTTCACTTCACTTCACTTCA 337

QY 242 TGTTCCTTCAATGAACAGCTGAGAGCTGAGGACAGGCTGTCTATTACTGTGGAGCT 301
DB 338 TGTATCTTCAATGAACAGCTGAGAGCTGAGGACAGGCTGTCTATTACTGTGGAGCT 397

QY 302 TGA-----CTACAGGCTCTGACTCTCTGGGGCAGGGAGTCTGTGTCACCGTCTCTCT 352
DB 398 AGAGGGGGGGCGGAGCAGCAGCTCTGACTTACTTGGGGCGGGGAAACCTTGGTCACTCTCT 457

QY 353 CA 354
DB 458 CA 459

RESULT 4

US-08-652-816A-21
; Sequence 21, Application US/08652816A
; Patent No. 5872215
; GENERAL INFORMATION:
; APPLICANT: Osbourn, JK

APPLICANT: Allen, DJ
APPLICANT: McCafferty, JG
TITLE OF INVENTION: Specific binding members, materials and
TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,816A
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525004.9
FILING DATE: 07-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/02240
FILING DATE: 02-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/244,597
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/33308
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 354 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-652-816A-21

Query Match 62.3%; Score 220.6; DB 2; Length 354;
Best Local Similarity 80.2%; Pred. No. 2.6e-59;
Matches 288; Conservative 0; Mismatches 59; Indels 12; Gaps 2;
QY 2 AGGTGACGCTGGTGGGCTGGGGCGGCTGGCAAGCTGGGGGCTCCCTGAGACTCT 61
DB 2 AGGTGACGCTGGTGGGCTGGGGCGGCTGGCCAGCTGGGGGCTCCCTGAGACTCT 61
QY 62 GGTGCGGAGCTCCCGGCTGAGGTTACCTTCAATACTACTACATGAGCTGGGTCGCC 121
DB 62 CTTGTGAGGCTCTGGATTGAG-----CGTCAGTAGCAATTACATGAGCTGGGTCGCC 115
QY 122 AGGCTCCAGGCGAGGGCTGGAGTGGTCTCACGTATTAGTAGTGGTATCCCAT 181
DB 116 AGTCTCCAGGGAAGGAGCTGGAATATGTTTCAGCTATTAGTAGTAATGGGGTAGCACAT 175

QY 182 GGTACGACAGCTCCGTGAAGGCGAGATTCAATCTCCAGAGAGAACGCCAACACACAC 241
DB 176 ACTACGACAGCTCCGTGAAGGCGAGATTCAATCTCCAGAGAGAAATCCAGAGACACGC 235
QY 242 TGTTCCTTCAATGAACAGCTGAGAGCTGAGGACAGGCTGCTATTACTGTGCGAGCT 301
DB 236 TGTATCTTCAATGAGCAGCTCCGAGAGCTGAGGACAGCGCTGTGTATTACTGTGCGAGAT 295
QY 302 TGA-----CTACAGGGTCTGACTCTCGGGGCGAGGAGTCTGGTCAACCGTCTCTCTCA 354
DB 296 TTATAAATCCCTACGGTATGACGCTCTGGGCGCAGGCGCACCCTGGTCAACCGTCTCTCTCA 354
RESULT 5
US-08-652-816A-22
Sequence 22. Application US/08652816A
Patent No. 5872215
GENERAL INFORMATION:
APPLICANT: Osbourn, JK
APPLICANT: Allen, DJ
APPLICANT: McCafferty, JG
TITLE OF INVENTION: Specific binding members, materials and
TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,816A
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525004.9
FILING DATE: 07-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/02240
FILING DATE: 02-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/244,597
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/33308
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 354 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

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; TOPOLOGY: linear
; US-08-652-816A-22
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: human lymphoblast
; CELL LINE: CGM1
; US-08-545-809A-48
Query Match 62.1%; Score 220; DB 2; Length 354;
Best Local Similarity 80.0%; Pred. No. 3.9e-59;
Matches 288; Conservative 0; Mismatches 60; Indels 12; Gaps 2;
QY 1 GAGGTGACGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCTGAGACTC 60
DB 1 GAGGTACACCTGGTGGAGTCTGGGAGAGCCCTTGTACAGCCTGGGGGTCCTGAGACTC 60
QY 61 TGGTGCAGCCTCCGGGTTTCAGGTTTCACTTCAATAACTACTACTAGTGGTCCGC 120
DB 61 TCCTGTGACGCTCTG-----GATTCACTTTAGCAGCTATGCCATGAGTGGTCCGC 114
QY 121 CAGGCTCAGGCGCAGGGCTGGAGTGGTCTCAGTATTAGTAGTGGTATGCCACA 180
DB 115 CAGGCTCAGGGAAGGGCTGGAGTGGTCTCAGTATTAGTGGTGGTGGTAGCACA 174
QY 181 TGGTACGACACTCCGTTGAAGGCGAGATTACCATCTCCAGAGAAAGCCCAACACA 240
DB 175 TACTACGACACTCCGTTGAAGGCGGCTTACCATCTCCAGAGACAATTCCAGAACACG 234
QY 241 CTGTTTCTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAG- 299
DB 235 CTGTATCTGCAATGAACAGCCTGAGAGCCGAGACACGGCTGTGTATTACTGTGCGAGA 294
QY 300 -----CTTGACTACAGGCTGACTCTCTGGGGCAGGGAGTCTGGTCACTCTCA 354
DB 295 GCTTTGGTTCGGGAGTTATAAGAGACTGGGGCCAGGGAACCTGGTCACTCTCTCA 354
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RESULT 6

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US-08-545-809A-48
; Sequence 48, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545.809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 743 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
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RESULT 7

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US-08-652-816A-24
; Sequence 24, Application US/08652816A
; Patent No. 5872215
; GENERAL INFORMATION:
; APPLICANT: Osbourn, JK
; APPLICANT: Allen, DJ
; APPLICANT: McCafferty, JG
; TITLE OF INVENTION: Specific binding members, materials and
; TITLE OF INVENTION: methods.
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,816A
; FILING DATE: 23-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9125579.4
; FILING DATE: 02-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9125579.8
; FILING DATE: 02-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206372.6
; FILING DATE: 23-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9525004.9
; FILING DATE: 07-DEC-1995
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; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: human lymphoblast
; CELL LINE: CGM1
; US-08-545-809A-48
Query Match 62.0%; Score 219.4; DB 3; Length 743;
Best Local Similarity 86.0%; Pred. No. 8.4e-59;
Matches 257; Conservative 0; Mismatches 36; Indels 6; Gaps 1;
QY 1 GAGGTGACGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCTGAGACTC 60
DB 334 GAGGTGACGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCTGAGACTC 393
QY 61 TGGTGCAGCCTCCGGGTTTCAGGTTTCACTTCAATAACTACTACTAGTGGTCCGC 120
DB 394 TCCTGTGACGCTCTG-----GATTCACTTTCAGTAGCTATAGCATGAACCTGGGTCCGC 447
QY 121 CAGGCTCCAGGCGCAGGGCTGGAGTGGTCTCAGTATTAGTAGTGGTATGCCACA 180
DB 448 CAGGCTCCAGGGAAGGGGCTGGAGTGGGTTTCATACATTAGTAGTAGTACCATA 507
QY 181 TGGTACGACACTCCGTTGAAGGCGCAGATTACCATCTCCAGAGAGAAAGCCCAACACA 240
DB 508 TACTACGACACTCTGTGAAGGCCGATTACCATCTCCAGAGACAATGCCAAGAACTCA 567
QY 241 CTGTTTCTTCAATGAACAGCCTTGAGAGCTGAGAGTGGAGACAGGCTGTCTATTACTGTGCGAG 299
DB 568 CTGTATCTGCAATGAACAGCCTTGAGAGCGGAGGACACGGCTGTGTATTACTGTGCGAG 626
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;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB 9610824.6
;; FILING DATE: 23-MAY-1996
;; PRIOR APPLICATION DATA: PCT/GB92/02240
;; FILING DATE: 02-DEC-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/244,597
;; FILING DATE: 01-JUN-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: David W. Clough
;; REGISTRATION NUMBER: 36,107
;; REFERENCE/DOCKET NUMBER: 28111/33308
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312-474-6300
;; INFORMATION FOR SEQ ID NO: 24:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 348 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; US-08-652-816A-24

Query Match 61.9%; Score 219.2; DB 2; Length 348;
Best Local Similarity 78.9%; Pred. No. 6.9e-59;
Matches 276; Conservative 0; Mismatches 68; Indels 6; Gaps 1;

QY 1 GAGGTGACGTGTTGGAGTCTGGGGGGCTTGGCAAGCTGGGGGGTCCCTGAGACTC 60
DB 1 GAGGTGACGTGTTGGAGTCTGGGGGGCTTGGCAAGCTGGGGGGTCCCTGAGACTC 60

QY 61 TGGTGGCAGCTCCGGGTTTCCAGTTCACCTTCAATAACTACTACATGGAGTGGTCCGC 120
DB 61 TCCTGTGACGCTCTG-----GATTCACCTTTGATGATTTATGGCATGAGTGGTCCGC 114

QY 121 CAGGCTCCAGGCGAGGGCTGGAGTGGTCTCAGTATTAGTAGTGGTGGTATCCCA 180
DB 115 CAAGCTCCAGGGAAGGGCTGGAGTGGTCTCTGGTATTATTTGGAATGGTGGTAGCACA 174

QY 181 TGGTACGACACTCCGTGAAGGCGAGATTACCATCTCCAGAGAGAGCGCAACACACA 240
DB 175 GGTATGACAGCTCTGTGAAGGCGGATTCACCATCTCCAGAGAGAGCGCAACAGAACTCC 234

QY 241 CTGTTCTTCAATGAACAGCTGAGAGCTGAGACAGCGTGTCTATTACTGTGGCAGC 300
DB 235 CTGTATCTTCAATGAACAGCTGAGAGCGGAGACAGCGGTGTATTACTGTGGCAAGA 294

QY 301 TTGACTACAGGCTGACTCTCTGGGGCCAGGGAGTCTGTGTCACCGTCTC 350
DB 295 AGCGGTATGCTGGATTATTGGGGCCAGGTACCTGTGTACCGTGTGTC 344

RESULT 8
US-08-545-809A-11
; Sequence 11, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95

;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/545,809A
;; FILING DATE: 27-MAR-1996
;; PRIOR APPLICATION DATA: PCT/JP93/00603
;; FILING DATE: 10-MAY-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Freeman, John W.
;; REGISTRATION NUMBER: 29,066
;; REFERENCE/DOCKET NUMBER: 06501/004001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-542-5070
;; TELEFAX: 617-542-8906
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 715 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: Genomic DNA
;; ORIGINAL SOURCE:
;; ORGANISM: Homo sapiens
;; CELL TYPE: human lymphoblast
;; CELL LINE: CGM1
;; US-08-545-809A-11

Query Match 61.7%; Score 218.4; DB 3; Length 715;
Best Local Similarity 85.9%; Pred. No. 1.7e-58;
Matches 256; Conservative 0; Mismatches 36; Indels 6; Gaps 1;

QY 2 AGGTGACGTGTTGGAGTCTGGGGGGCTTGGCAAGCTGGGGGGTCCCTGAGACTCT 61
DB 361 AGGTGACGTGTTGGAGTCTGGGGGGCTTGGCAAGCTGGGGGGTCCCTGAGACTCT 420

QY 62 GGTGCGCAGCTCCGGGTTTCCAGTTCACCTTCAATAACTACTACATGGAGTGGTCCGCC 121
DB 421 CCTGTGACGCTCTG-----GATTCACCTTCACTACTACTACATGAGTGGATCCGCC 474

QY 122 AGCTCCAGGCGAGGGCTGGAGTGGTCTCAGTATTAGTAGTGGTGGTATCCACAT 181
DB 475 AGGCTCCAGGGAAGGGCTGGAGTGGTCTTACATATTAGTAGTGGTGGTATACCATAT 534

QY 182 GGTACCCAGACTCCGTGAAGGCGAGATTTCACCATCTCCAGAGAGAGCGCAACACAC 241
DB 535 ACTACCCAGACTCTGTGAAGGCGGATTCACCATCTCCAGGGAACAGCGCAAGAACTCAC 594

QY 242 TGTTCCTTCAATGAACAGCTGAGAGCTGAGGACACGCGTGTCTATTACTGTGCGGAG 299
DB 595 TGTATCTGCAATGAACAGCTGAGAGCGGAGGACACGCGCGTGTATTACTGTGCGGAG 652

RESULT 9
US-08-545-809A-21
; Sequence 21, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

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;; OPERATING SYSTEM: Windows95
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/545.809A
;; FILING DATE: 27-MAR-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/JPS3/00603
;; FILING DATE: 10-MAY-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Freeman, John W.
;; REGISTRATION NUMBER: 29,066
;; REFERENCE/DOCKET NUMBER: 06501/004001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-542-5070
;; TELEFAX: 617-542-8906
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 21:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 519 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: Genomic DNA
;; ORIGINAL SOURCE:
;; ORGANISM: Homo sapiens
;; CELL TYPE: human lymphoblast
;; CELL LINE: CGM1
;; US-08-545-809A-21

Query Match 61.5%; Score 217.8; DB 3; Length 519;
Best Local Similarity 85.6%; Pred. No. 2.3e-58;
Matches 256; Conservative 0; Mismatches 37; Indels 6; Gaps 1;

Qy 1 GAGGTGCAGCTGGTGGAGTCTTGGGGGGCGGTTGGCAAAGCCTGGGGGTCCTCGAGACTC 60
Db 169 GAGGTGCAACTGGTGGAGTCTTGGGGGGCGGCTGGTCAAGCCTGGGGGTCCTCGAGACTC 228

Qy 61 TGGTGGCAGCTCGGGTTCAGGTTCACTTCACTTAATACTACTACATGAGTGGTCCGC 120
Db 229 TCCTGTGCAGCTCTG-----GATTCACCTTCAGTAGCTATAGCATGAATGGGTCCGC 282

Qy 121 CAGGCTCAGGGCAGGGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTGTATCCACACA 180
Db 283 CAGGCTTCAGGGAAGGGCTGGAGTGGGTCTTCATCCATTAGTAGTAGTAGTACATA 342

Qy 181 TGGTACGAGACTCCGTGAAGGGCAGATTACACATCTCCAGAGAGAACGCCAACACACA 240
Db 343 TACTACGAGACTCAGTGAAGGGCGATTACCATCTCCAGAGACAGCCCAAGAACTCA 402

Qy 241 CTGTTTCTTCAATGAACAGCTGAGAGCTGAGACAGGCTGTCTATTACTGTGCGAG 299
Db 403 CTGTATCTGCAATGAACAGCTGAGAGCTGAGAGCGGCTGTGTATTACTGTGCGAG 461

RESULT 10
US-08-026-320A-1
; Sequence 1, Application US/08026320A
; Patent No. 5419904
; GENERAL INFORMATION:
; APPLICANT: Irie, Reiko F
; TITLE OF INVENTION: HUMAN B-LYMPHOBLASTOID CELL LINE
; TITLE OF INVENTION: SECRETING ANTI-GANGLIOSIDE ANTIBODY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pons, Smith, Lande & Rose
; STREET: 2029 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States of America
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WordPerfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/026.320A
;; FILING DATE: 26-FEB-1993
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/609803
;; FILING DATE: 05-NOV-1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Oldenkamp, David J
;; REGISTRATION NUMBER: 29421
;; REFERENCE/DOCKET NUMBER: 94268
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 3107885046
;; TELEFAX: 3102771297
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 432 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Homo sapiens
;; CELL TYPE: Epstein Barr Virus Transformed B cell
;; CELL LINE: L612
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..432
;; OTHER INFORMATION: /function= "Heavy Chain"
;; OTHER INFORMATION: /product= "Immunoglobulin Variable Region"
;; OTHER INFORMATION: /standard name= "HuMab L612 Heavy Chain Variable
;; OTHER INFORMATION: Region Sequence"
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 148..162
;; OTHER INFORMATION: /function= "Complementary
;; OTHER INFORMATION: determining region 1 (CDR1)"
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 271..300
;; OTHER INFORMATION: /function= "Complementary
;; OTHER INFORMATION: determining region 2 (CDR2)"
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 397..429
;; OTHER INFORMATION: /function= "Complementary determining
;; OTHER INFORMATION: region 3 (CDR3)"
;; US-08-026-320A-1

Query Match 60.9%; Score 215.6; DB 1; Length 432;
Best Local Similarity 79.0%; Pred. No. 1e-57;
Matches 289; Conservative 0; Mismatches 59; Indels 18; Gaps 2;

Qy 1 GAGGTGCAGCTGGTGGAGTCTGGGGGGCGGTTGGCAAAGCCTGGGGGTCCTCGAGACTC 60
Db 58 GAGGTGCAGCTGTTGGATTCTGGGGGAGGCTTGGTACAGCTGGGGGTCCTCGAGACTC 117

Qy 61 TGGTGGCAGCTCCGGGTTTCAGGTTTCACTTCAATACTACTACATGAGTGGTCCGC 120
Db 118 TCCTGTGCAGCTCTG-----GATTCACCTTTAGCAGCTGTGCCATGAGTGGTCCGC 171

Qy 121 CAGGCTCCAGGGCAGGGCTGGAGTGGGTCTCAGCTATTAGTAGTAGTGTATCCACACA 180
Db 172 CAGGCTCCAGGGAAGGGCTGGAGTGGGTCTCAGCTATTAGTAGTAGTGTGTAGCACA 231

Qy 181 TGGTACGAGACTCCGTGAAGGGCAGATTACCATCTCCAGAGAGAACGCCAACACACA 240
Db 232 TACTACGAGACTCCGTGAAGGGCGGTTTACCATCTCCAGAGACAAATCCAAGAACACG 291
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QY 241 CTGTTCTTCAATGAACAGCCTGAGAGCTGAGACACGGCTGTCTATTACTGTGCGA-- 298
DB 292 TTGTATCTGCAATGAACAGCCTGAGAGCGGAGACACGGCTGTCTATTACTGTGCGAAA 351
QY 299 -----GCTTGACTACAGGCTGTGACTCTCTGGGGCCAGGAGTCTCTGGTCAACCGTC 348
DB 352 GGTGGCAACGATATTTTGACTGGTTATATGCTTTGGGGCCAGGGAACCTGGTCAACCGTC 411
QY 349 TCCTCA 354
DB 412 TCCTCA 417

RESULT 11
US-09-273-839A-11
; Sequence 11, Application US/09273839A
; Patent No. 6329156
; GENERAL INFORMATION:
; APPLICANT: Cirino, Nick M
; APPLICANT: Jackson, Paul J
; APPLICANT: Lehnert, Bruce B
; TITLE OF INVENTION: Disruption of Anthrax Toxin Binding to Cell Surface
; FILE REFERENCE: S-89,662
; CURRENT APPLICATION NUMBER: US/09/273,839A
; CURRENT FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 892
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-273-839A-11

Query Match 60.9%; Score 215.6; DB 4; Length 892;
Best Local Similarity 79.5%; Pred. No. 1.4e-57;
Matches 283; Conservative 0; Mismatches 64; Indels 9; Gaps 2;
QY 2 AGGTGACGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCCTGAGACTCT 61
DB 104 AGGTGACGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCCTGAGACTCT 163
QY 62 GGTGCGCAGCTCCCGGCTTCACTTCAATTAATACTACTACATGAGTGGGTCCGCC 121
DB 164 CTTGTGAGCTCTG-----GATTCACTTCAATACCATGCTATGGAATGGTCCGCC 217
QY 122 AGGTCCAGGCGAGGCTGGAGTGGTCTCACTGATTTAGTAGTGGTGGTATCCCAT 181
DB 218 AGGTCCAGGCGAGGCTGGAGTGGTCTCTGGTATTAATTTGGGATGGTGGTAGCAG 277
QY 182 GGTACGAGACTCCGTGAAGGGCAGATTACCATCTCCAGAGAGAACGCCAACACAC 241
DB 278 GTTATGAGACTCTGTGAAGGGCGGATTTCCCGCTCTCCAGAGAACGCCAACAACTCCC 337
QY 242 TGTTCTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCT 301
DB 338 TGATCTGCAATGAACAGCTGAGAGACGAGGACACGGCTGTCTATTACTGTGCGCAG 397
QY 302 TGA---CTACAGGCTCTGACTCTCTGGGGCCAGGAGTCTCTGGTCAACCGTCTCTCA 354
DB 398 CTAAGTGGGAGGATTTGACTTACTTGGGGCCAGGACCCCTGGTCAACCGTCTCTCA 453

RESULT 12
US-10-039-785-65
; Sequence 65, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Saicedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785

; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 747
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding T1006F07 scFv
US-10-039-785-65

Query Match 60.6%; Score 214.6; DB 4; Length 747;
Best Local Similarity 84.9%; Pred. No. 2.6e-57;
Matches 254; Conservative 0; Mismatches 39; Indels 6; Gaps 1;
QY 1 GAGTGCAGCTGTGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCCTGAGACTC 60
DB 1 GAGTGCAGCTGTGAGTCTGGGGCGGCTTGGTACAGCCTGGGGGTCCCTGAGACTC 60
QY 61 TGTGTGCGCAGCTCCCGGCTTCACTTCAATAAATACTACATGAGTGGTCCGC 120
DB 61 TCTGTGCGCAGCTCTG-----GATTCACTTTAGCAGCTATGCCATGAGTGGTCCGC 114
QY 121 CAGGCTCCAGGGCAGGGCTGGAGTGGGTCTCACTGATTTAGTAGTGGTGGTATCCACA 180
DB 115 CAGGCTCCAGGGAAGGGCTGGAGTGGGTCTCACTGATTTAGTAGTGGTGGTATCCACA 174
QY 181 TGTAGCAGCAGCTCCGTGAGGCGAGATTCACCATCTCCAGAGAGAACGCCAACACACA 240
DB 175 TACTACGACAGCTCCGTGAGGCGCGGTTCCACCATCTCCAGAGACAAATCCAAAGAACAG 234
QY 241 CTGTTTCTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTCTCTATTACTGTGCGAG 299
DB 235 CTGTATCTGCAATGAACAGCCTGAGAGCGGAGACACGGCCGTGTATTACTGTGCGAG 293

RESULT 13
US-08-545-809A-23
; Sequence 23, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

```

;
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 514 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: human lymphoblast
; CELL LINE: CGM1
; US-08-545-809A-23

Query Match 60.3%; Score 213.6; DB 3; Length 514;
Best Local Similarity 84.9%; Pred. No. 4.5e-57;
Matches 253; Conservative 0; Mismatches 39; Indels 6; Gaps 1;

Qy 1 GAGGTGACGCTGGTGGAGTCTGGGGCGGCTTGCAAGCCTGGGGGCTCCCTGAGACTC 60
Db 170 GAGGTGACGCTGGTGGAGTCTGGGGCGGCTTGCAAGCCTGGGGGCTCCCTGAGACTC 229
Qy 61 TGGTGCAGCCTCCGGGTTGAGTTCACCTTCAATACTACTACTGAGTGGTGGTCCGC 120
Db 230 TCCTGTGCAGCCTCTG-----GATTCACTTTAGCAGTATGTCATGAGTGGTGGTCCGC 283
Qy 121 CAGGCTCCAGGCGAGGCGCTGGAGTGGTCTCAGTATTAGTAGTGGTGGTATCCCA 180
Db 284 CAGGCTCCAGGCGAGGCGCTGGAGTGGTCTCAGTATTAGTAGTGGTGGTATCCCA 343
Qy 181 TGGTACGAGACTCCGTTGAAGGCGAGATTCAACCATCTCCAGAGAGAGCGCAACACA 240
Db 344 TACTACGAGACTCCGTTGAAGGCGGTTCAACCATCTCCAGAGAGAGATTCCAGAACAG 403
Qy 241 CTGTTTCTTCAATGAACAGCCTGAGAGCTGAGACACGGCTGTCTATTACTGTGCGA 298
Db 404 CTGTATCTGCAATGAACAGCCTGAGAGCTGAGACACGGCTGTCTATTACTGTGCGA 461

RESULT 14
US-08-428-197-35
Sequence 35, Application US/08428197
Patent No. 5891438
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,197
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10555
; FILING DATE: 29-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: PD-2630
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 351 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: SPA3-33
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..351
; US-08-428-197-35

Query Match 59.9%; Score 212.2; DB 2; Length 351;
Best Local Similarity 79.5%; Pred. No. 1e-56;
Matches 279; Conservative 0; Mismatches 63; Indels 9; Gaps 2;

Qy 7 CAGCTGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCTCGAGACTCTGGTGC 66
Db 7 CTGCTCGAGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGTGGCTTCTCTGT 66
Qy 67 GCAGCCTCCGGGTTGAGGTTTACCTTCAATAAATACTATACATGAGTGGGTCGCGCAGGCT 126
Db 67 GAAGCCTCTG-----GATTCCCTTTCAGTAACTATGGCATGAGTGGGTCGCGCAGGCT 120
Qy 127 CCAGGCGCAGGCGTGGAGTGGGTTCTCAGTATTAGTAGTAGTGGTATCCCAATGTAC 186
Db 121 CCAGGGAAGGCGTGGAGTGGGTTCTCAAGTATTAGTGAAGTGGTATGATAGTACATACTAC 180
Qy 187 GCAGACTCCGTGAAGGCGAGATTCAACCATCTCCAGAGAGAACGCCACACACACTGTTT 246
Db 181 GCGGACTCCGTGAAGGCGCGGTTTCAACCATCTCCAGAGAGAACGCCAAGAACTCACTGTAT 240
Qy 247 CTTCAATGAACAGCCTGAGAGCTGAGGACACGCGTGTCTATTACTGTGCGAGCTTGCAC- 305
Db 241 CTGCAATGAACAGCCTGAGAGCGGAGAGACGCGTGTGTATTACTGTGCGAGAGATGCA 300
Qy 306 --TACAGGGTCTGACTCTCTGGGCGCCAGGGAGTCTCTGTCAACCGTCTCTCA 354
Db 301 TGGGATGCAATTGATATCTCTGGGCGCCAGGAGCAATGGTCACTCTCTCA 351

RESULT 15
PCT-US93-10555-35
Sequence 35, Application PC/TUS9310555
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: PD-2630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 351 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: SpA3-33
FEATURE:
NAME/KEY: CDS
LOCATION: 1..351
PCT-US93-10555-35

Query Match 59.9%; Score 212.2; DB 5; Length 351;
Best Local Similarity 79.5%; Pred. No. 1e-56;
Matches 279; Conservative 0; Mismatches 63; Indels 9; Gaps 2;
QY 7 CAGCTGTGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGGTCCCTGAGACTCTGGTGC 66
Db |||||
7 CTGCTCAGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGTGGCCCTGAGACTCTCCTGT 66
QY 67 GCAGCCTCCGGGTCAGGTTCACTTCAATACTACTACATGACTGGGTCCGCCAGGCT 126
Db |||||
67 GAAGCCTCTG-----GATTCCCTTCAGTAACATATGGCATGAGCTGGGTCCGCCAGGCT 120
QY 127 CCAGGGCAGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGTATCCACATGGTAC 186
Db |||||
121 CCAGGGNAGGGGCTGGAGTGGGTCTCAAGTATTAGTGAAGTGGTGTATGATATCTAC 180
QY 187 GCAGACTCCGTGAAGGCGAGATTCAACATCTCCAGAGAGAACGCCAACACACTGTTT 246
Db |||||
181 GCCGACTCCGTGAAGGCGCGTTCCACCATCTCCAGAGACAACGCCAAGAACTCACTGTAT 240
QY 247 CTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGTTGAC- 305
Db |||||
241 CTGCAATGAACAGCCTGAGAGCGGAGACACGGCTGTGTATTACTGTGCGAGATGCA 300
QY 306 --TACAGGCTCTGACTCTCGGGCCAGGAGTCTCGGTACCGGTCTCTCTCA 354
Db |||||
301 TGGGATGCATTGTATATCTGGGGCCAGGACAAATGTCAGTCTCTCTCA 351

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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 19:01:43 ; Search time 511.438 Seconds
(without alignments)

2371.523 Million cell updates/sec

Title: US-09-019-441-4 COPY_58_411

Perfect score: 354

Sequence: 1 GAGGTGACGTGGTGGAGTC.....TCTGGTCACGGTCTCTCA 354

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2244575 seqs, 1713117285 residues

Total number of hits satisfying chosen parameters: 4489150

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	354	100.0	411	11	US-09-019-441-4
2	354	100.0	411	15	US-10-103-686-4
3	240	67.8	720	9	US-09-192-854-1
4	240	67.8	720	10	US-09-968-561A-1
5	240	67.8	720	13	US-09-968-744A-1
6	238.4	67.3	348	15	US-10-091-300-23
7	236.8	66.9	348	15	US-10-091-300-27
8	235.2	66.4	348	15	US-10-091-300-30
9	235.2	66.4	1710	12	US-10-291-265-99
10	233.6	66.0	1721	12	US-10-291-265-96
11	233.6	66.0	414	12	US-10-309-764-130
12	232	65.5	414	12	US-10-309-764-126
13	231	65.3	729	13	US-10-322-673-66
14	230.4	65.1	729	13	US-10-322-673-68
15	228.4	64.5	4026	13	US-09-949-039-1
					Sequence 4, Appli
					Sequence 4, Appli
					Sequence 1, Appli
					Sequence 1, Appli
					Sequence 1, Appli
					Sequence 23, Appli
					Sequence 27, Appli
					Sequence 30, Appli
					Sequence 99, Appli
					Sequence 96, Appli
					Sequence 130, Appli
					Sequence 126, Appli
					Sequence 66, Appli
					Sequence 68, Appli
					Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-019-441-4

; Sequence 4, Application US/09019441

; Publication No. US20030086921A1

; GENERAL INFORMATION:

; APPLICANT: REPT, Mitchell E.

; KLOETZER, William S.

; NAKAMURA, Takehiko

; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL

; ANTIBODIES AND USE THEREOF AS THERAPEUTICS

; NUMBER OF SEQUENCES: 35

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/019,441

; FILING DATE: 05-Feb-1998

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/803,085

; FILING DATE: 20-FEB-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Teskin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/DOCKET NUMBER: 012712-502

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 4:

Sequence	1, Appli	Sequence 134, App	Sequence 58, Appl	Sequence 70, Appl	Sequence 78, Appl	Sequence 94, Appl	Sequence 118, App	Sequence 102, App	Sequence 1, Appli	Sequence 5, Appli	Sequence 56, Appl	Sequence 74, Appl	Sequence 62, Appl	Sequence 66, Appl	Sequence 98, Appl	Sequence 122, App	Sequence 86, Appl	Sequence 60, Appl	Sequence 17, Appl	Sequence 31233, A	Sequence 90, Appl	Sequence 58, Appl	Sequence 58, Appl	Sequence 58, Appl	Sequence 58, Appl	Sequence 191, App	Sequence 67, Appl	Sequence 55, Appl	Sequence 82, Appl
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45	217.4	61.4	405	12	US-10-309-764-82																								

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SEQUENCE CHARACTERISTICS:
LENGTH: 411 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..411
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 58..411
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-019-441-4

Query Match      100.0%; Score 354; DB 11; Length 411;
Best Local Similarity 100.0%; Pred. No. 4.6e-102;
Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGTGCAGCTGGTGGAGTCTGGGGGGCGGCTTGGCAAAAGCCTGGGGGGTCCCTGAGACTC 60
Db |||||
Qy 58 GAGGTGCAGCTGGTGGAGTCTGGGGGGCGGCTTGGCAAAAGCCTGGGGGGTCCCTGAGACTC 117
Db |||||
Qy 61 TGGTGGCAGCTCCGGGTTCCAGGTTTCACTTCAATTAATACTACTGAGTGGTCCGC 120
Db |||||
Qy 118 TGGTGGCAGCTCCGGGTTCCAGGTTTCACTTCAATTAATACTACTGAGTGGTCCGC 177
Db |||||
Qy 121 CAGGCTCCAGGGCAGGGCTGGAGTGGGTTTCACTTATAGTAGTGGTGGTATCCACACA 180
Db |||||
Qy 178 CAGGCTCCAGGGCAGGGCTGGAGTGGGTTTCACTTATAGTAGTGGTGGTATCCACACA 237
Db |||||
Qy 181 TGGTACGAGACTCCGTGAAGGGCAGATTACCATCTCCAGAGAGAACGCCAACACACA 240
Db |||||
Qy 238 TGGTACGAGACTCCGTGAAGGGCAGATTACCATCTCCAGAGAGAACGCCAACACACA 297
Db |||||
Qy 241 CTGTTTCTTCAAAATGAACAGCTCAGAGCTCAGACACAGCGTGTCTATTACTGTGCGAGC 300
Db |||||
Qy 298 CTGTTTCTTCAAAATGAACAGCTCAGAGCTCAGACACAGCGTGTCTATTACTGTGCGAGC 357
Db |||||
Qy 301 TTGACTACAGGCTGTGACTCTCTGGGGCCAGGGAGTCTCTGTTACCGTCTCCTCA 354
Db |||||
Qy 358 TTGACTACAGGCTGTGACTCTCTGGGGCCAGGGAGTCTCTGTTACCGTCTCCTCA 411
Db |||||

RESULT 2
US-10-103-686-4
; Sequence 4, Application US/10103686
; Publication No. US20030059424A1
GENERAL INFORMATION:
APPLICANT: REFF, Mitchell E. S.
KLOETZER, William S.
NAKAMURA, Takehiko
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
ANTIBODIES AND USE THEREOF AS THERAPEUTICS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/103,686
FILING DATE: 25-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/803,085
```

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FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 411 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..411
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 58..411
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-103-686-4

Query Match      100.0%; Score 354; DB 15; Length 411;
Best Local Similarity 100.0%; Pred. No. 4.6e-102;
Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGTGCAGCTGGTGGAGTCTGGGGGGCGGCTTGGCAAAAGCCTGGGGGGTCCCTGAGACTC 60
Db |||||
Qy 61 TGGTGGCAGCTCCGGGTTCCAGGTTTCACTTCAATTAATACTACTGAGTGGTCCGC 120
Db |||||
Qy 118 TGGTGGCAGCTCCGGGTTCCAGGTTTCACTTCAATTAATACTACTGAGTGGTCCGC 177
Db |||||
Qy 121 CAGGCTCCAGGGCAGGGCTGGAGTGGGTTTCACTTATAGTAGTGGTGGTATCCACACA 180
Db |||||
Qy 178 CAGGCTCCAGGGCAGGGCTGGAGTGGGTTTCACTTATAGTAGTGGTGGTATCCACACA 237
Db |||||
Qy 181 TGGTACGAGACTCCGTGAAGGGCAGATTACCATCTCCAGAGAGAACGCCAACACACA 240
Db |||||
Qy 238 TGGTACGAGACTCCGTGAAGGGCAGATTACCATCTCCAGAGAGAACGCCAACACACA 297
Db |||||
Qy 241 CTGTTTCTTCAAAATGAACAGCTCAGAGCTCAGACACAGCGTGTCTATTACTGTGCGAGC 300
Db |||||
Qy 298 CTGTTTCTTCAAAATGAACAGCTCAGAGCTCAGACACAGCGTGTCTATTACTGTGCGAGC 357
Db |||||
Qy 301 TTGACTACAGGCTGTGACTCTCTGGGGCCAGGGAGTCTCTGTTACCGTCTCCTCA 354
Db |||||
Qy 358 TTGACTACAGGCTGTGACTCTCTGGGGCCAGGGAGTCTCTGTTACCGTCTCCTCA 411
Db |||||

RESULT 3
US-09-192-854-1
; Sequence 1, Application US/09192854
; Patent No. US20020068276A1
GENERAL INFORMATION:
APPLICANT: Winter, Greg
APPLICANT: Tomlinson, Ian
TITLE OF INVENTION: Methods for Selecting Functional Peptides
FILE REFERENCE: 3789/72916
CURRENT APPLICATION NUMBER: US/09/192,854
CURRENT FILING DATE: 1998-11-17
EARLIER FILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 212
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 720
TYPE: DNA
ORGANISM: Homo sapiens
US-09-192-854-1
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Query Match	67.8%;	Score 240;	DB 9;	Length 720;	
Best Local Similarity	82.6%;	Pred. No. 7e-66;			
Matches 289;	Conservative 0;	Mismatches 55;	Indels 6;	Gaps 17;	
QY	1	GAGGTGCAGCTGGTGGAGTCTCGGGGGCGGCTTGGCAAAGCTGGGGGGTCCCTCAGAGCTC	60		
DB	1	GAGGTGCAGCTGTTGGAGTCTCGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTC	60		
QY	61	TGTTGCGCAGCCTCCGGGTTTCAGGTTTCACCTTCAATTAATACTACTATGAGACTGGGTCCGC	120		
DB	61	TCCTGTGCAGCCTCTG-----GATTCAACCTTTAGCAGCTATGCCATGAGCTGGGTCCGC	114		
QY	121	CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTATCCCAACA	180		
DB	115	CAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTTCAGCTATTAGTGGTGGTGGTAGCACA	174		
QY	181	TGTTACGCAGACTCCGTGAGGGGCAGATTACCATCTCCAGAGAGAAGCCAAACAACA	240		
DB	175	TACTACGCAGACTCCGTGAAGGGCGGTTTCAACCATCTCCAGAGACAATTCCAGAACACG	234		
QY	241	CTGTTCCTTCAAATGAACAGCCTCAGAGACTCAGGACACGGCTGTCTATTACTGTGCGGAGC	300		
DB	235	CTGTATCTGCDAATGAACAGCCTCAGAGCCGAGGACAGGGCCGTATATTACTGTGCGAAA	294		
QY	301	TTGACTACAGGGTCTGACTCTGGGGCCAGGAGTCTCTGGTCAACGGTCTC	350		
DB	295	AGTTATGGTGCCTTTTGACTACTGGGGCCAGGGAACCTGGTTCACCGTCTC	344		

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RESULT 4
US-09-968-561A-1
; Sequence 1, Application US/09968561A
; Patent No. US2002016462A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phase Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-968-561A-1

```

[illegible]

Db	115	CAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACA	174
Qy	181	TGGTACGCAGACTCCGTGAAGGGCAGAGTATTCACCACTCTCCAGAGAGAACCCCAACAACACA	240
Db	175	TACTACGAGACTCCGTGAAGGGCCGGTTACCATCTCCAGAGACAATTCACGAAGAACGC	234
Qy	241	CTGTTTCTTCAAAATGAACAGCCTCAGAGCTGAGGACACGGCTGTCTATTATCTGTGCGAGC	300
Db	235	CTGTATCTGCAAAATGAACAGCCTCAGAGCCGAGGACACGGCCGTATATTATCTGTGCGAAA	294
Qy	301	TTGACTACAGGGTCTGACTCTCTGGGGCCAGGAGTCTCTGGTCAACCGTCTC	350
Db	295	AGTTATGCTGCTTTTGTACTCTGGGGCCAGGGAACCTTGGTCAACCGTCTC	344

RESULT 5

US-09-968-744A-1
; Sequence 1, Application US/09968744A
; Publication No. US20030148372A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073
; CURRENT APPLICATION NUMBER: US/09/968,744A
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-968-744A-1

Query Match	67.8%	Score 240;	DB 13;	Length 720;
Best Local Similarity	82.6%;	Pred. No. 7e-66;		
Matches 289;	Conservative 0;	Mismatches 55;	Indels 6;	Gaps 17;
QY	1	GAGGTGAGCTGGTGGAGTCTGGGGGGCGGCTGTGCAAGCCTGGGGGGTCCCTCAGAGCTC	60	
DB	1	GAGGTGAGCTGTTGGAGTCTGGGGGAGGCTTGTGTACAGCCTGGGGGGTCCCTGAGAGCTC	60	
QY	61	TGGTGGCAGAGCCTCCGGGTTTCAGGTTTCACCTTCAATAACTACTACTATGGACTGGGTCCGC	120	
DB	61	TCCTGTGCAGCCTCTG-----GATTCACTTTAGCAGCTATGCCATGAGCTGGGTCCGC	114	
QY	121	CAGGCTCCAGGCGAGGGGCTGGAGTGGGTCTCAGTATTAGTAGTAGTGGTATCCCAACA	180	
DB	115	CAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACA	174	
QY	181	TGGTACCAGAGACTCCGTGAGGGGAGATTCCACCATCTCCAGAGAGAACGCCAACACACA	240	
DB	175	TACTACGAGAGACTCCGTGAAGGGCCGGTTACCATTCTCCAGAGACAATTCCAGAACACG	234	
QY	241	CTGTGTTCTTCAAATGAACAGCCTCAGAGCTTGAGGACACGGGTGCTATTACTGTGCGGAGC	300	
DB	235	CTGTATCTGCANAATGAACAGCCTCAGAGCCGAGAGCGAGGACACGGCCGTATATTACTGTGCGGAA	294	
QY	301	TTGACTACAGGGTCTGACTCTGGGGGCGAGGAGTCTCTGGTTCACCGTCTC	350	
DB	295	AGTTATGGTGTCTTTTGACTACTGGGGCCAGGGAACCTGTGTCAACCGTCTC	344	

RESULT 6

US-10-091-300-23
; Sequence 23, Application US/10091300
; Publication No. US20030108545A1
; GENERAL INFORMATION:
; APPLICANT: Rockwell, Patricia
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth with a Vascular
; TITLE OF INVENTION: Endothelial Growth Factor Receptor Antagonist
; FILE REFERENCE: 11245/46211
; CURRENT APPLICATION NUMBER: US/10/091.300
; CURRENT FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 23
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Human
US-10-091-300-23

Query Match 67.3%; Score 238.4; DB 15; Length 348;
Best Local Similarity 82.3%; Pred. No. 1.9e-65;
Matches 288; Conservative 0; Mismatches 56; Indels 6; Gaps 1;

Qy	1	GAGGTGAGCTGGTGGAGTCTGGGGGGCTTGGCAAGCTGGGGGTCCTGAGACTC	60
Db	1	GAGGTGAGCTGGTGGAGTCTGGGGGGCTTGGCAAGCTGGGGGTCCTGAGACTC	60
Qy	61	TGGTGGCAGCTCCGGGCTTCAAGTTCACCTTCAATAACTACTAGTGGAGTGGGTC	120
Db	61	TCCTGTGAGCTCTG-----GATTCACTTCAAGTTCAGTATAGTGGTGGTCCGC	114
Qy	121	CAGGCTCCAGGGCAGGGCTGGAGTGGTCTCAGTATTTAGTAGTGGTATCCACA	180
Db	115	CAGGCTCCAGGGAAGGGCTGGAGTGGTCTCATTCCATTTAGTAGTGGTATCCACA	174
Qy	181	TGGTACGAGCTCCGTCGAGGGCAGATTACCATCTCCAGAGAGACGCCCAACACA	240
Db	175	TACTACGAGCTCAGTGAAGGCCGATTCCACCATCTCCAGAGAGACGCCCAAGACTCA	234
Qy	241	CTGTTTCTTCAAAATGAACAGCTTGAGAGCTGAGGACACGCTCTCTATTACTGTG	300
Db	235	CTGTATCTGCAAAATGAACAGCTTGAGAGCTGAGGACACGCTCTGTATTACTGTG	294
Qy	301	TTGACTACAGGGTCTGACTCTCTGGGGCAGGGAGTCTGTGTCACCGTCTC	350
Db	295	GTACACAGATGCTTTTGATATCTGGGGCAGGGACAATGTCACCGTCTC	344

RESULT 7

US-10-091-300-27
; Sequence 27, Application US/10091300
; Publication No. US20030108545A1
; GENERAL INFORMATION:
; APPLICANT: Rockwell, Patricia
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth with a Vascular
; TITLE OF INVENTION: Endothelial Growth Factor Receptor Antagonist
; FILE REFERENCE: 11245/46211
; CURRENT APPLICATION NUMBER: US/10/091.300
; CURRENT FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 27
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Human
US-10-091-300-27

Query Match 66.9%; Score 236.8; DB 15; Length 348;
Best Local Similarity 82.0%; Pred. No. 6e-65;
Matches 287; Conservative 0; Mismatches 57; Indels 6; Gaps 1;

Qy	1	GAGGTGAGCTGGTGGAGTCTGGGGGGCTTGGCAAGCTGGGGGTCCTGAGACTC	60
Db	1	GAGGTGAGCTGGTGGAGTCTGGGGGGCTTGGCAAGCTGGGGGTCCTGAGACTC	60
Qy	61	TGGTGGCAGCTCCGGGCTTCAAGTTCACCTTCAATAACTACTAGTGGTGGTCCGC	120
Db	61	TCCTGTGAGCTCTGGATTCA-----CCTTCAGTAGCTATAGCATGAACCTGGTCCGC	114
Qy	121	CAGGCTCCAGGGCAGGGCTGGAGTGGTCTCAGTATTTAGTAGTGGTATCCACA	180
Db	115	CAGGCTCCAGGGAAGGGCTGGAGTGGTCTCATTCCATTTAGTAGTGGTATCCACA	174
Qy	181	TGGTACGAGCTCCGTCGAGGGCAGATTACCATCTCCAGAGAGACGCCCAACACA	240
Db	175	TACTACGAGCTCAGTGAAGGCCGATTCCACCATCTCCAGAGAGACGCCCAAGACTCA	234
Qy	241	CTGTTTCTTCAAAATGAACAGCTTGAGAGCTGAGGACACGCTCTCTATTACTGTG	300
Db	235	CTGTATCTGCAAAATGAACAGCTTGAGAGCTGAGGACACGCTCTGTATTACTGTG	294
Qy	301	TTGACTACAGGGTCTGACTCTCTGGGGCAGGGAGTCTGTGTCACCGTCTC	350
Db	295	GTACACAGATGCTTTTGATATCTGGGGCAGGGACAATGTCACCGTCTC	344

RESULT 8

US-10-091-300-30
; Sequence 30, Application US/10091300
; Publication No. US20030108545A1
; GENERAL INFORMATION:
; APPLICANT: Rockwell, Patricia
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth with a Vascular
; TITLE OF INVENTION: Endothelial Growth Factor Receptor Antagonist
; FILE REFERENCE: 11245/46211
; CURRENT APPLICATION NUMBER: US/10/091.300
; CURRENT FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 30
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Human
US-10-091-300-30

Query Match 66.4%; Score 235.2; DB 15; Length 348;
Best Local Similarity 81.7%; Pred. No. 1.9e-64;
Matches 286; Conservative 0; Mismatches 58; Indels 6; Gaps 1;

Qy	1	GAGGTGAGCTGGTGGAGTCTGGGGGGCTTGGCAAGCTGGGGGTCCTGAGACTC	60
Db	1	GAGGTGAGCTGGTGGAGTCTGGGGGGCTTGGCAAGCTGGGGGTCCTGAGACTC	60
Qy	61	TGGTGGCAGCTCCGGGCTTCAAGTTCACCTTCAATAACTACTAGTGGTGGTCCGC	120
Db	61	TCCTGTGAGCTCTGGATTCA-----CCTTCAGTAGCTATAGCATGAACCTGGTCCGC	114
Qy	121	CAGGCTCCAGGGCAGGGCTGGAGTGGTCTCAGTATTTAGTAGTGGTATCCACA	180
Db	115	CAGGCTCCAGGGAAGGGCTGGAGTGGTCTCATTCCATTTAGTAGTGGTATCCACA	174
Qy	181	TGGTACGAGCTCCGTCGAGGGCAGATTACCATCTCCAGAGAGACGCCCAACACA	240
Db	175	TACTACGAGCTCAGTGAAGGCCGATTCCACCATCTCCAGAGAGACGCCCAAGACTCA	234
Qy	241	CTGTTTCTTCAAAATGAACAGCTTGAGAGCTGAGGACACGCTCTCTATTACTGTG	300
Db	235	CTGTATCTGCAAAATGAACAGCTTGAGAGCTGAGGACACGCTCTGTATTACTGTG	294
Qy	301	TTGACTACAGGGTCTGACTCTCTGGGGCAGGGAGTCTGTGTCACCGTCTC	350
Db	295	GTACACAGATGCTTTTGATATCTGGGGCAGGGACAATGTCACCGTCTC	344

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RESULT 9
US-10-291-265-99
; Sequence 99, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 99
; LENGTH: 1710
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1253)
US-10-291-265-99

Query Match 66.4%; Score 235.2; DB 12; Length 1710;
Best Local Similarity 81.7%; Pred. No. 3e-64;
Matches 286; Conservative 0; Mismatches 58; Indels 6; Gaps 1;

QY 1 GAGGTGACGCTGGTGGAGTCTGGGGGGGCTTGGCAAGCCTGGGGGGTCCCTGAGACTC 60
DB 219 GAGGTGACGCTGGTGGAGTCTGGGGGGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTC 278
QY 61 TGGTGGCAGCTCCGGGTTTCAAGTTCACCTTCAATAACTACTACATGGAGTGGGTCCGC 120
DB 279 TCCTGTGACGCTCTG-----GATTCACCTTTAGCAGTTTTCGATGAGTGGGTCCGC 332
QY 121 CAGGCTCCAGGCGAGGGGCTGGAGTGGGTCTCAGTATTAGTAGTAGTGGTGTATCCACA 180
DB 333 CAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCATCTATTAGTGGTAGTTCGGGTACCA 392
QY 181 TGGTACGACGCTCCGTGAAGGCGAGATTCACCATCTCCAGAGAGACGCAACACACA 240
DB 393 TACTACGACGACTCCGTGAAGGCGGTTTCAACATCTCCAGAGACAATTCGAAGAACACG 452
QY 241 CTGTTTCTTCAATGAACAGCCTGAGAGCTGAGAGTGGAGACACGGCTCTCTATTACTGTGCGAGC 300
DB 453 CTGTATCTGCAATGAACAGCCTGAGAGCGGAGACACGGCCGTATATTACTGTGCGAAA 512
QY 301 TTGACTACAGGCTGACTCTCTGGGCGCAGGAGTCTCTGTACCGTCTC 350
DB 513 CCGTTCCGTTATTGTTGACTACTGGGCGCAGGGAACCTCGTCAACCGTCTC 562

RESULT 11
US-10-309-764-130
; Sequence 130, Application US/10309764
; Publication No. US20030232009A1
; GENERAL INFORMATION:
; APPLICANT: Foltz, Ian
; APPLICANT: Babcock, John
; APPLICANT: Palathumpat, Raju
; APPLICANT: Yang, Xiao-dong
; APPLICANT: King, Chadwick T.
; TITLE OF INVENTION: ANTI-CDR45RB ANTIBODIES FOR USE IN
; FILE REFERENCE: ABGENIX.029A
; CURRENT APPLICATION NUMBER: US/10/309,764
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337,276
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 130
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-309-764-130

Query Match 66.0%; Score 233.6; DB 12; Length 414;
Best Local Similarity 82.3%; Pred. No. 6.4e-64;
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RESULT 9
US-10-291-265-99
; Sequence 99, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 99
; LENGTH: 1710
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1253)
US-10-291-265-99

Query Match 66.4%; Score 235.2; DB 12; Length 1710;
Best Local Similarity 81.7%; Pred. No. 3e-64;
Matches 286; Conservative 0; Mismatches 58; Indels 6; Gaps 1;

QY 1 GAGGTGACGCTGGTGGAGTCTGGGGGGGCTTGGCAAGCCTGGGGGGTCCCTGAGACTC 60
DB 219 GAGGTGACGCTGGTGGAGTCTGGGGGGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTC 278
QY 61 TGGTGGCAGCTCCGGGTTTCAAGTTCACCTTCAATAACTACTACATGGAGTGGGTCCGC 120
DB 279 TCCTGTGACGCTCTG-----GATTCACCTTTAGCAGTTTTCGATGAGTGGGTCCGC 332
QY 121 CAGGCTCCAGGCGAGGGGCTGGAGTGGGTCTCAGTATTAGTAGTAGTGGTGTATCCACA 180
DB 333 CAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCATCTATTAGTGGTAGTTCGGGTACCA 392
QY 181 TGGTACGACGCTCCGTGAAGGCGAGATTCACCATCTCCAGAGAGACGCAACACACA 240
DB 393 TACTACGACGACTCCGTGAAGGCGGTTTCAACATCTCCAGAGACAATTCGAAGAACACG 452
QY 241 CTGTTTCTTCAATGAACAGCCTGAGAGCTGAGAGTGGAGACACGGCTGTCTATTACTGTGCGAGC 300
DB 453 CTGTATCTGCAATGAACAGCCTGAGAGCGGAGACACGGCCGTATATTACTGTGCGAAA 512
QY 301 TTGACTACAGGCTGACTCTCTGGGCGCAGGAGTCTCTGTACCGTCTC 350
DB 513 CCGTTCCGTTATTGTTGACTACTGGGCGCAGGGAACCTCGTCAACCGTCTC 562

RESULT 10
US-10-291-265-96
; Sequence 96, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
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Matches 298; Conservative 0; Mismatches 49; Indels 15; Gaps 2;
Qy 2 AGGTGCAGCTGGTGGAGTCTGGGGGGCTTGGCAAGCCCTGGGGGTCCCTGAGACTCT 61
Db 59 AGGTGCAGCTGGTGGAGTCTGGGGGGCTTGGTCAAGCCCTGGAGGGTCCCTGAGACTCT 118
Qy 62 GGTGCGAGCTCCGGGTTACAGTTTCACTTCAATAACTACTACATGAGTGGGTCCGCC 121
Db 119 CCTGTGAGCTCTG-----GATTACCTTCAATGTCTACTACATGAGTGGATCCGCC 172
Qy 122 AGGTCCAGGCGAGGGCTGGAGTGGGTCTCACGTATTAGTAGTGGTATCCACAT 181
Db 173 AGGTCCAGGCGAGGGCTGGAGTGGGTCTCATACATTAGTACTAGTAGTGGCATTT 232
Qy 182 GGTACGAGACTCCGTGAGGGCAGATTCACTATCTCCAGAGAAAGCCCAACACAC 241
Db 233 ACTACGAGACTCTGTGAAGGGCCGATTCACTCTCCAGGCAATGCCAAGAACTCAC 292
Qy 242 TGTTCCTTCAATGAACAGCTGAGAGCTGAGGACAGCGTGTCTATTACTGTGCGAGCT 301
Db 293 TGTATCTGCAATGAACAGCTGAGAGCGGAGGACAGCGCGTGTATTACTGTGCGAGAA 352
Qy 302 TGACT-----ACAGGGTCTGACTCTCTGGGGCCAGGGAGTCTGGTCAACGCTCTCT 352
Db 353 GGACTGGATCTACGAGCTCTTTGACTACTTGGGGCCAGGGAACCTGGTCAACGCTCTCT 412
Qy 353 CA 354
Db 413 CA 414

RESULT 12

US-10-309-764-126
; Sequence 126, Application US/10309764
; Publication No. US20030232009A1
; GENERAL INFORMATION:
; APPLICANT: Foltz, Ian
; APPLICANT: Babcock, John
; APPLICANT: Palathumpat, Raju
; APPLICANT: Yang, Xiao-dong
; APPLICANT: King, Chadwick T.
; TITLE OF INVENTION: ANTI-CD45RB ANTIBODIES FOR USE IN
; TITLE OF INVENTION: TREATING AUTOIMMUNE DISEASE AND TRANSPLANT REJECTION
; FILE REFERENCE: AGENIX.029A
; CURRENT APPLICATION NUMBER: US/10/309,764
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337,276
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-309-764-126

Query Match 65.5%; Score 232; DB 12; Length 414;
Best Local Similarity 82.0%; Pred. No. 2.1e-63;
Matches 297; Conservative 0; Mismatches 50; Indels 15; Gaps 2;
Qy 2 AGGTGCAGCTGGTGGAGTCTGGGGGGCTTGGCAAGCCCTGGGGGTCCCTGAGACTCT 61
Db 59 AGGTGCAGCTGGTGGAGTCTGGGGGGCTTGGTCAAGCCCTGGAGGGTCCCTGAGACTCT 118
Qy 62 GGTGCGAGCTCCGGGTTACAGTTTCACTTCAATAACTACTACATGAGTGGGTCCGCC 121
Db 119 CCTGCGAGCTCTG-----GATTACCTTCAATTAATACTACTACATGAGTGGATCCGCC 172
Qy 122 AGGTCCAGGCGAGGGCTGGAGTGGGTCTCACGTATTAGTAGTGGTATCCACAT 181
Db 173 AGGTCCAGGGAAGGGCTGGAGTGGGTCTCATACATTAGTCTTGTAGTGGCAGTACCAT 232
Qy 182 GGTACGAGACTCCGTGAGGGCAGATTCACTATCTCCAGAGAGAAAGCCCAACACAC 241

Db 233 ACTACGAGACTCTGTGAAGGGCCGATTACCATCTCCAGGGCAACAGCCGAAGACTCAC 292
Qy 242 TGTTCCTTCAATGAACAGCTGAGAGCTGAGGACAGCGGTCTCTATTACTGTGCGAGCT 301
Db 293 TGTTCCTTCAATGAACAGCTGAGAGCGGAGGACAGCGCGGTGTATTACTGTGCGAGAA 352
Qy 302 TGAC-----TACAGGGTCTGACTCTCTGGGGCCAGGGAGTCTCTGGTCAACGCTCTCT 352
Db 353 GGGCGGCTACGGTACTACTTTTGACTACTTGGGGCCAGGGAACCTGGTCAACGCTCTCT 412
Qy 353 CA 354
Db 413 CA 414

RESULT 13

US-10-322-673-66
; Sequence 66, Application US/10322673
; Publication No. US20030180296A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF585
; CURRENT APPLICATION NUMBER: US/10/322,673
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 66
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding CM087C06 scFv
US-10-322-673-66

Query Match 65.3%; Score 231; DB 13; Length 729;
Best Local Similarity 81.1%; Pred. No. 5e-63;
Matches 283; Conservative 0; Mismatches 60; Indels 6; Gaps 1;
Qy 2 AGGTGCAGCTGGTGGAGTCTGGGGGGCTTGGCAAGCCCTGGGGGTCCCTGAGACTCT 61
Db 2 AGATGCAGCTGGTGCAGTCTGGGGGAGGCTTGGTCAAGCCCTGGAGGGTCCCTGAGACTCT 61
Qy 62 GGTGCGAGCTCCGGGTTACAGTTTCACTTCAATAACTACTACTACATGAGTGGGTCCGCC 121
Db 62 CCTGTGCGAGCTCTG-----GATTACCTTCACTACTACTACTAGTGGATCCGCC 115
Qy 122 AGGTCCAGGCGAGGGCTGGAGTGGGTCTCACGTATTAGTAGTGGTATCCACAT 181
Db 116 AGGTCCAGGGAAGGGCTGGAGTGGGTCTCAGCTATTAGTGGTGGTATGACAT 175
Qy 182 GGTACGAGACTCCGTGAGGGCAGATTCACTATCTCCAGAGAGAACCCCAACACAC 241
Db 176 ACTACGAGACTCCGTGAGGGCCGGTTCACTCTCCAGAGACAAATTCGAAGAACACGC 235
Qy 242 TGTTCCTTCAATGAACAGCTGAGAGCTGAGGACAGCGGTCTCTATTACTGTGCGAGCT 301
Db 236 TGTATCTGCAATGAACAGCTGAGAGCGGAGGACAGCGGTGTGTATTACTGTGCAAGAG 295
Qy 302 TGACTACAGGGTCTGACTCTCTGGGGCCAGGGAGTCTCTGGTCAACGCTCTC 350

Db 296 GAGGATCCACTTTTGATATCTGGGGCCGGGGGACAAATGGTCACCGTCTC 344
|||||

RESULT 14

US-10-322-673-68
; Sequence 68, Application US/10322673
; Publication No. US20030180296A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF585
; CURRENT APPLICATION NUMBER: US/10/322,673
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 68
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding CM085C11 scFv
US-10-322-673-68

Query Match 65.1%; Score 230.4; DB 13; Length 729;
Best Local Similarity 80.9%; Pred. No. 7.8e-63;
Matches 283; Conservative 0; Mismatches 61; Indels 6; Gaps 1;
Qy 1 GAGGTGCAGCTGTGGAGTCTCTGGGGGGCGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC 60
Db 1 GAGGTGCAGCTGTGGAGACCGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTC 60
Qy 61 TGGTGGCAGCCTCGGGGTCAGGTTCACTTCAATTAATACTAGTACGAGTGGTGGTCCGC 120
Db 61 TCCTGTGCAGCCTCTG-----GATTCACTTTAGCCCCCTATTACATGAGTGGTGGTCCGC 114
Qy 121 CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTGTATCCCA 180
Db 115 CAGGCTCCAGGGAAGGGGCTAGAGTGGGTCTCAGCTATTAGTGGTGGTGGTAGTATA 174
Qy 181 TGGTACGAGACTCCGTGAAGGGCAGATTCAACCATCTCCAGAGAGAACGCCAACACACA 240
Db 175 TACTACGAGACTCCGTGAAGGGCGGTTCAACCATCTCCAGAGACAATTCAGAACACG 234
Qy 241 CTGTTTCTTCAATGAACAGCCTGAGAGCTGAGACACGGCTGTCTATTACTGTGGAGC 300
Db 235 CTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCCCTATATTACTGTGGAGA 294
Qy 301 TTGACTACAGGCTGTGACTCTCTGGGGCAGGGAGTCTGTGTCACCGTCTC 350
Db 295 GGGGCATCTGGCCCTGACTACTCTGGGGCAGAGGGGACAAATGGTCAACCGTCTC 344
|||||

RESULT 15

US-09-949-039-1
; Sequence 1, Application US/09949039
; Publication No. US20030166160A1
; GENERAL INFORMATION:
; APPLICANT: HAWLEY, STEPHEN B.
; TITLE OF INVENTION: COMPOUNDS AND MOLECULAR COMPLEXES COMPRISING MULTIPLE
; TITLE OF INVENTION: BINDING REGIONS DIRECTED TO TRANSCYTOTIC LIGANDS

; FILE REFERENCE: 057220/1301
; CURRENT APPLICATION NUMBER: US/09/949,039
; CURRENT FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4026
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pSyn5AF DNA
; OTHER INFORMATION: sequence
US-09-949-039-1

Query Match 64.5%; Score 228.4; DB 13; Length 4026;
Best Local Similarity 81.7%; Pred. No. 5.3e-62;
Matches 291; Conservative 0; Mismatches 56; Indels 9; Gaps 2;
Qy 2 AGGTGCAGCTGTGGAGTCTCTGGGGGGCGGCTTGGCAAAGCCTGGGGGTCCCTGAGACTCT 61
Db 355 AGGTGCAGCTGTGGTGAATCAGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 414
Qy 62 GGTGGCAGCCTCCGGGTTCCAGTTTCACTTCAATTAATACTACTATGAGTGGTGGTCCGCC 121
Db 415 CTTGTGCAGCCTCTG-----GATTCACTTCACTAGTCTATGCTATGCACTGGTCCGCC 468
Qy 122 AGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTGGTATCCACAT 181
Db 469 AGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTGGTGGTGGTGGTGGT 528
Qy 182 GGTACGAGACTCCGTGAAGGGCAGATTCAACCATCTCCAGAGAGAACGCCAACACACAC 241
Db 529 ACTACGAGACTCCGTGAAGGGCGGTTCAACCATCTCCAGAGACAACGCCAAGAACTCAC 588
Qy 242 TGTTCCTTCAAAATGAACAGCCTGAGAGCTGAGAGACAGCGGTCTCTATTACTGTGCGAGCT 301
Db 589 TGTATCTGCAAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAG 648
Qy 302 TGACTACAGG-----TCTGACTCTCTGGGGCCAGGGAGTCTCTGTGTCACCGTCTCCTCA 354
Db 649 ATACCCGAGGGTACTTGGATCTCTGGGGCGGCTGGCACCCCTGGTCAACCGTCTCCTCA 704
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Job time : 513.438 secs

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